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(54) Title: **CORYNEBACTERIUM GLUTAMICUM GENES ENCODING PROTEINS INVOLVED IN CARBON METABOLISM AND ENERGY PRODUCTION**

(57) Abstract: Isolated nucleic acid molecules, designated SMP nucleic acid molecules, which encode novel SMP proteins from *Corynebacterium glutamicum* are described. The invention also provides antisense nucleic acid molecules, recombinant expression vectors containing SMP nucleic acid molecules, and host cells into which the expression vectors have been introduced. The invention still further provides isolated SMP proteins, mutated SMP proteins, fusion proteins, antigenic peptides and methods for the improvement of production of a desired compound from *C. glutamicum* based on genetic engineering of SMP genes in this organism.

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CORYNEBACTERIUM GLUTAMICUM
INVOLVED IN CARBON METABOLISM AND

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PROTEINS
ACTION

Related Applications

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30 contents of all of the aforementioned application are hereby expressly incorporated
herein by this reference.

Background of the Invention

Certain products and by-products of naturally-occurring metabolic processes in cells have utility in a wide array of industries, including the food, feed, cosmetics, and pharmaceutical industries. These molecules, collectively termed 'fine chemicals', include organic acids, both proteinogenic and non-proteinogenic amino acids, nucleotides and nucleosides, lipids and fatty acids, diols, carbohydrates, aromatic compounds, vitamins and cofactors, and enzymes. Their production is most conveniently performed through the large-scale culture of bacteria developed to produce and secrete large quantities of one or more desired molecules. One particularly useful organism for this purpose is *Corynebacterium glutamicum*, a gram positive, nonpathogenic bacterium. Through strain selection, a number of mutant strains have been developed which produce an array of desirable compounds. However, selection of strains improved for the production of a particular molecule is a time-consuming and difficult process.

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Summary of the Invention

The invention provides novel bacterial nucleic acid molecules which have a variety of uses. These uses include the identification of microorganisms which can be used to produce fine chemicals, the modulation of fine chemical production in *C. glutamicum* or related bacteria, the typing or identification of *C. glutamicum* or related bacteria, as reference points for mapping the *C. glutamicum* genome, and as markers for transformation. These novel nucleic acid molecules encode proteins, referred to herein as sugar metabolism and oxidative phosphorylation (SMP) proteins.

C. glutamicum is a gram positive, aerobic bacterium which is commonly used in industry for the large-scale production of a variety of fine chemicals, and also for the degradation of hydrocarbons (such as in petroleum spills) and for the oxidation of terpenoids. The SMP nucleic acid molecules of the invention, therefore, can be used to identify microorganisms which can be used to produce fine chemicals, e.g., by fermentation processes. Modulation of the expression of the SMP nucleic acids of the invention, or modification of the sequence of the SMP nucleic acid molecules of the invention, can be used to modulate the production of one or more fine chemicals from a

microorganism (e.g., to improve the yield or production of one or more fine chemicals from a *Corynebacterium* or *Brevibacterium* species).

The SMP nucleic acids of the invention may also be used to identify an organism as being *Corynebacterium glutamicum* or a close relative thereof, or to identify the
5 presence of *C. glutamicum* or a relative thereof in a mixed population of microorganisms. The invention provides the nucleic acid sequences of a number of *C. glutamicum* genes; by probing the extracted genomic DNA of a culture of a unique or mixed population of microorganisms under stringent conditions with a probe spanning a region of a *C. glutamicum* gene which is unique to this organism, one can ascertain
10 whether this organism is present. Although *Corynebacterium glutamicum* itself is nonpathogenic, it is related to species pathogenic in humans, such as *Corynebacterium diphtheriae* (the causative agent of diphtheria); the detection of such organisms is of significant clinical relevance.

The SMP nucleic acid molecules of the invention may also serve as reference
15 points for mapping of the *C. glutamicum* genome, or of genomes of related organisms. Similarly, these molecules, or variants or portions thereof, may serve as markers for genetically engineered *Corynebacterium* or *Brevibacterium* species.

The SMP proteins encoded by the novel nucleic acid molecules of the invention are capable of, for example, performing a function involved in the metabolism of carbon
20 compounds such as sugars or in the generation of energy molecules by processes such as oxidative phosphorylation in *Corynebacterium glutamicum*. Given the availability of cloning vectors for use in *Corynebacterium glutamicum*, such as those disclosed in Sinskey *et al.*, U.S. Patent No. 4,649,119, and techniques for genetic manipulation of *C. glutamicum* and the related *Brevibacterium* species (e.g., *lactofermentum*) (Yoshihama
25 *et al.*, *J. Bacteriol.* 162: 591-597 (1985); Katsumata *et al.*, *J. Bacteriol.* 159: 306-311 (1984); and Santamaria *et al.*, *J. Gen. Microbiol.* 130: 2237-2246 (1984)), the nucleic acid molecules of the invention may be utilized in the genetic engineering of this organism to make it a better or more efficient producer of one or more fine chemicals. This improved production or efficiency of production of a fine chemical may be due to a
30 direct effect of manipulation of a gene of the invention, or it may be due to an indirect effect of such manipulation.

There are a number of mechanisms by which the alteration of an SMP protein of the invention may directly affect the yield, production, and/or efficiency of production of a fine chemical from a *C. glutamicum* strain incorporating such an altered protein. The degradation of high-energy carbon molecules such as sugars, and the conversion of compounds such as NADH and FADH₂ to compounds containing high energy phosphate bonds via oxidative phosphorylation results in a number of compounds which themselves may be desirable fine chemicals, such as pyruvate, ATP, NADH, and a number of intermediate sugar compounds. Further, the energy molecules (such as ATP) and the reducing equivalents (such as NADH or NADPH) produced by these metabolic pathways are utilized in the cell to drive reactions which would otherwise be energetically unfavorable. Such unfavorable reactions include many biosynthetic pathways for fine chemicals. By improving the ability of the cell to utilize a particular sugar (*e.g.*, by manipulating the genes encoding enzymes involved in the degradation and conversion of that sugar into energy for the cell), one may increase the amount of energy available to permit unfavorable, yet desired metabolic reactions (*e.g.*, the biosynthesis of a desired fine chemical) to occur.

The mutagenesis of one or more SMP genes of the invention may also result in SMP proteins having altered activities which indirectly impact the production of one or more desired fine chemicals from *C. glutamicum*. For example, by increasing the efficiency of utilization of one or more sugars (such that the conversion of the sugar to useful energy molecules is improved), or by increasing the efficiency of conversion of reducing equivalents to useful energy molecules (*e.g.*, by improving the efficiency of oxidative phosphorylation, or the activity of the ATP synthase), one can increase the amount of these high-energy compounds available to the cell to drive normally unfavorable metabolic processes. These processes include the construction of cell walls, transcription, translation, and the biosynthesis of compounds necessary for growth and division of the cells (*e.g.*, nucleotides, amino acids, vitamins, lipids, etc.) (Lengeler *et al.* (1999) *Biology of Prokaryotes*, Thieme Verlag: Stuttgart, p. 88-109; 913-918; 875-899). By improving the growth and multiplication of these engineered cells, it is possible to increase both the viability of the cells in large-scale culture, and also to improve their rate of division, such that a relatively larger number of cells can survive in fermentor culture. The yield, production, or efficiency of production may be increased, at least

due to the presence of a greater number of viable cells, each producing the desired fine chemical. Also, many of the degradation products produced during sugar metabolism are utilized by the cell as precursors or intermediates in the production of other desirable products, such as fine chemicals. So, by increasing the ability of the cell to metabolize
5 sugars, the number of these degradation products available to the cell for other processes should also be increased.

The invention provides novel nucleic acid molecules which encode proteins, referred to herein as SMP proteins, which are capable of, for example, performing a function involved in the metabolism of carbon compounds such as sugars and the
10 generation of energy molecules by processes such as oxidative phosphorylation in *Corynebacterium glutamicum*. Nucleic acid molecules encoding an SMP protein are referred to herein as SMP nucleic acid molecules. In a preferred embodiment, the SMP protein participates in the conversion of carbon molecules and degradation products thereof to energy which is utilized by the cell for metabolic processes. Examples of
15 such proteins include those encoded by the genes set forth in Table 1.

Accordingly, one aspect of the invention pertains to isolated nucleic acid molecules (*e.g.*, cDNAs, DNAs, or RNAs) comprising a nucleotide sequence encoding an SMP protein or biologically active portions thereof, as well as nucleic acid fragments suitable as primers or hybridization probes for the detection or amplification of SMP-
20 encoding nucleic acid (*e.g.*, DNA or mRNA). In particularly preferred embodiments, the isolated nucleic acid molecule comprises one of the nucleotide sequences set forth as the odd-numbered SEQ ID NOs in the Sequence Listing (*e.g.*, SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:7....), or the coding region or a complement thereof of one of these nucleotide sequences. In other particularly preferred embodiments, the
25 isolated nucleic acid molecule of the invention comprises a nucleotide sequence which hybridizes to or is at least about 50%, preferably at least about 60%, more preferably at least about 70%, 80% or 90%, and even more preferably at least about 95%, 96%, 97%, 98%, 99% or more homologous to a nucleotide sequence set forth as an odd-numbered SEQ ID NO in the Sequence Listing (*e.g.*, SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5,
30 SEQ ID NO:7....), or a portion thereof. In other preferred embodiments, the isolated nucleic acid molecule encodes one of the amino acid sequences set forth as an even-numbered SEQ ID NO in the Sequence Listing (*e.g.*, SEQ ID NO:2, SEQ ID NO:4, SEQ

ID NO:6, SEQ ID NO:8:....). The preferred SMP proteins of the present invention also preferably possess at least one of the SMP activities described herein.

In another embodiment, the isolated nucleic acid molecule encodes a protein or portion thereof wherein the protein or portion thereof includes an amino acid sequence
5 which is sufficiently homologous to an amino acid sequence of the invention (*e.g.*, a sequence having an even-numbered SEQ ID NO: in the Sequence Listing), *e.g.*, sufficiently homologous to an amino acid sequence of the invention such that the protein or portion thereof maintains an SMP activity. Preferably, the protein or portion thereof encoded by the nucleic acid molecule maintains the ability to perform a function
10 involved in the metabolism of carbon compounds such as sugars or the generation of energy molecules (*e.g.*, ATP) by processes such as oxidative phosphorylation in *Corynebacterium glutamicum*. In one embodiment, the protein encoded by the nucleic acid molecule is at least about 50%, preferably at least about 60%, and more preferably at least about 70%, 80%, or 90% and most preferably at least about 95%, 96%, 97%,
15 98%, or 99% or more homologous to an amino acid sequence of the invention (*e.g.*, an entire amino acid sequence selected those having an even-numbered SEQ ID NO in the Sequence Listing). In another preferred embodiment, the protein is a full length *C. glutamicum* protein which is substantially homologous to an entire amino acid sequence of the invention (encoded by an open reading frame shown in the corresponding odd-
20 numbered SEQ ID NOs in the Sequence Listing (*e.g.*, SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:7....)).

In another preferred embodiment, the isolated nucleic acid molecule is derived from *C. glutamicum* and encodes a protein (*e.g.*, an SMP fusion protein) which includes a biologically active domain which is at least about 50% or more homologous to one of
25 the amino acid sequences of the invention (*e.g.*, a sequence of one of the even-numbered SEQ ID NOs in the Sequence Listing) and is able to perform a function involved in the metabolism of carbon compounds such as sugars or the generation of energy molecules (*e.g.*, ATP) by processes such as oxidative phosphorylation in *Corynebacterium glutamicum*, or has one or more of the activities set forth in Table 1, and which also
30 includes heterologous nucleic acid sequences encoding a heterologous polypeptide or regulatory regions.

In another embodiment, the isolated nucleic acid molecule is at least 15 nucleotides in length and hybridizes under stringent conditions to a nucleic acid molecule comprising a nucleotide sequence of the invention (*e.g.*, a sequence of an odd-numbered SEQ ID NO in the Sequence Listing) A. Preferably, the isolated nucleic acid molecule corresponds to a naturally-occurring nucleic acid molecule. More preferably, the isolated nucleic acid encodes a naturally-occurring *C. glutamicum* SMP protein, or a biologically active portion thereof.

Another aspect of the invention pertains to vectors, *e.g.*, recombinant expression vectors, containing the nucleic acid molecules of the invention, and host cells into which such vectors have been introduced. In one embodiment, such a host cell is used to produce an SMP protein by culturing the host cell in a suitable medium. The SMP protein can be then isolated from the medium or the host cell.

Yet another aspect of the invention pertains to a genetically altered microorganism in which an SMP gene has been introduced or altered. In one embodiment, the genome of the microorganism has been altered by introduction of a nucleic acid molecule of the invention encoding wild-type or mutated SMP sequence as a transgene. In another embodiment, an endogenous SMP gene within the genome of the microorganism has been altered, *e.g.*, functionally disrupted, by homologous recombination with an altered SMP gene. In another embodiment, an endogenous or introduced SMP gene in a microorganism has been altered by one or more point mutations, deletions, or inversions, but still encodes a functional SMP protein. In still another embodiment, one or more of the regulatory regions (*e.g.*, a promoter, repressor, or inducer) of an SMP gene in a microorganism has been altered (*e.g.*, by deletion, truncation, inversion, or point mutation) such that the expression of the SMP gene is modulated. In a preferred embodiment, the microorganism belongs to the genus *Corynebacterium* or *Brevibacterium*, with *Corynebacterium glutamicum* being particularly preferred. In a preferred embodiment, the microorganism is also utilized for the production of a desired compound, such as an amino acid, with lysine being particularly preferred.

In another aspect, the invention provides a method of identifying the presence or activity of *Corynebacterium diphtheriae* in a subject. This method includes detection of one or more of the nucleic acid or amino acid sequences of the invention (*e.g.*, the

sequences set forth in the Sequence Listing as SEQ ID NOs 1 through 782) in a subject, thereby detecting the presence or activity of *Corynebacterium diphtheriae* in the subject.

Still another aspect of the invention pertains to an isolated SMP protein or a portion, *e.g.*, a biologically active portion, thereof. In a preferred embodiment, the
5 isolated SMP protein or portion thereof is capable of performing a function involved in the metabolism of carbon compounds such as sugars or in the generation of energy molecules (*e.g.*, ATP) by processes such as oxidative phosphorylation in *Corynebacterium glutamicum*. In another preferred embodiment, the isolated SMP protein or portion thereof is sufficiently homologous to an amino acid sequence of the
10 invention (*e.g.*, a sequence of an even-numbered SEQ ID NO: in the Sequence Listing) such that the protein or portion thereof maintains the ability to perform a function involved in the metabolism of carbon compounds such as sugars or in the generation of energy molecules (*e.g.*, ATP) by processes such as oxidative phosphorylation in *Corynebacterium glutamicum*.

15 The invention also provides an isolated preparation of an SMP protein. In preferred embodiments, the SMP protein comprises an amino acid sequence of the invention (*e.g.*, a sequence of an even-numbered SEQ ID NO: of the Sequence Listing). In another preferred embodiment, the invention pertains to an isolated full length protein which is substantially homologous to an entire amino acid sequence of the invention
20 (*e.g.*, a sequence of an even-numbered SEQ ID NO: of the Sequence Listing) (encoded by an open reading frame set forth in a corresponding odd-numbered SEQ ID NO: of the Sequence Listing). In yet another embodiment, the protein is at least about 50%, preferably at least about 60%, and more preferably at least about 70%, 80%, or 90%, and most preferably at least about 95%, 96%, 97%, 98%, or 99% or more homologous
25 to an entire amino acid sequence of the invention (*e.g.*, a sequence of an even-numbered SEQ ID NO: of the Sequence Listing). In other embodiments, the isolated SMP protein comprises an amino acid sequence which is at least about 50% or more homologous to one of the amino acid sequences of the invention (*e.g.*, a sequence of an even-numbered SEQ ID NO: of the Sequence Listing) and is able to perform a function involved in the
30 metabolism of carbon compounds such as sugars or in the generation of energy molecules (*e.g.*, ATP) by processes such as oxidative phosphorylation in *Corynebacterium glutamicum*, or has one or more of the activities set forth in Table 1.

Alternatively, the isolated SMP protein can comprise an amino acid sequence which is encoded by a nucleotide sequence which hybridizes, *e.g.*, hybridizes under stringent conditions, or is at least about 50%, preferably at least about 60%, more preferably at least about 70%, 80%, or 90%, and even more preferably at least about 5 95%, 96%, 97%, 98,%, or 99% or more homologous to a nucleotide sequence of one of the even-numbered SEQ ID NOs set forth in the Sequence Listing. It is also preferred that the preferred forms of SMP proteins also have one or more of the SMP bioactivities described herein.

The SMP polypeptide, or a biologically active portion thereof, can be operatively 10 linked to a non-SMP polypeptide to form a fusion protein. In preferred embodiments, this fusion protein has an activity which differs from that of the SMP protein alone. In other preferred embodiments, this fusion protein performs a function involved in the metabolism of carbon compounds such as sugars or in the generation of energy molecules (*e.g.*, ATP) by processes such as oxidative phosphorylation in 15 *Corynebacterium glutamicum*. In particularly preferred embodiments, integration of this fusion protein into a host cell modulates production of a desired compound from the cell.

In another aspect, the invention provides methods for screening molecules which modulate the activity of an SMP protein, either by interacting with the protein itself or a 20 substrate or binding partner of the SMP protein, or by modulating the transcription or translation of an SMP nucleic acid molecule of the invention.

Another aspect of the invention pertains to a method for producing a fine chemical. This method involves the culturing of a cell containing a vector directing the expression of an SMP nucleic acid molecule of the invention, such that a fine chemical 25 is produced. In a preferred embodiment, this method further includes the step of obtaining a cell containing such a vector, in which a cell is transfected with a vector directing the expression of an SMP nucleic acid. In another preferred embodiment, this method further includes the step of recovering the fine chemical from the culture. In a particularly preferred embodiment, the cell is from the genus *Corynebacterium* or 30 *Brevibacterium*, or is selected from those strains set forth in Table 3.

Another aspect of the invention pertains to methods for modulating production of a molecule from a microorganism. Such methods include contacting the cell with an

agent which modulates SMP protein activity or SMP nucleic acid expression such that a cell associated activity is altered relative to this same activity in the absence of the agent. In a preferred embodiment, the cell is modulated for one or more *C. glutamicum* carbon metabolism pathways or for the production of energy through processes such as oxidative phosphorylation, such that the yields or rate of production of a desired fine chemical by this microorganism is improved. The agent which modulates SMP protein activity can be an agent which stimulates SMP protein activity or SMP nucleic acid expression. Examples of agents which stimulate SMP protein activity or SMP nucleic acid expression include small molecules, active SMP proteins, and nucleic acids encoding SMP proteins that have been introduced into the cell. Examples of agents which inhibit SMP activity or expression include small molecules and antisense SMP nucleic acid molecules.

Another aspect of the invention pertains to methods for modulating yields of a desired compound from a cell, involving the introduction of a wild-type or mutant SMP gene into a cell, either maintained on a separate plasmid or integrated into the genome of the host cell. If integrated into the genome, such integration can be random, or it can take place by homologous recombination such that the native gene is replaced by the introduced copy, causing the production of the desired compound from the cell to be modulated. In a preferred embodiment, said yields are increased. In another preferred embodiment, said chemical is a fine chemical. In a particularly preferred embodiment, said fine chemical is an amino acid. In especially preferred embodiments, said amino acid is L-lysine.

Detailed Description of the Invention

The present invention provides SMP nucleic acid and protein molecules which are involved in the metabolism of carbon compounds such as sugars and the generation of energy molecules by processes such as oxidative phosphorylation in *Corynebacterium glutamicum*. The molecules of the invention may be utilized in the modulation of production of fine chemicals from microorganisms, such as *C. glutamicum*, either directly (*e.g.*, where overexpression or optimization of a glycolytic pathway protein has a direct impact on the yield, production, and/or efficiency of production of, *e.g.*, pyruvate from modified *C. glutamicum*), or may have an indirect

impact which nonetheless results in an increase of yield, production, and/or efficiency of production of the desired compound (*e.g.*, where modulation of proteins involved in oxidative phosphorylation results in alterations in the amount of energy available to perform necessary metabolic processes and other cellular functions, such as nucleic acid and protein biosynthesis and transcription/translation). Aspects of the invention are further explicated below.

I. Fine Chemicals

The term 'fine chemical' is art-recognized and includes molecules produced by an organism which have applications in various industries, such as, but not limited to, the pharmaceutical, agriculture, and cosmetics industries. Such compounds include organic acids, such as tartaric acid, itaconic acid, and diaminopimelic acid, both proteinogenic and non-proteinogenic amino acids, purine and pyrimidine bases, nucleosides, and nucleotides (as described *e.g.* in Kuninaka, A. (1996) Nucleotides and related compounds, p. 561-612, in Biotechnology vol. 6, Rehm *et al.*, eds. VCH: Weinheim, and references contained therein), lipids, both saturated and unsaturated fatty acids (*e.g.*, arachidonic acid), diols (*e.g.*, propane diol, and butane diol), carbohydrates (*e.g.*, hyaluronic acid and trehalose), aromatic compounds (*e.g.*, aromatic amines, vanillin, and indigo), vitamins and cofactors (as described in Ullmann's Encyclopedia of Industrial Chemistry, vol. A27, "Vitamins", p. 443-613 (1996) VCH: Weinheim and references therein; and Ong, A.S., Niki, E. & Packer, L. (1995) "Nutrition, Lipids, Health, and Disease" Proceedings of the UNESCO/Confederation of Scientific and Technological Associations in Malaysia, and the Society for Free Radical Research – Asia, held Sept. 1-3, 1994 at Penang, Malaysia, AOCS Press, (1995)), enzymes, polyketides (Cane *et al.* (1998) *Science* 282: 63-68), and all other chemicals described in Gutcho (1983) Chemicals by Fermentation, Noyes Data Corporation, ISBN: 0818805086 and references therein. The metabolism and uses of certain of these fine chemicals are further explicated below.

A. Amino Acid Metabolism and Uses

Amino acids comprise the basic structural units of all proteins, and as such are essential for normal cellular functioning in all organisms. The term "amino acid" is art-

recognized. The proteinogenic amino acids, of which there are 20 species, serve as structural units for proteins, in which they are linked by peptide bonds, while the nonproteinogenic amino acids (hundreds of which are known) are not normally found in proteins (see Ulmann's Encyclopedia of Industrial Chemistry, vol. A2, p. 57-97 VCH:

5 Weinheim (1985)). Amino acids may be in the D- or L- optical configuration, though L-amino acids are generally the only type found in naturally-occurring proteins.

Biosynthetic and degradative pathways of each of the 20 proteinogenic amino acids have been well characterized in both prokaryotic and eukaryotic cells (see, for example, Stryer, L. Biochemistry, 3rd edition, pages 578-590 (1988)). The 'essential' amino acids
10 (histidine, isoleucine, leucine, lysine, methionine, phenylalanine, threonine, tryptophan, and valine), so named because they are generally a nutritional requirement due to the complexity of their biosyntheses, are readily converted by simple biosynthetic pathways to the remaining 11 'nonessential' amino acids (alanine, arginine, asparagine, aspartate, cysteine, glutamate, glutamine, glycine, proline, serine, and tyrosine). Higher animals
15 do retain the ability to synthesize some of these amino acids, but the essential amino acids must be supplied from the diet in order for normal protein synthesis to occur.

Aside from their function in protein biosynthesis, these amino acids are interesting chemicals in their own right, and many have been found to have various applications in the food, feed, chemical, cosmetics, agriculture, and pharmaceutical
20 industries. Lysine is an important amino acid in the nutrition not only of humans, but also of monogastric animals such as poultry and swine. Glutamate is most commonly used as a flavor additive (mono-sodium glutamate, MSG) and is widely used throughout the food industry, as are aspartate, phenylalanine, glycine, and cysteine. Glycine, L-methionine and tryptophan are all utilized in the pharmaceutical industry. Glutamine,
25 valine, leucine, isoleucine, histidine, arginine, proline, serine and alanine are of use in both the pharmaceutical and cosmetics industries. Threonine, tryptophan, and D/ L-methionine are common feed additives. (Leuchtenberger, W. (1996) Amino acids – technical production and use, p. 466-502 in Rehm *et al.* (eds.) Biotechnology vol. 6, chapter 14a, VCH: Weinheim). Additionally, these amino acids have been found to be
30 useful as precursors for the synthesis of synthetic amino acids and proteins, such as N-acetylcysteine, S-carboxymethyl-L-cysteine, (S)-5-hydroxytryptophan, and others

described in Ulmann's Encyclopedia of Industrial Chemistry, vol. A2, p. 57-97, VCH: Weinheim, 1985.

The biosynthesis of these natural amino acids in organisms capable of producing them, such as bacteria, has been well characterized (for review of bacterial amino acid biosynthesis and regulation thereof, see Umbarger, H.E.(1978) *Ann. Rev. Biochem.* 47: 533-606). Glutamate is synthesized by the reductive amination of α -ketoglutarate, an intermediate in the citric acid cycle. Glutamine, proline, and arginine are each subsequently produced from glutamate. The biosynthesis of serine is a three-step process beginning with 3-phosphoglycerate (an intermediate in glycolysis), and resulting in this amino acid after oxidation, transamination, and hydrolysis steps. Both cysteine and glycine are produced from serine; the former by the condensation of homocysteine with serine, and the latter by the transferal of the side-chain β -carbon atom to tetrahydrofolate, in a reaction catalyzed by serine transhydroxymethylase. Phenylalanine, and tyrosine are synthesized from the glycolytic and pentose phosphate pathway precursors erythrose 4-phosphate and phosphoenolpyruvate in a 9-step biosynthetic pathway that differ only at the final two steps after synthesis of prephenate. Tryptophan is also produced from these two initial molecules, but its synthesis is an 11-step pathway. Tyrosine may also be synthesized from phenylalanine, in a reaction catalyzed by phenylalanine hydroxylase. Alanine, valine, and leucine are all biosynthetic products of pyruvate, the final product of glycolysis. Aspartate is formed from oxaloacetate, an intermediate of the citric acid cycle. Asparagine, methionine, threonine, and lysine are each produced by the conversion of aspartate. Isoleucine is formed from threonine. A complex 9-step pathway results in the production of histidine from 5-phosphoribosyl-1-pyrophosphate, an activated sugar.

Amino acids in excess of the protein synthesis needs of the cell cannot be stored, and are instead degraded to provide intermediates for the major metabolic pathways of the cell (for review see Stryer, L. *Biochemistry* 3rd ed. Ch. 21 "Amino Acid Degradation and the Urea Cycle" p. 495-516 (1988)). Although the cell is able to convert unwanted amino acids into useful metabolic intermediates, amino acid production is costly in terms of energy, precursor molecules, and the enzymes necessary to synthesize them. Thus it is not surprising that amino acid biosynthesis is regulated by feedback inhibition, in which the presence of a particular amino acid serves to slow or entirely stop its own

production (for overview of feedback mechanisms in amino acid biosynthetic pathways, see Stryer, L. Biochemistry, 3rd ed. Ch. 24: "Biosynthesis of Amino Acids and Heme" p. 575-600 (1988)). Thus, the output of any particular amino acid is limited by the amount of that amino acid present in the cell.

5

B. Vitamin, Cofactor, and Nutraceutical Metabolism and Uses

Vitamins, cofactors, and nutraceuticals comprise another group of molecules which the higher animals have lost the ability to synthesize and so must ingest, although they are readily synthesized by other organisms such as bacteria. These molecules are
10 either bioactive substances themselves, or are precursors of biologically active substances which may serve as electron carriers or intermediates in a variety of metabolic pathways. Aside from their nutritive value, these compounds also have significant industrial value as coloring agents, antioxidants, and catalysts or other processing aids. (For an overview of the structure, activity, and industrial applications
15 of these compounds, see, for example, Ullman's Encyclopedia of Industrial Chemistry, "Vitamins" vol. A27, p. 443-613, VCH: Weinheim, 1996.) The term "vitamin" is art-recognized, and includes nutrients which are required by an organism for normal functioning, but which that organism cannot synthesize by itself. The group of vitamins may encompass cofactors and nutraceutical compounds. The language "cofactor"
20 includes nonproteinaceous compounds required for a normal enzymatic activity to occur. Such compounds may be organic or inorganic; the cofactor molecules of the invention are preferably organic. The term "nutraceutical" includes dietary supplements having health benefits in plants and animals, particularly humans. Examples of such molecules are vitamins, antioxidants, and also certain lipids (e.g., polyunsaturated fatty
25 acids).

The biosynthesis of these molecules in organisms capable of producing them, such as bacteria, has been largely characterized (Ullman's Encyclopedia of Industrial Chemistry, "Vitamins" vol. A27, p. 443-613, VCH: Weinheim, 1996; Michal, G. (1999) Biochemical Pathways: An Atlas of Biochemistry and Molecular Biology, John Wiley
30 & Sons; Ong, A.S., Niki, E. & Packer, L. (1995) "Nutrition, Lipids, Health, and Disease" Proceedings of the UNESCO/Confederation of Scientific and Technological

Associations in Malaysia, and the Society for Free Radical Research – Asia, held Sept. 1-3, 1994 at Penang, Malaysia, AOCS Press: Champaign, IL X, 374 S).

Thiamin (vitamin B₁) is produced by the chemical coupling of pyrimidine and thiazole moieties. Riboflavin (vitamin B₂) is synthesized from guanosine-5'-triphosphate (GTP) and ribose-5'-phosphate. Riboflavin, in turn, is utilized for the synthesis of flavin mononucleotide (FMN) and flavin adenine dinucleotide (FAD). The family of compounds collectively termed 'vitamin B₆' (e.g., pyridoxine, pyridoxamine, pyridoxa-5'-phosphate, and the commercially used pyridoxin hydrochloride) are all derivatives of the common structural unit, 5-hydroxy-6-methylpyridine. Pantothenate (pantothenic acid, (R)-(+)-N-(2,4-dihydroxy-3,3-dimethyl-1-oxobutyl)- β -alanine) can be produced either by chemical synthesis or by fermentation. The final steps in pantothenate biosynthesis consist of the ATP-driven condensation of β -alanine and pantoic acid. The enzymes responsible for the biosynthesis steps for the conversion to pantoic acid, to β -alanine and for the condensation to pantothenic acid are known. The metabolically active form of pantothenate is Coenzyme A, for which the biosynthesis proceeds in 5 enzymatic steps. Pantothenate, pyridoxal-5'-phosphate, cysteine and ATP are the precursors of Coenzyme A. These enzymes not only catalyze the formation of pantothenate, but also the production of (R)-pantoic acid, (R)-pantolacton, (R)-panthenol (provitamin B₅), pantetheine (and its derivatives) and coenzyme A.

Biotin biosynthesis from the precursor molecule pimeloyl-CoA in microorganisms has been studied in detail and several of the genes involved have been identified. Many of the corresponding proteins have been found to also be involved in Fe-cluster synthesis and are members of the nifS class of proteins. Lipoic acid is derived from octanoic acid, and serves as a coenzyme in energy metabolism, where it becomes part of the pyruvate dehydrogenase complex and the α -ketoglutarate dehydrogenase complex. The folates are a group of substances which are all derivatives of folic acid, which in turn is derived from L-glutamic acid, p-amino-benzoic acid and 6-methylpterin. The biosynthesis of folic acid and its derivatives, starting from the metabolism intermediates guanosine-5'-triphosphate (GTP), L-glutamic acid and p-amino-benzoic acid has been studied in detail in certain microorganisms.

Corrinoids (such as the cobalamines and particularly vitamin B₁₂) and porphyrines belong to a group of chemicals characterized by a tetrapyrrole ring system.

The biosynthesis of vitamin B₁₂ is sufficiently complex that it has not yet been completely characterized, but many of the enzymes and substrates involved are now known. Nicotinic acid (nicotinate), and nicotinamide are pyridine derivatives which are also termed 'niacin'. Niacin is the precursor of the important coenzymes NAD
5 (nicotinamide adenine dinucleotide) and NADP (nicotinamide adenine dinucleotide phosphate) and their reduced forms.

The large-scale production of these compounds has largely relied on cell-free chemical syntheses, though some of these chemicals have also been produced by large-scale culture of microorganisms, such as riboflavin, Vitamin B₆, pantothenate, and
10 biotin. Only Vitamin B₁₂ is produced solely by fermentation, due to the complexity of its synthesis. *In vitro* methodologies require significant inputs of materials and time, often at great cost.

C. Purine, Pyrimidine, Nucleoside and Nucleotide Metabolism and Uses

15 Purine and pyrimidine metabolism genes and their corresponding proteins are important targets for the therapy of tumor diseases and viral infections. The language "purine" or "pyrimidine" includes the nitrogenous bases which are constituents of nucleic acids, co-enzymes, and nucleotides. The term "nucleotide" includes the basic structural units of nucleic acid molecules, which are comprised of a nitrogenous base, a
20 pentose sugar (in the case of RNA, the sugar is ribose; in the case of DNA, the sugar is D-deoxyribose), and phosphoric acid. The language "nucleoside" includes molecules which serve as precursors to nucleotides, but which are lacking the phosphoric acid moiety that nucleotides possess. By inhibiting the biosynthesis of these molecules, or their mobilization to form nucleic acid molecules, it is possible to inhibit RNA and DNA
25 synthesis; by inhibiting this activity in a fashion targeted to cancerous cells, the ability of tumor cells to divide and replicate may be inhibited. Additionally, there are nucleotides which do not form nucleic acid molecules, but rather serve as energy stores (*i.e.*, AMP) or as coenzymes (*i.e.*, FAD and NAD).

Several publications have described the use of these chemicals for these medical
30 indications, by influencing purine and/or pyrimidine metabolism (*e.g.* Christopherson, R.I. and Lyons, S.D. (1990) "Potent inhibitors of *de novo* pyrimidine and purine biosynthesis as chemotherapeutic agents." *Med. Res. Reviews* 10: 505-548). Studies of

enzymes involved in purine and pyrimidine metabolism have been focused on the development of new drugs which can be used, for example, as immunosuppressants or anti-proliferants (Smith, J.L., (1995) "Enzymes in nucleotide synthesis." *Curr. Opin. Struct. Biol.* 5: 752-757; (1995) *Biochem Soc. Transact.* 23: 877-902). However, purine and pyrimidine bases, nucleosides and nucleotides have other utilities: as intermediates in the biosynthesis of several fine chemicals (e.g., thiamine, S-adenosyl-methionine, folates, or riboflavin), as energy carriers for the cell (e.g., ATP or GTP), and for chemicals themselves, commonly used as flavor enhancers (e.g., IMP or GMP) or for several medicinal applications (see, for example, Kuninaka, A. (1996) *Nucleotides and Related Compounds in Biotechnology* vol. 6, Rehm *et al.*, eds. VCH: Weinheim, p. 561-612). Also, enzymes involved in purine, pyrimidine, nucleoside, or nucleotide metabolism are increasingly serving as targets against which chemicals for crop protection, including fungicides, herbicides and insecticides, are developed.

The metabolism of these compounds in bacteria has been characterized (for reviews see, for example, Zalkin, H. and Dixon, J.E. (1992) "*de novo* purine nucleotide biosynthesis", in: *Progress in Nucleic Acid Research and Molecular Biology*, vol. 42, Academic Press:, p. 259-287; and Michal, G. (1999) "Nucleotides and Nucleosides", Chapter 8 in: *Biochemical Pathways: An Atlas of Biochemistry and Molecular Biology*, Wiley: New York). Purine metabolism has been the subject of intensive research, and is essential to the normal functioning of the cell. Impaired purine metabolism in higher animals can cause severe disease, such as gout. Purine nucleotides are synthesized from ribose-5-phosphate, in a series of steps through the intermediate compound inosine-5'-phosphate (IMP), resulting in the production of guanosine-5'-monophosphate (GMP) or adenosine-5'-monophosphate (AMP), from which the triphosphate forms utilized as nucleotides are readily formed. These compounds are also utilized as energy stores, so their degradation provides energy for many different biochemical processes in the cell. Pyrimidine biosynthesis proceeds by the formation of uridine-5'-monophosphate (UMP) from ribose-5-phosphate. UMP, in turn, is converted to cytidine-5'-triphosphate (CTP). The deoxy- forms of all of these nucleotides are produced in a one step reduction reaction from the diphosphate ribose form of the nucleotide to the diphosphate deoxyribose form of the nucleotide. Upon phosphorylation, these molecules are able to participate in DNA synthesis.

D. Trehalose Metabolism and Uses

Trehalose consists of two glucose molecules, bound in α , α -1,1 linkage. It is commonly used in the food industry as a sweetener, an additive for dried or frozen foods, and in beverages. However, it also has applications in the pharmaceutical, cosmetics and biotechnology industries (see, for example, Nishimoto *et al.*, (1998) U.S. Patent No. 5,759,610; Singer, M.A. and Lindquist, S. (1998) *Trends Biotech.* 16: 460-467; Paiva, C.L.A. and Panek, A.D. (1996) *Biotech. Ann. Rev.* 2: 293-314; and Shiosaka, M. (1997) *J. Japan* 172: 97-102). Trehalose is produced by enzymes from many microorganisms and is naturally released into the surrounding medium, from which it can be collected using methods known in the art.

II. Sugar and Carbon Molecule Utilization and Oxidative Phosphorylation

Carbon is a critically important element for the formation of all organic compounds, and thus is a nutritional requirement not only for the growth and division of *C. glutamicum*, but also for the overproduction of fine chemicals from this microorganism. Sugars, such as mono-, di-, or polysaccharides, are particularly good carbon sources, and thus standard growth media typically contain one or more of: glucose, fructose, mannose, galactose, ribose, sorbose, ribulose, lactose, maltose, sucrose, raffinose, starch, or cellulose (Ullmann's Encyclopedia of Industrial Chemistry (1987) vol. A9, "Enzymes", VCH: Weinheim). Alternatively, more complex forms of sugar may be utilized in the media, such as molasses, or other by-products of sugar refinement. Other compounds aside from the sugars may be used as alternate carbon sources, including alcohols (*e.g.*, ethanol or methanol), alkanes, sugar alcohols, fatty acids, and organic acids (*e.g.*, acetic acid or lactic acid). For a review of carbon sources and their utilization by microorganisms in culture, see: Ullman's Encyclopedia of Industrial Chemistry (1987) vol. A9, "Enzymes", VCH: Weinheim; Stoppok, E. and Buchholz, K. (1996) "Sugar-based raw materials for fermentation applications" in Biotechnology (Rehm, H.J. *et al.*, eds.) vol. 6, VCH: Weinheim, p. 5-29; Rehm, H.J. (1980) *Industrielle Mikrobiologie*, Springer: Berlin; Bartholomew, W.H., and Reiman, H.B. (1979). Economics of Fermentation Processes, in: Peppler, H.J. and Perlman, D., eds. *Microbial Technology* 2nd ed., vol. 2, chapter 18, Academic Press: New York; and

Kočkova-Kratachvilova, A. (1981) Characteristics of Industrial Microorganisms, in: Rehm, H.J. and Reed, G., eds. Handbook of Biotechnology, vol. 1, chapter 1, Verlag Chemie: Weinheim.

After uptake, these energy-rich carbon molecules must be processed such that they are able to be degraded by one of the major sugar metabolic pathways. Such pathways lead directly to useful degradation products, such as ribose-5-phosphate and phosphoenolpyruvate, which may be subsequently converted to pyruvate. Three of the most important pathways in bacteria for sugar metabolism include the Embden-Meyerhoff-Parnas (EMP) pathway (also known as the glycolytic or fructose bisphosphate pathway), the hexosemonophosphate (HMP) pathway (also known as the pentose shunt or pentose phosphate pathway), and the Entner-Doudoroff (ED) pathway (for review, see Michal, G. (1999) Biochemical Pathways: An Atlas of Biochemistry and Molecular Biology, Wiley: New York, and Stryer, L. (1988) Biochemistry, Chapters 13-19, Freeman: New York, and references therein).

The EMP pathway converts hexose molecules to pyruvate, and in the process produces 2 molecules of ATP and 2 molecules of NADH. Starting with glucose-1-phosphate (which may be either directly taken up from the medium, or alternatively may be generated from glycogen, starch, or cellulose), the glucose molecule is isomerized to fructose-6-phosphate, is phosphorylated, and split into two 3-carbon molecules of glyceraldehyde-3-phosphate. After dehydrogenation, phosphorylation, and successive rearrangements, pyruvate results.

The HMP pathway converts glucose to reducing equivalents, such as NADPH, and produces pentose and tetrose compounds which are necessary as intermediates and precursors in a number of other metabolic pathways. In the HMP pathway, glucose-6-phosphate is converted to ribulose-5-phosphate by two successive dehydrogenase reactions (which also release two NADPH molecules), and a carboxylation step. Ribulose-5-phosphate may also be converted to xyulose-5-phosphate and ribose-5-phosphate; the former can undergo a series of biochemical steps to glucose-6-phosphate, which may enter the EMP pathway, while the latter is commonly utilized as an intermediate in other biosynthetic pathways within the cell.

The ED pathway begins with the compound glucose or gluconate, which is subsequently phosphorylated and dehydrated to form 2-dehydro-3-deoxy-6-P-gluconate.

Glucuronate and galacturonate may also be converted to 2-dehydro-3-deoxy-6-P-gluconate through more complex biochemical pathways. This product molecule is subsequently cleaved into glyceraldehyde-3-P and pyruvate; glyceraldehyde-3-P may itself also be converted to pyruvate.

5 The EMP and HMP pathways share many features, including intermediates and enzymes. The EMP pathway provides the greatest amount of ATP, but it does not produce ribose-5-phosphate, an important precursor for, *e.g.*, nucleic acid biosynthesis, nor does it produce erythrose-4-phosphate, which is important for amino acid biosynthesis. Microorganisms that are capable of using only the EMP pathway for
10 glucose utilization are thus not able to grow on simple media with glucose as the sole carbon source. They are referred to as fastidious organisms, and their growth requires inputs of complex organic compounds, such as those found in yeast extract.

In contrast, the HMP pathway produces all of the precursors necessary for both nucleic acid and amino acid biosynthesis, yet yields only half the amount of ATP energy
15 that the EMP pathway does. The HMP pathway also produces NADPH, which may be used for redox reactions in biosynthetic pathways. The HMP pathway does not directly produce pyruvate, however, and thus these microorganisms must also possess this portion of the EMP pathway. It is therefore not surprising that a number of microorganisms, particularly the facultative anaerobes, have evolved such that they
20 possess both of these pathways.

The ED pathway has thus far has only been found in bacteria. Although this pathway is linked partly to the HMP pathway in the reverse direction for precursor formation, the ED pathway directly forms pyruvate by the aldolase cleavage of 3-ketodeoxy-6-phosphogluconate. The ED pathway can exist on its own and is utilized by
25 the majority of strictly aerobic microorganisms. The net result is similar to that of the HMP pathway, although one mole of ATP can be formed only if the carbon atoms are converted into pyruvate, instead of into precursor molecules.

The pyruvate molecules produced through any of these pathways can be readily converted into energy via the Krebs cycle (also known as the citric acid cycle, the citrate
30 cycle, or the tricarboxylic acid cycle (TCA cycle)). In this process, pyruvate is first decarboxylated, resulting in the production of one molecule of NADH, 1 molecule of acetyl-CoA, and 1 molecule of CO₂. The acetyl group of acetyl CoA then reacts with

the 4 carbon unit, oxaloacetate, leading to the formation of citric acid, a 6 carbon organic acid. Dehydration and two additional CO₂ molecules are released. Ultimately, oxaloacetate is regenerated and can serve again as an acetyl acceptor, thus completing the cycle. The electrons released during the oxidation of intermediates in the TCA cycle are transferred to NAD⁺ to yield NADH.

During respiration, the electrons from NADH are transferred to molecular oxygen or other terminal electron acceptors. This process is catalyzed by the respiratory chain, an electron transport system containing both integral membrane proteins and membrane associated proteins. This system serves two basic functions: first, to accept electrons from an electron donor and to transfer them to an electron acceptor, and second, to conserve some of the energy released during electron transfer by the synthesis of ATP. Several types of oxidation-reduction enzymes and electron transport proteins are known to be involved in such processes, including the NADH dehydrogenases, flavin-containing electron carriers, iron sulfur proteins, and cytochromes. The NADH dehydrogenases are located at the cytoplasmic surface of the plasma membrane, and transfer hydrogen atoms from NADH to flavoproteins, in turn accepting electrons from NADH. The flavoproteins are a group of electron carriers possessing a flavin prosthetic group which is alternately reduced and oxidized as it accepts and transfers electrons. Three flavins are known to participate in these reactions: riboflavin, flavin-adenine dinucleotide (FAD) and flavin-mononucleotide (FMN). Iron sulfur proteins contain a cluster of iron and sulfur atoms which are not bonded to a heme group, but which still are able to participate in dehydration and rehydration reactions. Succinate dehydrogenase and aconitase are exemplary iron-sulfur proteins; their iron-sulfur complexes serve to accept and transfer electrons as part of the overall electron-transport chain. The cytochromes are proteins containing an iron porphyrin ring (heme). There are a number of different classes of cytochromes, differing in their reduction potentials. Functionally, these cytochromes form pathways in which electrons may be transferred to other cytochromes having increasingly more positive reduction potentials. A further class of non-protein electron carriers is known: the lipid-soluble quinones (e.g., coenzyme Q). These molecules also serve as hydrogen atom acceptors and electron donors.

The action of the respiratory chain generates a proton gradient across the cell membrane, resulting in proton motive force. This force is utilized by the cell to synthesize ATP, via the membrane-spanning enzyme, ATP synthase. This enzyme is a multiprotein complex in which the transport of H^+ molecules through the membrane results in the physical rotation of the intracellular subunits and concomitant phosphorylation of ADP to form ATP (for review, see Fillingame, R.H. and Divall, S. (1999) *Novartis Found. Symp.* 221: 218-229, 229-234).

Non-hexose carbon substrates may also serve as carbon and energy sources for cells. Such substrates may first be converted to hexose sugars in the gluconeogenesis pathway, where glucose is first synthesized by the cell and then is degraded to produce energy. The starting material for this reaction is phosphoenolpyruvate (PEP), which is one of the key intermediates in the glycolytic pathway. PEP may be formed from substrates other than sugars, such as acetic acid, or by decarboxylation of oxaloacetate (itself an intermediate in the TCA cycle). By reversing the glycolytic pathway (utilizing a cascade of enzymes different than those of the original glycolysis pathway), glucose-6-phosphate may be formed. The conversion of pyruvate to glucose requires the utilization of 6 high energy phosphate bonds, whereas glycolysis only produces 2 ATP in the conversion of glucose to pyruvate. However, the complete oxidation of glucose (glycolysis, conversion of pyruvate into acetyl CoA, citric acid cycle, and oxidative phosphorylation) yields between 36-38 ATP, so the net loss of high energy phosphate bonds experienced during gluconeogenesis is offset by the overall greater gain in such high-energy molecules produced by the oxidation of glucose.

III. Elements and Methods of the Invention

The present invention is based, at least in part, on the discovery of novel molecules, referred to herein as SMP nucleic acid and protein molecules, which participate in the conversion of sugars to useful degradation products and energy (*e.g.*, ATP) in *C. glutamicum* or which may participate in the production of useful energy-rich molecules (*e.g.*, ATP) by other processes, such as oxidative phosphorylation. In one embodiment, the SMP molecules participate in the metabolism of carbon compounds such as sugars or the generation of energy molecules (*e.g.*, ATP) by processes such as oxidative phosphorylation in *Corynebacterium glutamicum*. In a preferred embodiment,

the activity of the SMP molecules of the present invention to contribute to carbon metabolism or energy production in *C. glutamicum* has an impact on the production of a desired fine chemical by this organism. In a particularly preferred embodiment, the SMP molecules of the invention are modulated in activity, such that the *C. glutamicum*

5 metabolic and energetic pathways in which the SMP proteins of the invention participate are modulated in yield, production, and/or efficiency of production, which either directly or indirectly modulates the yield, production, and/or efficiency of production of a desired fine chemical by *C. glutamicum*.

The language, "SMP protein" or "SMP polypeptide" includes proteins which are

10 capable of performing a function involved in the metabolism of carbon compounds such as sugars and the generation of energy molecules by processes such as oxidative phosphorylation in *Corynebacterium glutamicum*. Examples of SMP proteins include those encoded by the SMP genes set forth in Table 1 and by the odd-numbered SEQ ID NOs. The terms "SMP gene" or "SMP nucleic acid sequence" include nucleic acid

15 sequences encoding an SMP protein, which consist of a coding region and also corresponding untranslated 5' and 3' sequence regions. Examples of SMP genes include those set forth in Table 1. The terms "production" or "productivity" are art-recognized and include the concentration of the fermentation product (for example, the desired fine chemical) formed within a given time and a given fermentation volume (*e.g.*, kg product

20 per hour per liter). The term "efficiency of production" includes the time required for a particular level of production to be achieved (for example, how long it takes for the cell to attain a particular rate of output of a fine chemical). The term "yield" or "product/carbon yield" is art-recognized and includes the efficiency of the conversion of the carbon source into the product (*i.e.*, fine chemical). This is generally written as, for

25 example, kg product per kg carbon source. By increasing the yield or production of the compound, the quantity of recovered molecules, or of useful recovered molecules of that compound in a given amount of culture over a given amount of time is increased. The terms "biosynthesis" or a "biosynthetic pathway" are art-recognized and include the synthesis of a compound, preferably an organic compound, by a cell from intermediate

30 compounds in what may be a multistep and highly regulated process. The terms "degradation" or a "degradation pathway" are art-recognized and include the breakdown of a compound, preferably an organic compound, by a cell to degradation

products (generally speaking, smaller or less complex molecules) in what may be a multistep and highly regulated process. The term "degradation product" is art-recognized and includes breakdown products of a compound. Such products may themselves have utility as precursor (starting point) or intermediate molecules necessary
5 for the biosynthesis of other compounds by the cell. The language "metabolism" is art-recognized and includes the totality of the biochemical reactions that take place in an organism. The metabolism of a particular compound, then, (*e.g.*, the metabolism of an amino acid such as glycine) comprises the overall biosynthetic, modification, and degradation pathways in the cell related to this compound.

10 In another embodiment, the SMP molecules of the invention are capable of modulating the production of a desired molecule, such as a fine chemical, in a microorganism such as *C. glutamicum*. There are a number of mechanisms by which the alteration of an SMP protein of the invention may directly affect the yield, production, and/or efficiency of production of a fine chemical from a *C. glutamicum*
15 strain incorporating such an altered protein. The degradation of high-energy carbon molecules such as sugars, and the conversion of compounds such as NADH and FADH₂ to more useful forms via oxidative phosphorylation results in a number of compounds which themselves may be desirable fine chemicals, such as pyruvate, ATP, NADH, and a number of intermediate sugar compounds. Further, the energy molecules (such as
20 ATP) and the reducing equivalents (such as NADH or NADPH) produced by these metabolic pathways are utilized in the cell to drive reactions which would otherwise be energetically unfavorable. Such unfavorable reactions include many biosynthetic pathways for fine chemicals. By improving the ability of the cell to utilize a particular sugar (*e.g.*, by manipulating the genes encoding enzymes involved in the degradation
25 and conversion of that sugar into energy for the cell), one may increase the amount of energy available to permit unfavorable, yet desired metabolic reactions (*e.g.*, the biosynthesis of a desired fine chemical) to occur.

The mutagenesis of one or more SMP genes of the invention may also result in SMP proteins having altered activities which indirectly impact the production of one or
30 more desired fine chemicals from *C. glutamicum*. For example, by increasing the efficiency of utilization of one or more sugars (such that the conversion of the sugar to useful energy molecules is improved), or by increasing the efficiency of conversion of

reducing equivalents to useful energy molecules (*e.g.*, by improving the efficiency of oxidative phosphorylation, or the activity of the ATP synthase), one can increase the amount of these high-energy compounds available to the cell to drive normally unfavorable metabolic processes. These processes include the construction of cell walls, transcription, translation, and the biosynthesis of compounds necessary for growth and division of the cells (*e.g.*, nucleotides, amino acids, vitamins, lipids, etc.) (Lengeler *et al.* (1999) *Biology of Prokaryotes*, Thieme Verlag: Stuttgart, p. 88-109; 913-918; 875-899). By improving the growth and multiplication of these engineered cells, it is possible to increase both the viability of the cells in large-scale culture, and also to improve their rate of division, such that a relatively larger number of cells can survive in fermentor culture. The yield, production, or efficiency of production may be increased, at least due to the presence of a greater number of viable cells, each producing the desired fine chemical. Further, a number of the degradation and intermediate compounds produced during sugar metabolism are necessary precursors and intermediates for other biosynthetic pathways throughout the cell. For example, many amino acids are synthesized directly from compounds normally resulting from glycolysis or the TCA cycle (*e.g.*, serine is synthesized from 3-phosphoglycerate, an intermediate in glycolysis). Thus, by increasing the efficiency of conversion of sugars to useful energy molecules, it is also possible to increase the amount of useful degradation products as well.

The isolated nucleic acid sequences of the invention are contained within the genome of a *Corynebacterium glutamicum* strain available through the American Type Culture Collection, given designation ATCC 13032. The nucleotide sequence of the isolated *C. glutamicum* SMP DNAs and the predicted amino acid sequences of the *C. glutamicum* SMP proteins are shown in the Sequence Listing as odd-numbered SEQ ID NOs and even-numbered SEQ ID NOs, respectively. Computational analyses were performed which classified and/or identified these nucleotide sequences as sequences which encode proteins having a function involved in the metabolism of carbon compounds such as sugars or in the generation of energy molecules by processes such as oxidative phosphorylation in *Corynebacterium glutamicum*.

The present invention also pertains to proteins which have an amino acid sequence which is substantially homologous to an amino acid sequence of the invention

(e.g., the sequence of an even-numbered SEQ ID NO of the Sequence Listing). As used herein, a protein which has an amino acid sequence which is substantially homologous to a selected amino acid sequence is least about 50% homologous to the selected amino acid sequence, e.g., the entire selected amino acid sequence. A protein which has an amino acid sequence which is substantially homologous to a selected amino acid sequence can also be least about 50-60%, preferably at least about 60-70%, and more preferably at least about 70-80%, 80-90%, or 90-95%, and most preferably at least about 96%, 97%, 98%, 99% or more homologous to the selected amino acid sequence.

An SMP protein or a biologically active portion or fragment thereof of the invention can participate in the metabolism of carbon compounds such as sugars or in the generation of energy molecules (e.g., ATP) by processes such as oxidative phosphorylation in *Corynebacterium glutamicum*, or can have one or more of the activities set forth in Table 1.

Various aspects of the invention are described in further detail in the following subsections:

A. Isolated Nucleic Acid Molecules

One aspect of the invention pertains to isolated nucleic acid molecules that encode SMP polypeptides or biologically active portions thereof, as well as nucleic acid fragments sufficient for use as hybridization probes or primers for the identification or amplification of SMP-encoding nucleic acid (e.g., SMP DNA). As used herein, the term "nucleic acid molecule" is intended to include DNA molecules (e.g., cDNA or genomic DNA) and RNA molecules (e.g., mRNA) and analogs of the DNA or RNA generated using nucleotide analogs. This term also encompasses untranslated sequence located at both the 3' and 5' ends of the coding region of the gene: at least about 100 nucleotides of sequence upstream from the 5' end of the coding region and at least about 20 nucleotides of sequence downstream from the 3' end of the coding region of the gene. The nucleic acid molecule can be single-stranded or double-stranded, but preferably is double-stranded DNA. An "isolated" nucleic acid molecule is one which is separated from other nucleic acid molecules which are present in the natural source of the nucleic acid. Preferably, an "isolated" nucleic acid is free of sequences which naturally flank the nucleic acid (i.e., sequences located at the 5' and 3' ends of the nucleic acid) in the

genomic DNA of the organism from which the nucleic acid is derived. For example, in various embodiments, the isolated SMP nucleic acid molecule can contain less than about 5 kb, 4kb, 3kb, 2kb, 1 kb, 0.5 kb or 0.1 kb of nucleotide sequences which naturally flank the nucleic acid molecule in genomic DNA of the cell from which the nucleic acid is derived (e.g., a *C. glutamicum* cell). Moreover, an "isolated" nucleic acid molecule, such as a DNA molecule, can be substantially free of other cellular material, or culture medium when produced by recombinant techniques, or chemical precursors or other chemicals when chemically synthesized.

A nucleic acid molecule of the present invention, e.g., a nucleic acid molecule having a nucleotide sequence of an odd-numbered SEQ ID NO of the Sequence Listing, or a portion thereof, can be isolated using standard molecular biology techniques and the sequence information provided herein. For example, a *C. glutamicum* SMP DNA can be isolated from a *C. glutamicum* library using all or portion of one of the odd-numbered SEQ ID NO sequences of the Sequence Listing as a hybridization probe and standard hybridization techniques (e.g., as described in Sambrook, J., Fritsh, E. F., and Maniatis, T. *Molecular Cloning: A Laboratory Manual*. 2nd, ed., Cold Spring Harbor Laboratory, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY, 1989). Moreover, a nucleic acid molecule encompassing all or a portion of one of the nucleic acid sequences of the invention (e.g., an odd-numbered SEQ ID NO:) can be isolated by the polymerase chain reaction using oligonucleotide primers designed based upon this sequence (e.g., a nucleic acid molecule encompassing all or a portion of one of the nucleic acid sequences of the invention (e.g., an odd-numbered SEQ ID NO of the Sequence Listing) can be isolated by the polymerase chain reaction using oligonucleotide primers designed based upon this same sequence). For example, mRNA can be isolated from normal endothelial cells (e.g., by the guanidinium-thiocyanate extraction procedure of Chirgwin *et al.* (1979) *Biochemistry* 18: 5294-5299) and DNA can be prepared using reverse transcriptase (e.g., Moloney MLV reverse transcriptase, available from Gibco/BRL, Bethesda, MD; or AMV reverse transcriptase, available from Seikagaku America, Inc., St. Petersburg, FL). Synthetic oligonucleotide primers for polymerase chain reaction amplification can be designed based upon one of the nucleotide sequences shown in the Sequence Listing. A nucleic acid of the invention can be amplified using cDNA or, alternatively, genomic DNA, as a template and

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appropriate oligonucleotide primers according to standard PCR amplification techniques. The nucleic acid so amplified can be cloned into an appropriate vector and characterized by DNA sequence analysis. Furthermore, oligonucleotides corresponding to an SMP nucleotide sequence can be prepared by standard synthetic techniques, *e.g.*,
5 using an automated DNA synthesizer.

In a preferred embodiment, an isolated nucleic acid molecule of the invention comprises one of the nucleotide sequences shown in the Sequence Listing. The nucleic acid sequences of the invention, as set forth in the Sequence Listing, correspond to the *Corynebacterium glutamicum* SMP DNAs of the invention. This DNA comprises
10 sequences encoding SMP proteins (*i.e.*, the "coding region", indicated in each odd-numbered SEQ ID NO: sequence in the Sequence Listing), as well as 5' untranslated sequences and 3' untranslated sequences, also indicated in each odd-numbered SEQ ID NO: in the Sequence Listing.. Alternatively, the nucleic acid molecule can comprise only the coding region of any of the sequences in nucleic acid sequences of the
15 Sequence Listing.

For the purposes of this application, it will be understood that each of the nucleic acid and amino acid sequences set forth in the Sequence Listing has an identifying RXA, RXN, or RXS number having the designation "RXA," "RXN," or "RXS" followed by 5 digits (*i.e.*, RXA01626, RXN00043, or RXS0735). Each of the nucleic acid sequences
20 comprises up to three parts: a 5' upstream region, a coding region, and a downstream region. Each of these three regions is identified by the same RXA, RXN, or RXS designation to eliminate confusion. The recitation "one of the odd-numbered sequences of the Sequence Listing", then, refers to any of the nucleic acid sequences in the Sequence Listing, which may also be distinguished by their differing RXA, RXN, or
25 RXS designations. The coding region of each of these sequences is translated into a corresponding amino acid sequence, which is also set forth in the Sequence Listing, as an even-numbered SEQ ID NO: immediately following the corresponding nucleic acid sequence. For example, the coding region for RXA02735 is set forth in SEQ ID NO:1, while the amino acid sequence which it encodes is set forth as SEQ ID NO:2. The
30 sequences of the nucleic acid molecules of the invention are identified by the same RXA, RXN, or RXS designations as the amino acid molecules which they encode, such that they can be readily correlated. For example, the amino acid sequence designated

RXA00042 is a translation of the coding region of the nucleotide sequence of nucleic acid molecule RXA00042, and the amino acid sequence designated RXN00043 is a translation of the coding region of the nucleotide sequence of nucleic acid molecule RXN00043. The correspondence between the RXA, RXN and RXS nucleotide and
5 amino acid sequences of the invention and their assigned SEQ ID NOs is set forth in Table 1.

Several of the genes of the invention are "F-designated genes". An F-designated gene includes those genes set forth in Table 1 which have an 'F' in front of the RXA designation. For example, SEQ ID NO:11, designated, as indicated on Table 1, as
10 "F RXA01312", is an F-designated gene, as are SEQ ID NOs: 29, 33, and 39 (designated on Table 1 as "F RXA02803", "F RXA02854", and "F RXA01365", respectively).

In one embodiment, the nucleic acid molecules of the present invention are not intended to include those compiled in Table 2. In the case of the *dapD* gene, a sequence
15 for this gene was published in Wehrmann, A., *et al.* (1998) *J. Bacteriol.* 180(12): 3159-3165. However, the sequence obtained by the inventors of the present application is significantly longer than the published version. It is believed that the published version relied on an incorrect start codon, and thus represents only a fragment of the actual coding region.

20 In another preferred embodiment, an isolated nucleic acid molecule of the invention comprises a nucleic acid molecule which is a complement of one of the nucleotide sequences of the invention (*e.g.*, a sequence of an odd-numbered SEQ ID NO: of the Sequence Listing), or a portion thereof. A nucleic acid molecule which is complementary to one of the nucleotide sequences of the invention is one which is
25 sufficiently complementary to one of the nucleotide sequences shown in the Sequence Listing (*e.g.*, the sequence of an odd-numbered SEQ ID NO:) such that it can hybridize to one of the nucleotide sequences of the invention, thereby forming a stable duplex.

In still another preferred embodiment, an isolated nucleic acid molecule of the invention comprises a nucleotide sequence which is at least about 50%, 51%, 52%, 53%,
30 54%, 55%, 56%, 57%, 58%, 59%, or 60%, preferably at least about 61%, 62%, 63%, 64%, 65%, 66%, 67%, 68%, 69%, or 70%, more preferably at least about 71%, 72%, 73%, 74%, 75%, 76%, 77%, 78%, 79%, or 80%, 81%, 82%, 83%, 84%, 85%, 86%,

87%, 88%, 89%, or 90%, or 91%, 92%, 93%, 94%, and even more preferably at least about 95%, 96%, 97%, 98%, 99% or more homologous to a nucleotide sequence of the invention (*e.g.*, a sequence of an odd-numbered SEQ ID NO: of the Sequence Listing), or a portion thereof. Ranges and identity values intermediate to the above-recited
5 ranges, (*e.g.*, 70-90% identical or 80-95% identical) are also intended to be encompassed by the present invention. For example, ranges of identity values using a combination of any of the above values recited as upper and/or lower limits are intended to be included. In an additional preferred embodiment, an isolated nucleic acid molecule of the invention comprises a nucleotide sequence which hybridizes, *e.g.*,
10 hybridizes under stringent conditions, to one of the nucleotide sequences of the invention, or a portion thereof.

Moreover, the nucleic acid molecule of the invention can comprise only a portion of the coding region of the sequence of one of the odd-numbered SEQ ID NOs of the Sequence Listing, for example a fragment which can be used as a probe or primer
15 or a fragment encoding a biologically active portion of an SMP protein. The nucleotide sequences determined from the cloning of the SMP genes from *C. glutamicum* allows for the generation of probes and primers designed for use in identifying and/or cloning SMP homologues in other cell types and organisms, as well as SMP homologues from other *Corynebacteria* or related species. The probe/primer typically comprises
20 substantially purified oligonucleotide. The oligonucleotide typically comprises a region of nucleotide sequence that hybridizes under stringent conditions to at least about 12, preferably about 25, more preferably about 40, 50 or 75 consecutive nucleotides of a sense strand of one of the nucleotide sequences of the invention (*e.g.*, a sequence of one of the odd-numbered SEQ ID NOs of the Sequence Listing), an anti-sense sequence of
25 one of these sequences, or naturally occurring mutants thereof. Primers based on a nucleotide sequence of the invention can be used in PCR reactions to clone SMP homologues. Probes based on the SMP nucleotide sequences can be used to detect transcripts or genomic sequences encoding the same or homologous proteins. In preferred embodiments, the probe further comprises a label group attached thereto, *e.g.*
30 the label group can be a radioisotope, a fluorescent compound, an enzyme, or an enzyme co-factor. Such probes can be used as a part of a diagnostic test kit for identifying cells which misexpress an SMP protein, such as by measuring a level of an SMP-encoding

nucleic acid in a sample of cells, *e.g.*, detecting SMP mRNA levels or determining whether a genomic SMP gene has been mutated or deleted.

In one embodiment, the nucleic acid molecule of the invention encodes a protein or portion thereof which includes an amino acid sequence which is sufficiently
5 homologous to an amino acid sequence of the invention (*e.g.*, a sequence of an even-numbered SEQ ID NO of the Sequence Listing) such that the protein or portion thereof maintains the ability to perform a function involved in the metabolism of carbon compounds such as sugars or in the generation of energy molecules (*e.g.*, ATP) by processes such as oxidative phosphorylation in *Corynebacterium glutamicum*. As used
10 herein, the language "sufficiently homologous" refers to proteins or portions thereof which have amino acid sequences which include a minimum number of identical or equivalent (*e.g.*, an amino acid residue which has a similar side chain as an amino acid residue in a sequence of one of the even-numbered SEQ ID NOs of the Sequence Listing) amino acid residues to an amino acid sequence of the invention such that the
15 protein or portion thereof is able to perform a function involved in the metabolism of carbon compounds such as sugars or in the generation of energy molecules (*e.g.*, ATP) by processes such as oxidative phosphorylation in *Corynebacterium glutamicum*. Protein members of such sugar metabolic pathways or energy producing systems, as described herein, may play a role in the production and secretion of one or more fine
20 chemicals. Examples of such activities are also described herein. Thus, "the function of an SMP protein" contributes either directly or indirectly to the yield, production, and/or efficiency of production of one or more fine chemicals. Examples of SMP protein activities are set forth in Table 1.

In another embodiment, the protein is at least about 50-60%, preferably at least
25 about 60-70%, and more preferably at least about 70-80%, 80-90%, 90-95%, and most preferably at least about 96%, 97%, 98%, 99% or more homologous to an entire amino acid sequence of the invention (*e.g.*, a sequence of an even-numbered SEQ ID NO: of the Sequence Listing).

Portions of proteins encoded by the SMP nucleic acid molecules of the invention
30 are preferably biologically active portions of one of the SMP proteins. As used herein, the term "biologically active portion of an SMP protein" is intended to include a portion, *e.g.*, a domain/motif, of an SMP protein that participates in the metabolism of carbon

compounds such as sugars, or in energy-generating pathways in *C. glutamicum*, or has an activity as set forth in Table 1. To determine whether an SMP protein or a biologically active portion thereof can participate in the metabolism of carbon compounds or in the production of energy-rich molecules in *C. glutamicum*, an assay of enzymatic activity may be performed. Such assay methods are well known to those of ordinary skill in the art, as detailed in Example 8 of the Exemplification.

Additional nucleic acid fragments encoding biologically active portions of an SMP protein can be prepared by isolating a portion of one of the amino acid sequences of the invention (*e.g.*, a sequence of an even-numbered SEQ ID NO: of the Sequence Listing), expressing the encoded portion of the SMP protein or peptide (*e.g.*, by recombinant expression *in vitro*) and assessing the activity of the encoded portion of the SMP protein or peptide.

The invention further encompasses nucleic acid molecules that differ from one of the nucleotide sequences of the invention (*e.g.*, a sequence of an odd-numbered SEQ ID NO: of the Sequence Listing) (and portions thereof) due to degeneracy of the genetic code and thus encode the same SMP protein as that encoded by the nucleotide sequences of the invention. In another embodiment, an isolated nucleic acid molecule of the invention has a nucleotide sequence encoding a protein having an amino acid sequence shown in the Sequence Listing (*e.g.*, an even-numbered SEQ ID NO:). In a still further embodiment, the nucleic acid molecule of the invention encodes a full length *C. glutamicum* protein which is substantially homologous to an amino acid of the invention (encoded by an open reading frame shown in an odd-numbered SEQ ID NO: of the Sequence Listing).

It will be understood by one of ordinary skill in the art that in one embodiment the sequences of the invention are not meant to include the sequences of the prior art, such as those Genbank sequences set forth in Tables 2 or 4 which were available prior to the present invention. In one embodiment, the invention includes nucleotide and amino acid sequences having a percent identity to a nucleotide or amino acid sequence of the invention which is greater than that of a sequence of the prior art (*e.g.*, a Genbank sequence (or the protein encoded by such a sequence) set forth in Tables 2 or 4). For example, the invention includes a nucleotide sequence which is greater than and/or at least 58% identical to the nucleotide sequence designated RXA00014 (SEQ ID NO:41),

- a nucleotide sequence which is greater than and/or at least % identical to the nucleotide sequence designated RXA00195 (SEQ ID NO:399), and a nucleotide sequence which is greater than and/or at least 42% identical to the nucleotide sequence designated RXA00196 (SEQ ID NO:401). One of ordinary skill in the art would be able to
- 5 calculate the lower threshold of percent identity for any given sequence of the invention by examining the GAP-calculated percent identity scores set forth in Table 4 for each of the three top hits for the given sequence, and by subtracting the highest GAP-calculated percent identity from 100 percent. One of ordinary skill in the art will also appreciate that nucleic acid and amino acid sequences having percent identities greater than the
- 10 lower threshold so calculated (*e.g.*, at least 50%, 51%, 52%, 53%, 54%, 55%, 56%, 57%, 58%, 59%, or 60%, preferably at least about 61%, 62%, 63%, 64%, 65%, 66%, 67%, 68%, 69%, or 70%, more preferably at least about 71%, 72%, 73%, 74%, 75%, 76%, 77%, 78%, 79%, or 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, or 90%, or 91%, 92%, 93%, 94%, and even more preferably at least about 95%, 96%, 97%,
- 15 98%, 99% or more identical) are also encompassed by the invention.

- In addition to the *C. glutamicum* SMP nucleotide sequences set forth in the Sequence Listing as odd-numbered SEQ ID NOs, it will be appreciated by those of ordinary skill in the art that DNA sequence polymorphisms that lead to changes in the amino acid sequences of SMP proteins may exist within a population (*e.g.*, the *C.*
- 20 *glutamicum* population). Such genetic polymorphism in the SMP gene may exist among individuals within a population due to natural variation. As used herein, the terms "gene" and "recombinant gene" refer to nucleic acid molecules comprising an open reading frame encoding an SMP protein, preferably a *C. glutamicum* SMP protein. Such natural variations can typically result in 1-5% variance in the nucleotide sequence of the
- 25 SMP gene. Any and all such nucleotide variations and resulting amino acid polymorphisms in SMP that are the result of natural variation and that do not alter the functional activity of SMP proteins are intended to be within the scope of the invention.

- Nucleic acid molecules corresponding to natural variants and non-*C. glutamicum* homologues of the *C. glutamicum* SMP DNA of the invention can be isolated based on
- 30 their homology to the *C. glutamicum* SMP nucleic acid disclosed herein using the *C. glutamicum* DNA, or a portion thereof, as a hybridization probe according to standard hybridization techniques under stringent hybridization conditions. Accordingly, in

another embodiment, an isolated nucleic acid molecule of the invention is at least 15 nucleotides in length and hybridizes under stringent conditions to the nucleic acid molecule comprising a nucleotide sequence of of an odd-numbered SEQ ID NO: of the Sequence Listing. In other embodiments, the nucleic acid is at least 30, 50, 100, 250 or
5 more nucleotides in length. As used herein, the term "hybridizes under stringent conditions" is intended to describe conditions for hybridization and washing under which nucleotide sequences at least 60% homologous to each other typically remain hybridized to each other. Preferably, the conditions are such that sequences at least about 65%, more preferably at least about 70%, and even more preferably at least about
10 75% or more homologous to each other typically remain hybridized to each other. Such stringent conditions are known to those of ordinary skill in the art and can be found in *Current Protocols in Molecular Biology*, John Wiley & Sons, N.Y. (1989), 6.3.1-6.3.6. A preferred, non-limiting example of stringent hybridization conditions are hybridization in 6X sodium chloride/sodium citrate (SSC) at about 45°C, followed by
15 one or more washes in 0.2 X SSC, 0.1% SDS at 50-65°C. Preferably, an isolated nucleic acid molecule of the invention that hybridizes under stringent conditions to a nucleotide sequence of the invention corresponds to a naturally-occurring nucleic acid molecule. As used herein, a "naturally-occurring" nucleic acid molecule refers to an RNA or DNA molecule having a nucleotide sequence that occurs in nature (*e.g.*,
20 encodes a natural protein). In one embodiment, the nucleic acid encodes a natural *C. glutamicum* SMP protein.

In addition to naturally-occurring variants of the SMP sequence that may exist in the population, one of ordinary skill in the art will further appreciate that changes can be introduced by mutation into a nucleotide sequence of the invention, thereby leading to
25 changes in the amino acid sequence of the encoded SMP protein, without altering the functional ability of the SMP protein. For example, nucleotide substitutions leading to amino acid substitutions at "non-essential" amino acid residues can be made in a nucleotide sequence of the invention. A "non-essential" amino acid residue is a residue that can be altered from the wild-type sequence of one of the SMP proteins (*e.g.*, an
30 even-numbered SEQ ID NO: of the Sequence Listing) without altering the activity of said SMP protein, whereas an "essential" amino acid residue is required for SMP protein activity. Other amino acid residues, however, (*e.g.*, those that are not conserved or only

semi-conserved in the domain having SMP activity) may not be essential for activity and thus are likely to be amenable to alteration without altering SMP activity.

Accordingly, another aspect of the invention pertains to nucleic acid molecules encoding SMP proteins that contain changes in amino acid residues that are not essential for SMP activity. Such SMP proteins differ in amino acid sequence from a sequence of an even-numbered SEQ ID NO: of the Sequence Listing yet retain at least one of the SMP activities described herein. In one embodiment, the isolated nucleic acid molecule comprises a nucleotide sequence encoding a protein, wherein the protein comprises an amino acid sequence at least about 50% homologous to an amino acid sequence of the invention and is capable of participate in the metabolism of carbon compounds such as sugars, or in the biosynthesis of high-energy compounds in *C. glutamicum*, or has one or more activities set forth in Table 1. Preferably, the protein encoded by the nucleic acid molecule is at least about 50-60% homologous to the amino acid sequence of one of the odd-numbered SEQ ID NOs of the Sequence Listing, more preferably at least about 60-70% homologous to one of these sequences, even more preferably at least about 70-80%, 80-90%, 90-95% homologous to one of these sequences, and most preferably at least about 96%, 97%, 98%, or 99% homologous to one of the amino acid sequences of the invention.

To determine the percent homology of two amino acid sequences (*e.g.*, one of the amino acid sequences of the invention and a mutant form thereof) or of two nucleic acids, the sequences are aligned for optimal comparison purposes (*e.g.*, gaps can be introduced in the sequence of one protein or nucleic acid for optimal alignment with the other protein or nucleic acid). The amino acid residues or nucleotides at corresponding amino acid positions or nucleotide positions are then compared. When a position in one sequence (*e.g.*, one of the amino acid sequences the invention) is occupied by the same amino acid residue or nucleotide as the corresponding position in the other sequence (*e.g.*, a mutant form of the amino acid sequence), then the molecules are homologous at that position (*i.e.*, as used herein amino acid or nucleic acid "homology" is equivalent to amino acid or nucleic acid "identity"). The percent homology between the two sequences is a function of the number of identical positions shared by the sequences (*i.e.*, % homology = # of identical positions/total # of positions x 100).

An isolated nucleic acid molecule encoding an SMP protein homologous to a protein sequence of the invention (*e.g.*, a sequence of an even-numbered SEQ ID NO: of the Sequence Listing) can be created by introducing one or more nucleotide substitutions, additions or deletions into a nucleotide sequence of the invention such that

5 one or more amino acid substitutions, additions or deletions are introduced into the encoded protein. Mutations can be introduced into one of the nucleotide sequences of the invention by standard techniques, such as site-directed mutagenesis and PCR-mediated mutagenesis. Preferably, conservative amino acid substitutions are made at one or more predicted non-essential amino acid residues. A "conservative amino acid

10 substitution" is one in which the amino acid residue is replaced with an amino acid residue having a similar side chain. Families of amino acid residues having similar side chains have been defined in the art. These families include amino acids with basic side chains (*e.g.*, lysine, arginine, histidine), acidic side chains (*e.g.*, aspartic acid, glutamic acid), uncharged polar side chains (*e.g.*, glycine, asparagine, glutamine, serine,

15 threonine, tyrosine, cysteine), nonpolar side chains (*e.g.*, alanine, valine, leucine, isoleucine, proline, phenylalanine, methionine, tryptophan), beta-branched side chains (*e.g.*, threonine, valine, isoleucine) and aromatic side chains (*e.g.*, tyrosine, phenylalanine, tryptophan, histidine). Thus, a predicted nonessential amino acid residue in an SMP protein is preferably replaced with another amino acid residue from the same

20 side chain family. Alternatively, in another embodiment, mutations can be introduced randomly along all or part of an SMP coding sequence, such as by saturation mutagenesis, and the resultant mutants can be screened for an SMP activity described herein to identify mutants that retain SMP activity. Following mutagenesis of the nucleotide sequence of one of the odd-numbered SEQ ID NOs of the Sequence Listing,

25 the encoded protein can be expressed recombinantly and the activity of the protein can be determined using, for example, assays described herein (see Example 8 of the Exemplification).

In addition to the nucleic acid molecules encoding SMP proteins described above, another aspect of the invention pertains to isolated nucleic acid molecules which

30 are antisense thereto. An "antisense" nucleic acid comprises a nucleotide sequence which is complementary to a "sense" nucleic acid encoding a protein, *e.g.*, complementary to the coding strand of a double-stranded DNA molecule or

complementary to an mRNA sequence. Accordingly, an antisense nucleic acid can hydrogen bond to a sense nucleic acid. The antisense nucleic acid can be complementary to an entire SMP coding strand, or to only a portion thereof. In one embodiment, an antisense nucleic acid molecule is antisense to a "coding region" of the coding strand of a nucleotide sequence encoding an SMP protein. The term "coding region" refers to the region of the nucleotide sequence comprising codons which are translated into amino acid residues (*e.g.*, the entire coding region of NO. 3 (RXA01626) comprises nucleotides 1 to 345). In another embodiment, the antisense nucleic acid molecule is antisense to a "noncoding region" of the coding strand of a nucleotide sequence encoding SMP. The term "noncoding region" refers to 5' and 3' sequences which flank the coding region that are not translated into amino acids (*i.e.*, also referred to as 5' and 3' untranslated regions).

Given the coding strand sequences encoding SMP disclosed herein (*e.g.*, the sequences set forth as odd-numbered SEQ ID NOs in the Sequence Listing), antisense nucleic acids of the invention can be designed according to the rules of Watson and Crick base pairing. The antisense nucleic acid molecule can be complementary to the entire coding region of SMP mRNA, but more preferably is an oligonucleotide which is antisense to only a portion of the coding or noncoding region of SMP mRNA. For example, the antisense oligonucleotide can be complementary to the region surrounding the translation start site of SMP mRNA. An antisense oligonucleotide can be, for example, about 5, 10, 15, 20, 25, 30, 35, 40, 45 or 50 nucleotides in length. An antisense nucleic acid of the invention can be constructed using chemical synthesis and enzymatic ligation reactions using procedures known in the art. For example, an antisense nucleic acid (*e.g.*, an antisense oligonucleotide) can be chemically synthesized using naturally occurring nucleotides or variously modified nucleotides designed to increase the biological stability of the molecules or to increase the physical stability of the duplex formed between the antisense and sense nucleic acids, *e.g.*, phosphorothioate derivatives and acridine substituted nucleotides can be used. Examples of modified nucleotides which can be used to generate the antisense nucleic acid include 5-fluorouracil, 5-bromouracil, 5-chlorouracil, 5-iodouracil, hypoxanthine, xanthine, 4-acetylcytosine, 5-(carboxyhydroxymethyl) uracil, 5-carboxymethylaminomethyl-2-thiouridine, 5-carboxymethylaminomethyluracil, dihydrouracil, beta-D-

galactosylqueosine, inosine, N6-isopentenyladenine, 1-methylguanine, 1-methylinosine, 2,2-dimethylguanine, 2-methyladenine, 2-methylguanine, 3-methylcytosine, 5-methylcytosine, N6-adenine, 7-methylguanine, 5-methylaminomethyluracil, 5-methoxyaminomethyl-2-thiouracil, beta-D-mannosylqueosine, 5'-methoxycarboxymethyluracil, 5-methoxyuracil, 2-methylthio-N6-isopentenyladenine, uracil-5-oxyacetic acid (v), wybutoxosine, pseudouracil, queosine, 2-thiocytosine, 5-methyl-2-thiouracil, 2-thiouracil, 4-thiouracil, 5-methyluracil, uracil-5-oxyacetic acid methylester, uracil-5-oxyacetic acid (v), 5-methyl-2-thiouracil, 3-(3-amino-3-N-2-carboxypropyl) uracil, (acp3)w, and 2,6-diaminopurine. Alternatively, the antisense nucleic acid can be produced biologically using an expression vector into which a nucleic acid has been subcloned in an antisense orientation (*i.e.*, RNA transcribed from the inserted nucleic acid will be of an antisense orientation to a target nucleic acid of interest, described further in the following subsection).

The antisense nucleic acid molecules of the invention are typically administered to a cell or generated *in situ* such that they hybridize with or bind to cellular mRNA and/or genomic DNA encoding an SMP protein to thereby inhibit expression of the protein, *e.g.*, by inhibiting transcription and/or translation. The hybridization can be by conventional nucleotide complementarity to form a stable duplex, or, for example, in the case of an antisense nucleic acid molecule which binds to DNA duplexes, through specific interactions in the major groove of the double helix. The antisense molecule can be modified such that it specifically binds to a receptor or an antigen expressed on a selected cell surface, *e.g.*, by linking the antisense nucleic acid molecule to a peptide or an antibody which binds to a cell surface receptor or antigen. The antisense nucleic acid molecule can also be delivered to cells using the vectors described herein. To achieve sufficient intracellular concentrations of the antisense molecules, vector constructs in which the antisense nucleic acid molecule is placed under the control of a strong prokaryotic, viral, or eukaryotic promoter are preferred.

In yet another embodiment, the antisense nucleic acid molecule of the invention is an α -anomeric nucleic acid molecule. An α -anomeric nucleic acid molecule forms specific double-stranded hybrids with complementary RNA in which, contrary to the usual β -units, the strands run parallel to each other (Gaultier *et al.* (1987) *Nucleic Acids. Res.* 15:6625-6641). The antisense nucleic acid molecule can also comprise a 2'-o-

methylribonucleotide (Inoue *et al.* (1987) *Nucleic Acids Res.* 15:6131-6148) or a chimeric RNA-DNA analogue (Inoue *et al.* (1987) *FEBS Lett.* 215:327-330).

In still another embodiment, an antisense nucleic acid of the invention is a ribozyme. Ribozymes are catalytic RNA molecules with ribonuclease activity which are
5 capable of cleaving a single-stranded nucleic acid, such as an mRNA, to which they have a complementary region. Thus, ribozymes (*e.g.*, hammerhead ribozymes (described in Haselhoff and Gerlach (1988) *Nature* 334:585-591)) can be used to catalytically cleave SMP mRNA transcripts to thereby inhibit translation of SMP mRNA. A ribozyme having specificity for an SMP-encoding nucleic acid can be
10 designed based upon the nucleotide sequence of an SMP cDNA disclosed herein (*i.e.*, SEQ ID NO. 3 (RXA01626)). For example, a derivative of a *Tetrahymena* L-19 IVS RNA can be constructed in which the nucleotide sequence of the active site is complementary to the nucleotide sequence to be cleaved in an SMP-encoding mRNA. See, *e.g.*, Cech *et al.* U.S. Patent No. 4,987,071 and Cech *et al.* U.S. Patent No.
15 5,116,742. Alternatively, SMP mRNA can be used to select a catalytic RNA having a specific ribonuclease activity from a pool of RNA molecules. See, *e.g.*, Bartel, D. and Szostak, J.W. (1993) *Science* 261:1411-1418.

Alternatively, SMP gene expression can be inhibited by targeting nucleotide sequences complementary to the regulatory region of an SMP nucleotide sequence (*e.g.*,
20 an SMP promoter and/or enhancers) to form triple helical structures that prevent transcription of an SMP gene in target cells. See generally, Helene, C. (1991) *Anticancer Drug Des.* 6(6):569-84; Helene, C. *et al.* (1992) *Ann. N.Y. Acad. Sci.* 660:27-36; and Maher, L.J. (1992) *Bioassays* 14(12):807-15.

25 B. Recombinant Expression Vectors and Host Cells

Another aspect of the invention pertains to vectors, preferably expression vectors, containing a nucleic acid encoding an SMP protein (or a portion thereof). As used herein, the term "vector" refers to a nucleic acid molecule capable of transporting another nucleic acid to which it has been linked. One type of vector is a "plasmid",
30 which refers to a circular double stranded DNA loop into which additional DNA segments can be ligated. Another type of vector is a viral vector, wherein additional DNA segments can be ligated into the viral genome. Certain vectors are capable of

- 40 -

autonomous replication in a host cell into which they are introduced (*e.g.*, bacterial vectors having a bacterial origin of replication and episomal mammalian vectors). Other vectors (*e.g.*, non-episomal mammalian vectors) are integrated into the genome of a host cell upon introduction into the host cell, and thereby are replicated along with the host genome. Moreover, certain vectors are capable of directing the expression of genes to which they are operatively linked. Such vectors are referred to herein as "expression vectors". In general, expression vectors of utility in recombinant DNA techniques are often in the form of plasmids. In the present specification, "plasmid" and "vector" can be used interchangeably as the plasmid is the most commonly used form of vector.

5 However, the invention is intended to include such other forms of expression vectors, such as viral vectors (*e.g.*, replication defective retroviruses, adenoviruses and adeno-associated viruses), which serve equivalent functions.

The recombinant expression vectors of the invention comprise a nucleic acid of the invention in a form suitable for expression of the nucleic acid in a host cell, which means that the recombinant expression vectors include one or more regulatory sequences, selected on the basis of the host cells to be used for expression, which is operatively linked to the nucleic acid sequence to be expressed. Within a recombinant expression vector, "operably linked" is intended to mean that the nucleotide sequence of interest is linked to the regulatory sequence(s) in a manner which allows for expression of the nucleotide sequence (*e.g.*, in an *in vitro* transcription/translation system or in a host cell when the vector is introduced into the host cell). The term "regulatory sequence" is intended to include promoters, enhancers and other expression control elements (*e.g.*, polyadenylation signals). Such regulatory sequences are described, for example, in Goeddel; *Gene Expression Technology: Methods in Enzymology* 185, Academic Press, San Diego, CA (1990). Regulatory sequences include those which direct constitutive expression of a nucleotide sequence in many types of host cell and those which direct expression of the nucleotide sequence only in certain host cells.

15 Preferred regulatory sequences are, for example, promoters such as *cos*-, *tac*-, *trp*-, *tet*-, *trp-tet*-, *lpp*-, *lac*-, *lpp-lac*-, *lacI^q*-, T7-, T5-, T3-, *gal*-, *trc*-, *ara*-, SP6-, *amy*, SPO2, λ -P_R- or λ P_L, which are used preferably in bacteria. Additional regulatory sequences are, for example, promoters from yeasts and fungi, such as ADC1, MF α , AC, P-60, CYC1, GAPDH, TEF, *rp28*, ADH, promoters from plants such as CaMV/35S, SSU, OCS, *lib4*,

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usp, STLS1, B33, nos or ubiquitin- or phaseolin-promoters. It is also possible to use artificial promoters. It will be appreciated by those of ordinary skill in the art that the design of the expression vector can depend on such factors as the choice of the host cell to be transformed, the level of expression of protein desired, etc. The expression vectors
5 of the invention can be introduced into host cells to thereby produce proteins or peptides, including fusion proteins or peptides, encoded by nucleic acids as described herein (*e.g.*, SMP proteins, mutant forms of SMP proteins, fusion proteins, etc.).

The recombinant expression vectors of the invention can be designed for expression of SMP proteins in prokaryotic or eukaryotic cells. For example, SMP genes
10 can be expressed in bacterial cells such as *C. glutamicum*, insect cells (using baculovirus expression vectors), yeast and other fungal cells (see Romanos, M.A. *et al.* (1992) "Foreign gene expression in yeast: a review", *Yeast* 8: 423-488; van den Hondel, C.A.M.J.J. *et al.* (1991) "Heterologous gene expression in filamentous fungi" in: More Gene Manipulations in Fungi, J.W. Bennet & L.L. Lasure, eds., p. 396-428: Academic
15 Press: San Diego; and van den Hondel, C.A.M.J.J. & Punt, P.J. (1991) "Gene transfer systems and vector development for filamentous fungi, in: Applied Molecular Genetics of Fungi, Peberdy, J.F. *et al.*, eds., p. 1-28, Cambridge University Press: Cambridge), algae and multicellular plant cells (see Schmidt, R. and Willmitzer, L. (1988) High efficiency *Agrobacterium tumefaciens* -mediated transformation of *Arabidopsis*
20 *thaliana* leaf and cotyledon explants" *Plant Cell Rep*: 583-586), or mammalian cells. Suitable host cells are discussed further in Goeddel, *Gene Expression Technology: Methods in Enzymology* 185, Academic Press, San Diego, CA (1990). Alternatively, the recombinant expression vector can be transcribed and translated *in vitro*, for example using T7 promoter regulatory sequences and T7 polymerase.

25 Expression of proteins in prokaryotes is most often carried out with vectors containing constitutive or inducible promoters directing the expression of either fusion or non-fusion proteins. Fusion vectors add a number of amino acids to a protein encoded therein, usually to the amino terminus of the recombinant protein but also to the C-terminus or fused within suitable regions in the proteins. Such fusion vectors
30 typically serve three purposes: 1) to increase expression of recombinant protein; 2) to increase the solubility of the recombinant protein; and 3) to aid in the purification of the recombinant protein by acting as a ligand in affinity purification. Often, in fusion

expression vectors, a proteolytic cleavage site is introduced at the junction of the fusion moiety and the recombinant protein to enable separation of the recombinant protein from the fusion moiety subsequent to purification of the fusion protein. Such enzymes, and their cognate recognition sequences, include Factor Xa, thrombin and enterokinase.

- 5 Typical fusion expression vectors include pGEX (Pharmacia Biotech Inc; Smith, D.B. and Johnson, K.S. (1988) *Gene* 67:31-40), pMAL (New England Biolabs, Beverly, MA) and pRIT5 (Pharmacia, Piscataway, NJ) which fuse glutathione S-transferase (GST), maltose E binding protein, or protein A, respectively, to the target recombinant protein. In one embodiment, the coding sequence of the SMP protein is cloned into a
- 10 pGEX expression vector to create a vector encoding a fusion protein comprising, from the N-terminus to the C-terminus, GST-thrombin cleavage site-X protein. The fusion protein can be purified by affinity chromatography using glutathione-agarose resin. Recombinant SMP protein unfused to GST can be recovered by cleavage of the fusion protein with thrombin.
- 15 Examples of suitable inducible non-fusion *E. coli* expression vectors include pTrc (Amann *et al.*, (1988) *Gene* 69:301-315), pLG338, pACYC184, pBR322, pUC18, pUC19, pKC30, pRep4, pHS1, pHS2, pPLc236, pMBL24, pLG200, pUR290, pIN-III113-B1, λ gt11, pBdCl, and pET 11d (Studier *et al.*, *Gene Expression Technology: Methods in Enzymology* 185, Academic Press, San Diego, California (1990) 60-89; and
- 20 Pouwels *et al.*, eds. (1985) *Cloning Vectors*. Elsevier: New York ISBN 0 444 904018). Target gene expression from the pTrc vector relies on host RNA polymerase transcription from a hybrid trp-lac fusion promoter. Target gene expression from the pET 11d vector relies on transcription from a T7 gn10-lac fusion promoter mediated by a coexpressed viral RNA polymerase (T7 gn1). This viral polymerase is supplied by
- 25 host strains BL21(DE3) or HMS174(DE3) from a resident λ prophage harboring a T7 gn1 gene under the transcriptional control of the lacUV 5 promoter. For transformation of other varieties of bacteria, appropriate vectors may be selected. For example, the plasmids pIJ101, pIJ364, pIJ702 and pIJ361 are known to be useful in transforming *Streptomyces*, while plasmids pUB110, pC194, or pBD214 are suited for transformation
- 30 of *Bacillus* species. Several plasmids of use in the transfer of genetic information into *Corynebacterium* include pHM1519, pBL1, pSA77, or pAJ667 (Pouwels *et al.*, eds. (1985) *Cloning Vectors*. Elsevier: New York ISBN 0 444 904018).

One strategy to maximize recombinant protein expression is to express the protein in a host bacteria with an impaired capacity to proteolytically cleave the recombinant protein (Gottesman, S., *Gene Expression Technology: Methods in Enzymology* 185, Academic Press, San Diego, California (1990) 119-128). Another
5 strategy is to alter the nucleic acid sequence of the nucleic acid to be inserted into an expression vector so that the individual codons for each amino acid are those preferentially utilized in the bacterium chosen for expression, such as *C. glutamicum* (Wada *et al.* (1992) *Nucleic Acids Res.* 20:2111-2118). Such alteration of nucleic acid sequences of the invention can be carried out by standard DNA synthesis techniques.

10 In another embodiment, the SMP protein expression vector is a yeast expression vector. Examples of vectors for expression in yeast *S. cerevisiae* include pYepSec1 (Baldari, *et al.*, (1987) *Embo J.* 6:229-234), 2 μ , pAG-1, Yep6, Yep13, pEMBLYe23, pMFa (Kurjan and Herskowitz, (1982) *Cell* 30:933-943), pJRY88 (Schultz *et al.*, (1987) *Gene* 54:113-123), and pYES2 (Invitrogen Corporation, San Diego, CA). Vectors and
15 methods for the construction of vectors appropriate for use in other fungi, such as the filamentous fungi, include those detailed in: van den Hondel, C.A.M.J.J. & Punt, P.J. (1991) "Gene transfer systems and vector development for filamentous fungi, in: Applied Molecular Genetics of Fungi, J.F. Peberdy, *et al.*, eds., p. 1-28, Cambridge University Press: Cambridge, and Pouwels *et al.*, eds. (1985) *Cloning Vectors*. Elsevier:
20 New York (IBSN 0 444 904018).

Alternatively, the SMP proteins of the invention can be expressed in insect cells using baculovirus expression vectors. Baculovirus vectors available for expression of proteins in cultured insect cells (*e.g.*, Sf 9 cells) include the pAc series (Smith *et al.* (1983) *Mol. Cell Biol.* 3:2156-2165) and the pVL series (Lucklow and Summers (1989)
25 *Virology* 170:31-39).

In another embodiment, the SMP proteins of the invention may be expressed in unicellular plant cells (such as algae) or in plant cells from higher plants (*e.g.*, the spermatophytes, such as crop plants). Examples of plant expression vectors include those detailed in: Becker, D., Kemper, E., Schell, J. and Masterson, R. (1992) "New
30 plant binary vectors with selectable markers located proximal to the left border", *Plant Mol. Biol.* 20: 1195-1197; and Bevan, M.W. (1984) "Binary *Agrobacterium* vectors for plant transformation", *Nucl. Acid. Res.* 12: 8711-8721, and include pLGV23, pGHIac+,

pBIN19, pAK2004, and pDH51 (Pouwels *et al.*, eds. (1985) Cloning Vectors. Elsevier: New York ISBN 0 444 904018).

In yet another embodiment, a nucleic acid of the invention is expressed in mammalian cells using a mammalian expression vector. Examples of mammalian expression vectors include pCDM8 (Seed, B. (1987) *Nature* 329:840) and pMT2PC (Kaufman *et al.* (1987) *EMBO J.* 6:187-195). When used in mammalian cells, the expression vector's control functions are often provided by viral regulatory elements. For example, commonly used promoters are derived from polyoma, Adenovirus 2, cytomegalovirus and Simian Virus 40. For other suitable expression systems for both prokaryotic and eukaryotic cells see chapters 16 and 17 of Sambrook, J., Fritsch, E. F., and Maniatis, T. *Molecular Cloning: A Laboratory Manual. 2nd, ed., Cold Spring Harbor Laboratory, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY, 1989.*

In another embodiment, the recombinant mammalian expression vector is capable of directing expression of the nucleic acid preferentially in a particular cell type (*e.g.*, tissue-specific regulatory elements are used to express the nucleic acid). Tissue-specific regulatory elements are known in the art. Non-limiting examples of suitable tissue-specific promoters include the albumin promoter (liver-specific; Pinkert *et al.* (1987) *Genes Dev.* 1:268-277), lymphoid-specific promoters (Calame and Eaton (1988) *Adv. Immunol.* 43:235-275), in particular promoters of T cell receptors (Winoto and Baltimore (1989) *EMBO J.* 8:729-733) and immunoglobulins (Banerji *et al.* (1983) *Cell* 33:729-740; Queen and Baltimore (1983) *Cell* 33:741-748), neuron-specific promoters (*e.g.*, the neurofilament promoter; Byrne and Ruddle (1989) *PNAS* 86:5473-5477), pancreas-specific promoters (Edlund *et al.* (1985) *Science* 230:912-916), and mammary gland-specific promoters (*e.g.*, milk whey promoter; U.S. Patent No. 4,873,316 and European Application Publication No. 264,166). Developmentally-regulated promoters are also encompassed, for example the murine hox promoters (Kessel and Gruss (1990) *Science* 249:374-379) and the α -fetoprotein promoter (Campes and Tilghman (1989) *Genes Dev.* 3:537-546).

The invention further provides a recombinant expression vector comprising a DNA molecule of the invention cloned into the expression vector in an antisense orientation. That is, the DNA molecule is operatively linked to a regulatory sequence in

a manner which allows for expression (by transcription of the DNA molecule) of an RNA molecule which is antisense to SMP mRNA. Regulatory sequences operatively linked to a nucleic acid cloned in the antisense orientation can be chosen which direct the continuous expression of the antisense RNA molecule in a variety of cell types, for instance viral promoters and/or enhancers, or regulatory sequences can be chosen which direct constitutive, tissue specific or cell type specific expression of antisense RNA. The antisense expression vector can be in the form of a recombinant plasmid, phagemid or attenuated virus in which antisense nucleic acids are produced under the control of a high efficiency regulatory region, the activity of which can be determined by the cell type into which the vector is introduced. For a discussion of the regulation of gene expression using antisense genes see Weintraub, H. *et al.*, Antisense RNA as a molecular tool for genetic analysis, *Reviews - Trends in Genetics*, Vol. 1(1) 1986.

Another aspect of the invention pertains to host cells into which a recombinant expression vector of the invention has been introduced. The terms "host cell" and "recombinant host cell" are used interchangeably herein. It is understood that such terms refer not only to the particular subject cell but to the progeny or potential progeny of such a cell. Because certain modifications may occur in succeeding generations due to either mutation or environmental influences, such progeny may not, in fact, be identical to the parent cell, but are still included within the scope of the term as used herein.

A host cell can be any prokaryotic or eukaryotic cell. For example, an SMP protein can be expressed in bacterial cells such as *C. glutamicum*, insect cells, yeast or mammalian cells (such as Chinese hamster ovary cells (CHO) or COS cells). Other suitable host cells are known to one of ordinary skill in the art. Microorganisms related to *Corynebacterium glutamicum* which may be conveniently used as host cells for the nucleic acid and protein molecules of the invention are set forth in Table 3.

Vector DNA can be introduced into prokaryotic or eukaryotic cells via conventional transformation or transfection techniques. As used herein, the terms "transformation" and "transfection", "conjugation" and "transduction" are intended to refer to a variety of art-recognized techniques for introducing foreign nucleic acid (*e.g.*, linear DNA or RNA (*e.g.*, a linearized vector or a gene construct alone without a vector) or nucleic acid in the form of a vector (*e.g.*, a plasmid, phage, phasmid, phagemid,

transposon or other DNA) into a host cell, including calcium phosphate or calcium chloride co-precipitation, DEAE-dextran-mediated transfection, lipofection, natural competence, chemical-mediated transfer, or electroporation. Suitable methods for transforming or transfecting host cells can be found in Sambrook, *et al.* (*Molecular Cloning: A Laboratory Manual*. 2nd, ed., Cold Spring Harbor Laboratory, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY, 1989), and other laboratory manuals.

For stable transfection of mammalian cells, it is known that, depending upon the expression vector and transfection technique used, only a small fraction of cells may integrate the foreign DNA into their genome. In order to identify and select these integrants, a gene that encodes a selectable marker (*e.g.*, resistance to antibiotics) is generally introduced into the host cells along with the gene of interest. Preferred selectable markers include those which confer resistance to drugs, such as G418, hygromycin and methotrexate. Nucleic acid encoding a selectable marker can be introduced into a host cell on the same vector as that encoding an SMP protein or can be introduced on a separate vector. Cells stably transfected with the introduced nucleic acid can be identified by, for example, drug selection (*e.g.*, cells that have incorporated the selectable marker gene will survive, while the other cells die).

To create a homologous recombinant microorganism, a vector is prepared which contains at least a portion of an SMP gene into which a deletion, addition or substitution has been introduced to thereby alter, *e.g.*, functionally disrupt, the SMP gene. Preferably, this SMP gene is a *Corynebacterium glutamicum* SMP gene, but it can be a homologue from a related bacterium or even from a mammalian, yeast, or insect source. In a preferred embodiment, the vector is designed such that, upon homologous recombination, the endogenous SMP gene is functionally disrupted (*i.e.*, no longer encodes a functional protein; also referred to as a "knock out" vector). Alternatively, the vector can be designed such that, upon homologous recombination, the endogenous SMP gene is mutated or otherwise altered but still encodes functional protein (*e.g.*, the upstream regulatory region can be altered to thereby alter the expression of the endogenous SMP protein). In the homologous recombination vector, the altered portion of the SMP gene is flanked at its 5' and 3' ends by additional nucleic acid of the SMP gene to allow for homologous recombination to occur between the exogenous SMP gene carried by the vector and an endogenous SMP gene in a microorganism. The additional

flanking SMP nucleic acid is of sufficient length for successful homologous recombination with the endogenous gene. Typically, several kilobases of flanking DNA (both at the 5' and 3' ends) are included in the vector (see *e.g.*, Thomas, K.R., and Capecchi, M.R. (1987) Cell 51: 503 for a description of homologous recombination
5 vectors). The vector is introduced into a microorganism (*e.g.*, by electroporation) and cells in which the introduced SMP gene has homologously recombined with the endogenous SMP gene are selected, using art-known techniques.

In another embodiment, recombinant microorganisms can be produced which contain selected systems which allow for regulated expression of the introduced gene.
10 For example, inclusion of an SMP gene on a vector placing it under control of the lac operon permits expression of the SMP gene only in the presence of IPTG. Such regulatory systems are well known in the art.

In another embodiment, an endogenous SMP gene in a host cell is disrupted (*e.g.*, by homologous recombination or other genetic means known in the art) such that
15 expression of its protein product does not occur. In another embodiment, an endogenous or introduced SMP gene in a host cell has been altered by one or more point mutations, deletions, or inversions, but still encodes a functional SMP protein. In still another embodiment, one or more of the regulatory regions (*e.g.*, a promoter, repressor, or inducer) of an SMP gene in a microorganism has been altered (*e.g.*, by deletion,
20 truncation, inversion, or point mutation) such that the expression of the SMP gene is modulated. One of ordinary skill in the art will appreciate that host cells containing more than one of the described SMP gene and protein modifications may be readily produced using the methods of the invention, and are meant to be included in the present invention.

25 A host cell of the invention, such as a prokaryotic or eukaryotic host cell in culture, can be used to produce (*i.e.*, express) an SMP protein. Accordingly, the invention further provides methods for producing SMP proteins using the host cells of the invention. In one embodiment, the method comprises culturing the host cell of invention (into which a recombinant expression vector encoding an SMP protein has
30 been introduced, or into which genome has been introduced a gene encoding a wild-type or altered SMP protein) in a suitable medium until SMP protein is produced. In another

embodiment, the method further comprises isolating SMP proteins from the medium or the host cell.

C. Isolated SMP Proteins

5 Another aspect of the invention pertains to isolated SMP proteins, and biologically active portions thereof. An "isolated" or "purified" protein or biologically active portion thereof is substantially free of cellular material when produced by recombinant DNA techniques, or chemical precursors or other chemicals when chemically synthesized. The language "substantially free of cellular material" includes
10 preparations of SMP protein in which the protein is separated from cellular components of the cells in which it is naturally or recombinantly produced. In one embodiment, the language "substantially free of cellular material" includes preparations of SMP protein having less than about 30% (by dry weight) of non-SMP protein (also referred to herein as a "contaminating protein"), more preferably less than about 20% of non-SMP protein,
15 still more preferably less than about 10% of non-SMP protein, and most preferably less than about 5% non-SMP protein. When the SMP protein or biologically active portion thereof is recombinantly produced, it is also preferably substantially free of culture medium, *i.e.*, culture medium represents less than about 20%, more preferably less than about 10%, and most preferably less than about 5% of the volume of the protein
20 preparation. The language "substantially free of chemical precursors or other chemicals" includes preparations of SMP protein in which the protein is separated from chemical precursors or other chemicals which are involved in the synthesis of the protein. In one embodiment, the language "substantially free of chemical precursors or other chemicals" includes preparations of SMP protein having less than about 30% (by
25 dry weight) of chemical precursors or non-SMP chemicals, more preferably less than about 20% chemical precursors or non-SMP chemicals, still more preferably less than about 10% chemical precursors or non-SMP chemicals, and most preferably less than about 5% chemical precursors or non-SMP chemicals. In preferred embodiments, isolated proteins or biologically active portions thereof lack contaminating proteins from
30 the same organism from which the SMP protein is derived. Typically, such proteins are produced by recombinant expression of, for example, a *C. glutamicum* SMP protein in a microorganism such as *C. glutamicum*.

An isolated SMP protein or a portion thereof of the invention can participate in the metabolism of carbon compounds such as sugars, or in the production of energy compounds (*e.g.*, by oxidative phosphorylation) utilized to drive unfavorable metabolic pathways, or has one or more of the activities set forth in Table 1. In preferred

5 embodiments, the protein or portion thereof comprises an amino acid sequence which is sufficiently homologous to an amino acid sequence of the invention (*e.g.*, a sequence of an even-numbered SEQ ID NO: of the Sequence Listing) such that the protein or portion thereof maintains the ability to perform a function involved in the metabolism of carbon compounds such as sugars or in the generation of energy molecules by processes such as

10 oxidative phosphorylation in *Corynebacterium glutamicum*. The portion of the protein is preferably a biologically active portion as described herein. In another preferred embodiment, an SMP protein of the invention has an amino acid sequence set forth as an even-numbered SEQ ID NO: of the Sequence Listing. In yet another preferred embodiment, the SMP protein has an amino acid sequence which is encoded by a

15 nucleotide sequence which hybridizes, *e.g.*, hybridizes under stringent conditions, to a nucleotide sequence of the invention (*e.g.*, a sequence of an odd-numbered SEQ ID NO: of the Sequence Listing). In still another preferred embodiment, the SMP protein has an amino acid sequence which is encoded by a nucleotide sequence that is at least about 50%, 51%, 52%, 53%, 54%, 55%, 56%, 57%, 58%, 59%, or 60%, preferably at least

20 about 61%, 62%, 63%, 64%, 65%, 66%, 67%, 68%, 69%, or 70%, more preferably at least about 71%, 72%, 73%, 74%, 75%, 76%, 77%, 78%, 79%, or 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, or 90%, or 91%, 92%, 93%, 94%, and even more preferably at least about 95%, 96%, 97%, 98%, 99% or more homologous to one of the nucleic acid sequences of the invention, or a portion thereof. Ranges and identity

25 values intermediate to the above-recited values, (*e.g.*, 70-90% identical or 80-95% identical) are also intended to be encompassed by the present invention. For example, ranges of identity values using a combination of any of the above values recited as upper and/or lower limits are intended to be included. The preferred SMP proteins of the present invention also preferably possess at least one of the SMP activities described

30 herein. For example, a preferred SMP protein of the present invention includes an amino acid sequence encoded by a nucleotide sequence which hybridizes, *e.g.*, hybridizes under stringent conditions, to a nucleotide sequence of the invention, and

which can perform a function involved in the metabolism of carbon compounds such as sugars or in the generation of energy molecules (*e.g.*, ATP) by processes such as oxidative phosphorylation in *Corynebacterium glutamicum*, or which has one or more of the activities set forth in Table 1.

- 5 In other embodiments, the SMP protein is substantially homologous to an amino acid sequence of the invention (*e.g.*, a sequence of an even-numbered SEQ ID NO: of the Sequence Listing) and retains the functional activity of the protein of one of the amino acid sequences of the invention yet differs in amino acid sequence due to natural variation or mutagenesis, as described in detail in subsection I above. Accordingly, in
- 10 another embodiment, the SMP protein is a protein which comprises an amino acid sequence which is at least about 50%, 51%, 52%, 53%, 54%, 55%, 56%, 57%, 58%, 59%, or 60%, preferably at least about 61%, 62%, 63%, 64%, 65%, 66%, 67%, 68%, 69%, or 70%, more preferably at least about 71%, 72%, 73%, 74%, 75%, 76%, 77%, 78%, 79%, or 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, or 90%, or
- 15 91%, 92%, 93%, 94%, and even more preferably at least about 95%, 96%, 97%, 98%, 99% or more homologous to an entire amino acid sequence of the invention and which has at least one of the SMP activities described herein. Ranges and identity values intermediate to the above-recited values, (*e.g.*, 70-90% identical or 80-95% identical) are also intended to be encompassed by the present invention. For example, ranges of
- 20 identity values using a combination of any of the above values recited as upper and/or lower limits are intended to be included. In another embodiment, the invention pertains to a full length *C. glutamicum* protein which is substantially homologous to an entire amino acid sequence of the invention.

- Biologically active portions of an SMP protein include peptides comprising
- 25 amino acid sequences derived from the amino acid sequence of an SMP protein, *e.g.*, an amino acid sequence of an even-numbered SEQ ID NO: of the Sequence Listing or the amino acid sequence of a protein homologous to an SMP protein, which include fewer amino acids than a full length SMP protein or the full length protein which is homologous to an SMP protein, and exhibit at least one activity of an SMP protein.
- 30 Typically, biologically active portions (peptides, *e.g.*, peptides which are, for example, 5, 10, 15, 20, 30, 35, 36, 37, 38, 39, 40, 50, 100 or more amino acids in length) comprise a domain or motif with at least one activity of an SMP protein. Moreover, other

biologically active portions, in which other regions of the protein are deleted, can be prepared by recombinant techniques and evaluated for one or more of the activities described herein. Preferably, the biologically active portions of an SMP protein include one or more selected domains/motifs or portions thereof having biological activity.

5 SMP proteins are preferably produced by recombinant DNA techniques. For example, a nucleic acid molecule encoding the protein is cloned into an expression vector (as described above), the expression vector is introduced into a host cell (as described above) and the SMP protein is expressed in the host cell. The SMP protein can then be isolated from the cells by an appropriate purification scheme using standard
10 protein purification techniques. Alternative to recombinant expression, an SMP protein, polypeptide, or peptide can be synthesized chemically using standard peptide synthesis techniques. Moreover, native SMP protein can be isolated from cells (*e.g.*, endothelial cells), for example using an anti-SMP antibody, which can be produced by standard techniques utilizing an SMP protein or fragment thereof of this invention.

15 The invention also provides SMP chimeric or fusion proteins. As used herein, an SMP "chimeric protein" or "fusion protein" comprises an SMP polypeptide operatively linked to a non-SMP polypeptide. An "SMP polypeptide" refers to a polypeptide having an amino acid sequence corresponding to an SMP protein, whereas a "non-SMP polypeptide" refers to a polypeptide having an amino acid sequence corresponding to a
20 protein which is not substantially homologous to the SMP protein, *e.g.*, a protein which is different from the SMP protein and which is derived from the same or a different organism. Within the fusion protein, the term "operatively linked" is intended to indicate that the SMP polypeptide and the non-SMP polypeptide are fused in-frame to each other. The non-SMP polypeptide can be fused to the N-terminus or C-terminus of
25 the SMP polypeptide. For example, in one embodiment the fusion protein is a GST-SMP fusion protein in which the SMP sequences are fused to the C-terminus of the GST sequences. Such fusion proteins can facilitate the purification of recombinant SMP proteins. In another embodiment, the fusion protein is an SMP protein containing a heterologous signal sequence at its N-terminus. In certain host cells (*e.g.*, mammalian
30 host cells), expression and/or secretion of an SMP protein can be increased through use of a heterologous signal sequence.

Preferably, an SMP chimeric or fusion protein of the invention is produced by standard recombinant DNA techniques. For example, DNA fragments coding for the different polypeptide sequences are ligated together in-frame in accordance with conventional techniques, for example by employing blunt-ended or stagger-ended
5 termini for ligation, restriction enzyme digestion to provide for appropriate termini, filling-in of cohesive ends as appropriate, alkaline phosphatase treatment to avoid undesirable joining, and enzymatic ligation. In another embodiment, the fusion gene can be synthesized by conventional techniques including automated DNA synthesizers. Alternatively, PCR amplification of gene fragments can be carried out using anchor
10 primers which give rise to complementary overhangs between two consecutive gene fragments which can subsequently be annealed and reamplified to generate a chimeric gene sequence (see, for example, *Current Protocols in Molecular Biology*, Ausubel *et al.*, eds. John Wiley & Sons: 1992). Moreover, many expression vectors are commercially available that already encode a fusion moiety (*e.g.*, a GST polypeptide).
15 An SMP-encoding nucleic acid can be cloned into such an expression vector such that the fusion moiety is linked in-frame to the SMP protein.

Homologues of the SMP protein can be generated by mutagenesis, *e.g.*, discrete point mutation or truncation of the SMP protein. As used herein, the term "homologue" refers to a variant form of the SMP protein which acts as an agonist or antagonist of the
20 activity of the SMP protein. An agonist of the SMP protein can retain substantially the same, or a subset, of the biological activities of the SMP protein. An antagonist of the SMP protein can inhibit one or more of the activities of the naturally occurring form of the SMP protein, by, for example, competitively binding to a downstream or upstream member of the sugar molecule metabolic cascade or the energy-producing pathway
25 which includes the SMP protein.

In an alternative embodiment, homologues of the SMP protein can be identified by screening combinatorial libraries of mutants, *e.g.*, truncation mutants, of the SMP protein for SMP protein agonist or antagonist activity. In one embodiment, a variegated library of SMP variants is generated by combinatorial mutagenesis at the nucleic acid
30 level and is encoded by a variegated gene library. A variegated library of SMP variants can be produced by, for example, enzymatically ligating a mixture of synthetic oligonucleotides into gene sequences such that a degenerate set of potential SMP

sequences is expressible as individual polypeptides, or alternatively, as a set of larger fusion proteins (*e.g.*, for phage display) containing the set of SMP sequences therein. There are a variety of methods which can be used to produce libraries of potential SMP homologues from a degenerate oligonucleotide sequence. Chemical synthesis of a
5 degenerate gene sequence can be performed in an automatic DNA synthesizer, and the synthetic gene then ligated into an appropriate expression vector. Use of a degenerate set of genes allows for the provision, in one mixture, of all of the sequences encoding the desired set of potential SMP sequences. Methods for synthesizing degenerate oligonucleotides are known in the art (see, *e.g.*, Narang, S.A. (1983) *Tetrahedron* 39:3;
10 Itakura *et al.* (1984) *Annu. Rev. Biochem.* 53:323; Itakura *et al.* (1984) *Science* 198:1056; Ike *et al.* (1983) *Nucleic Acid Res.* 11:477.

In addition, libraries of fragments of the SMP protein coding can be used to generate a variegated population of SMP fragments for screening and subsequent selection of homologues of an SMP protein. In one embodiment, a library of coding
15 sequence fragments can be generated by treating a double stranded PCR fragment of an SMP coding sequence with a nuclease under conditions wherein nicking occurs only about once per molecule, denaturing the double stranded DNA, renaturing the DNA to form double stranded DNA which can include sense/antisense pairs from different nicked products, removing single stranded portions from reformed duplexes by
20 treatment with S1 nuclease, and ligating the resulting fragment library into an expression vector. By this method, an expression library can be derived which encodes N-terminal, C-terminal and internal fragments of various sizes of the SMP protein.

Several techniques are known in the art for screening gene products of combinatorial libraries made by point mutations or truncation, and for screening cDNA
25 libraries for gene products having a selected property. Such techniques are adaptable for rapid screening of the gene libraries generated by the combinatorial mutagenesis of SMP homologues. The most widely used techniques, which are amenable to high through-put analysis, for screening large gene libraries typically include cloning the gene library into replicable expression vectors, transforming appropriate cells with the resulting library of
30 vectors, and expressing the combinatorial genes under conditions in which detection of a desired activity facilitates isolation of the vector encoding the gene whose product was detected. Recursive ensemble mutagenesis (REM), a new technique which enhances the

frequency of functional mutants in the libraries, can be used in combination with the screening assays to identify SMP homologues (Arkin and Yourvan (1992) *PNAS* 89:7811-7815; Delgrave *et al.* (1993) *Protein Engineering* 6(3):327-331).

In another embodiment, cell based assays can be exploited to analyze a
5 variegated SMP library, using methods well known in the art.

D. Uses and Methods of the Invention

The nucleic acid molecules, proteins, protein homologues, fusion proteins, primers, vectors, and host cells described herein can be used in one or more of the
10 following methods: identification of *C. glutamicum* and related organisms; mapping of genomes of organisms related to *C. glutamicum*; identification and localization of *C. glutamicum* sequences of interest; evolutionary studies; determination of SMP protein regions required for function; modulation of an SMP protein activity; modulation of the metabolism of one or more sugars; modulation of high-energy molecule production in a
15 cell (*i.e.*, ATP, NADPH); and modulation of cellular production of a desired compound, such as a fine chemical.

The SMP nucleic acid molecules of the invention have a variety of uses. First, they may be used to identify an organism as being *Corynebacterium glutamicum* or a close relative thereof. Also, they may be used to identify the presence of *C. glutamicum*
20 or a relative thereof in a mixed population of microorganisms. The invention provides the nucleic acid sequences of a number of *C. glutamicum* genes; by probing the extracted genomic DNA of a culture of a unique or mixed population of microorganisms under stringent conditions with a probe spanning a region of a *C. glutamicum* gene which is unique to this organism, one can ascertain whether this organism is present.
25 Although *Corynebacterium glutamicum* itself is nonpathogenic, it is related to pathogenic species, such as *Corynebacterium diphtheriae*. *Corynebacterium diphtheriae* is the causative agent of diphtheria, a rapidly developing, acute, febrile infection which involves both local and systemic pathology. In this disease, a local lesion develops in the upper respiratory tract and involves necrotic injury to epithelial cells; the bacilli
30 secrete toxin which is disseminated through this lesion to distal susceptible tissues of the body. Degenerative changes brought about by the inhibition of protein synthesis in these tissues, which include heart, muscle, peripheral nerves, adrenals, kidneys, liver and

spleen, result in the systemic pathology of the disease. Diphtheria continues to have high incidence in many parts of the world, including Africa, Asia, Eastern Europe and the independent states of the former Soviet Union. An ongoing epidemic of diphtheria in the latter two regions has resulted in at least 5,000 deaths since 1990.

5 In one embodiment, the invention provides a method of identifying the presence or activity of *Corynebacterium diphtheriae* in a subject. This method includes detection of one or more of the nucleic acid or amino acid sequences of the invention (*e.g.*, the sequences set forth as odd-numbered or even-numbered SEQ ID NOs, respectively, in the Sequence Listing) in a subject, thereby detecting the presence or activity of
10 *Corynebacterium diphtheriae* in the subject. *C. glutamicum* and *C. diphtheriae* are related bacteria, and many of the nucleic acid and protein molecules in *C. glutamicum* are homologous to *C. diphtheriae* nucleic acid and protein molecules, and can therefore be used to detect *C. diphtheriae* in a subject.

 The nucleic acid and protein molecules of the invention may also serve as
15 markers for specific regions of the genome. This has utility not only in the mapping of the genome, but also for functional studies of *C. glutamicum* proteins. For example, to identify the region of the genome to which a particular *C. glutamicum* DNA-binding protein binds, the *C. glutamicum* genome could be digested, and the fragments incubated with the DNA-binding protein. Those which bind the protein may be additionally probed
20 with the nucleic acid molecules of the invention, preferably with readily detectable labels; binding of such a nucleic acid molecule to the genome fragment enables the localization of the fragment to the genome map of *C. glutamicum*, and, when performed multiple times with different enzymes, facilitates a rapid determination of the nucleic acid sequence to which the protein binds. Further, the nucleic acid molecules of the
25 invention may be sufficiently homologous to the sequences of related species such that these nucleic acid molecules may serve as markers for the construction of a genomic map in related bacteria, such as *Brevibacterium lactofermentum*.

 The SMP nucleic acid molecules of the invention are also useful for evolutionary and protein structural studies. The metabolic and energy-releasing processes in which
30 the molecules of the invention participate are utilized by a wide variety of prokaryotic and eukaryotic cells; by comparing the sequences of the nucleic acid molecules of the present invention to those encoding similar enzymes from other organisms, the

evolutionary relatedness of the organisms can be assessed. Similarly, such a comparison permits an assessment of which regions of the sequence are conserved and which are not, which may aid in determining those regions of the protein which are essential for the functioning of the enzyme. This type of determination is of value for protein
5 engineering studies and may give an indication of what the protein can tolerate in terms of mutagenesis without losing function.

Manipulation of the SMP nucleic acid molecules of the invention may result in the production of SMP proteins having functional differences from the wild-type SMP proteins. These proteins may be improved in efficiency or activity, may be present in
10 greater numbers in the cell than is usual, or may be decreased in efficiency or activity.

The invention provides methods for screening molecules which modulate the activity of an SMP protein, either by interacting with the protein itself or a substrate or binding partner of the SMP protein, or by modulating the transcription or translation of an SMP nucleic acid molecule of the invention. In such methods, a microorganism
15 expressing one or more SMP proteins of the invention is contacted with one or more test compounds, and the effect of each test compound on the activity or level of expression of the SMP protein is assessed.

There are a number of mechanisms by which the alteration of an SMP protein of the invention may directly affect the yield, production, and/or efficiency of production
20 of a fine chemical from a *C. glutamicum* strain incorporating such an altered protein. The degradation of high-energy carbon molecules such as sugars, and the conversion of compounds such as NADH and FADH₂ to more useful forms via oxidative phosphorylation results in a number of compounds which themselves may be desirable fine chemicals, such as pyruvate, ATP, NADH, and a number of intermediate sugar
25 compounds. Further, the energy molecules (such as ATP) and the reducing equivalents (such as NADH or NADPH) produced by these metabolic pathways are utilized in the cell to drive reactions which would otherwise be energetically unfavorable. Such unfavorable reactions include many biosynthetic pathways for fine chemicals. By improving the ability of the cell to utilize a particular sugar (*e.g.*, by manipulating the
30 genes encoding enzymes involved in the degradation and conversion of that sugar into energy for the cell), one may increase the amount of energy available to permit

unfavorable, yet desired metabolic reactions (e.g., the biosynthesis of a desired fine chemical) to occur.

Further, modulation of one or more pathways involved in sugar utilization permits optimization of the conversion of the energy contained within the sugar molecule to the production of one or more desired fine chemicals. For example, by reducing the activity of enzymes involved in, for example, gluconeogenesis, more ATP is available to drive desired biochemical reactions (such as fine chemical biosyntheses) in the cell. Also, the overall production of energy molecules from sugars may be modulated to ensure that the cell maximizes its energy production from each sugar molecule. Inefficient sugar utilization can lead to excess CO₂ production and excess energy, which may result in futile metabolic cycles. By improving the metabolism of sugar molecules, the cell should be able to function more efficiently, with a need for fewer carbon molecules. This should result in an improved fine chemical product: sugar molecule ratio (improved carbon yield), and permits a decrease in the amount of sugars that must be added to the medium in large-scale fermentor culture of such engineered *C. glutamicum*.

The mutagenesis of one or more SMP genes of the invention may also result in SMP proteins having altered activities which indirectly impact the production of one or more desired fine chemicals from *C. glutamicum*. For example, by increasing the efficiency of utilization of one or more sugars (such that the conversion of the sugar to useful energy molecules is improved), or by increasing the efficiency of conversion of reducing equivalents to useful energy molecules (e.g., by improving the efficiency of oxidative phosphorylation, or the activity of the ATP synthase), one can increase the amount of these high-energy compounds available to the cell to drive normally unfavorable metabolic processes. These processes include the construction of cell walls, transcription, translation, and the biosynthesis of compounds necessary for growth and division of the cells (e.g., nucleotides, amino acids, vitamins, lipids, etc.) (Lengeler *et al.* (1999) *Biology of Prokaryotes*, Thieme Verlag: Stuttgart, p. 88-109; 913-918; 875-899). By improving the growth and multiplication of these engineered cells, it is possible to increase both the viability of the cells in large-scale culture, and also to improve their rate of division, such that a relatively larger number of cells can survive in fermentor culture. The yield, production, or efficiency of production may be increased, at least

due to the presence of a greater number of viable cells, each producing the desired fine chemical.

Further, many of the degradation products produced during sugar metabolism are themselves utilized by the cell as precursors or intermediates for the production of a number of other useful compounds, some of which are fine chemicals. For example, pyruvate is converted into the amino acid alanine, and ribose-5-phosphate is an integral part of, for example, nucleotide molecules. The amount and efficiency of sugar metabolism, then, has a profound effect on the availability of these degradation products in the cell. By increasing the ability of the cell to process sugars, either in terms of efficiency of existing pathways (*e.g.*, by engineering enzymes involved in these pathways such that they are optimized in activity), or by increasing the availability of the enzymes involved in such pathways (*e.g.*, by increasing the number of these enzymes present in the cell), it is possible to also increase the availability of these degradation products in the cell, which should in turn increase the production of many different other desirable compounds in the cell (*e.g.*, fine chemicals).

The aforementioned mutagenesis strategies for SMP proteins to result in increased yields of a fine chemical from *C. glutamicum* are not meant to be limiting; variations on these strategies will be readily apparent to one of ordinary skill in the art. Using such strategies, and incorporating the mechanisms disclosed herein, the nucleic acid and protein molecules of the invention may be utilized to generate *C. glutamicum* or related strains of bacteria expressing mutated SMP nucleic acid and protein molecules such that the yield, production, and/or efficiency of production of a desired compound is improved. This desired compound may be any product produced by *C. glutamicum*, which includes the final products of biosynthesis pathways and intermediates of naturally-occurring metabolic pathways, as well as molecules which do not naturally occur in the metabolism of *C. glutamicum*, but which are produced by a *C. glutamicum* strain of the invention.

This invention is further illustrated by the following examples which should not be construed as limiting. The contents of all references, patent applications, patents, published patent applications, Tables, and the sequence listing cited throughout this application are hereby incorporated by reference.

TABLE 1: GENES IN THE APPLICATION

HMP:

<u>Nucleic Acid</u> <u>SEQ ID NO</u>	<u>Amino Acid</u> <u>SEQ ID NO</u>	<u>Identification Code</u>	<u>Contig.</u>	<u>NT Start</u>	<u>NT Stop</u>	<u>Function</u>
1	2	RXS02735	VW0074	14576	15280	6-Phosphoglucolactonase
3	4	RXA01626	GR00452	4270	3926	L-ribose-phosphate 4-epimerase
5	6	RXA02245	GR00654	13639	14295	RIBULOSE-PHOSPHATE 3-EPIMERASE (EC 5.1.3.1)
7	8	RXA01015	GR00290	346	5	RIBOSE 5-PHOSPHATE ISOMERASE (EC 5.3.1.6)

TCA:

<u>Nucleic Acid</u> <u>SEQ ID NO</u>	<u>Amino Acid</u> <u>SEQ ID NO</u>	<u>Identification Code</u>	<u>Contig.</u>	<u>NT Start</u>	<u>NT Stop</u>	<u>Function</u>
9	10	RXN01312	VW0082	20803	18785	SUCCINATE DEHYDROGENASE FLAVOPROTEIN SUBUNIT (EC 1.3.99.1)
11	12	F RXA01312	GR00380	2690	1614	SUCCINATE DEHYDROGENASE FLAVOPROTEIN SUBUNIT (EC 1.3.99.1)
13	14	RXN00231	VW0083	15484	14015	SUCCINATE-SEMIALDEHYDE DEHYDROGENASE (NADP+) (EC 1.2.1.16)
15	16	RXA01311	GR00380	1611	865	SUCCINATE DEHYDROGENASE IRON-SULFUR PROTEIN (EC 1.3.99.1)
17	18	RXA01535	GR00427	1354	2760	FUMARATE HYDRATASE PRECURSOR (EC 4.2.1.2)
19	20	RXA00517	GR00131	1407	2447	MALATE DEHYDROGENASE (EC 1.1.1.37)
21	22	RXA01350	GR00392	1844	2827	MALATE DEHYDROGENASE (EC 1.1.1.37)

EMB-Pathway

<u>Nucleic Acid</u> <u>SEQ ID NO</u>	<u>Amino Acid</u> <u>SEQ ID NO</u>	<u>Identification Code</u>	<u>Contig.</u>	<u>NT Start</u>	<u>NT Stop</u>	<u>Function</u>
23	24	RXA02149	GR00639	17786	18754	GLUCOKINASE (EC 2.7.1.2)
25	26	RXA01814	GR00515	2571	910	PHOSPHOGLUCOMUTASE (EC 5.4.2.2) / PHOSPHOMANNOMUTASE (EC 5.4.2.8)
27	28	RXN02803	VW0086	1	657	PHOSPHOGLUCOMUTASE (EC 5.4.2.2) / PHOSPHOMANNOMUTASE (EC 5.4.2.8)
29	30	F RXA02803	GR00784	2	400	PHOSPHOGLUCOMUTASE (EC 5.4.2.2) / PHOSPHOMANNOMUTASE (EC 5.4.2.8)
31	32	RXN03076	VW0043	1624	35	PHOSPHOGLUCOMUTASE (EC 5.4.2.2) / PHOSPHOMANNOMUTASE (EC 5.4.2.8)
33	34	F RXA02854	GR10002	1588	5	PHOSPHOGLUCOMUTASE (EC 5.4.2.2) / PHOSPHOMANNOMUTASE (EC 5.4.2.8)
35	36	RXA00511	GR00129	1	513	PHOSPHOGLUCOMUTASE (EC 5.4.2.2) / PHOSPHOMANNOMUTASE (EC 5.4.2.8)

Table 1 (continued)

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig.	NT Start	NT Stop	Function
37	38	RXN01365	VV0091	1476	103	PHOSPHOGLUCOMUTASE (EC 5.4.2.2) / PHOSPHOMANNOMUTASE (EC 5.4.2.8)
39	40	F RXA01365	GR00397	897	4	PHOSPHOGLUCOMUTASE (EC 5.4.2.2) / PHOSPHOMANNOMUTASE (EC 5.4.2.8)
41	42	RXA00098	GR00014	6525	8144	GLUCOSE-6-PHOSPHATE ISOMERASE (GPI) (EC 5.3.1.9)
43	44	RXA01989	GR00578	1	630	GLUCOSE-6-PHOSPHATE ISOMERASE A (GPI A) (EC 5.3.1.9)
45	46	RXA00340	GR00059	1549	2694	PHOSPHOGLYCERATE MUTASE (EC 5.4.2.1)
47	48	RXA02492	GR00720	2201	2917	PHOSPHOGLYCERATE MUTASE (EC 5.4.2.1)
49	50	RXA00381	GR00082	1451	846	PHOSPHOGLYCERATE MUTASE (EC 5.4.2.1)
51	52	RXA02122	GR00636	6511	5813	PHOSPHOGLYCERATE MUTASE (EC 5.4.2.1)
53	54	RXA00206	GR00032	6171	5134	6-PHOSPHOFRUCTOKINASE (EC 2.7.1.11)
55	56	RXA01243	GR00359	2302	3261	1-PHOSPHOFRUCTOKINASE (EC 2.7.1.56)
57	58	RXA01882	GR00538	1165	2154	1-PHOSPHOFRUCTOKINASE (EC 2.7.1.56)
59	60	RXA01702	GR00479	1397	366	FRUCTOSE-BISPHOSPHATE ALDOOLASE (EC 4.1.2.13)
61	62	RXA02258	GR00654	26451	27227	TRIOSEPHOSPHATE ISOMERASE (EC 5.3.1.1)
63	64	RXN01225	VV0064	6382	4943	GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE (EC 1.2.1.12)
65	66	F RXA01225	GR00354	5302	6741	GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE HOMOLOG
67	68	RXA02256	GR00654	23934	24935	GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE
69	70	RXA02257	GR00654	25155	26369	PHOSPHOGLYCERATE KINASE (EC 2.7.2.3)
71	72	RXA00235	GR00036	2365	1091	ENOLASE (EC 4.2.1.11)
73	74	RXA01093	GR00306	1552	122	PYRUVATE KINASE (EC 2.7.1.40)
75	76	RXN02675	VV0098	72801	70945	PYRUVATE KINASE (EC 2.7.1.40)
77	78	F RXA02675	GR00754	2	364	PYRUVATE KINASE (EC 2.7.1.40)
79	80	F RXA02695	GR00755	2949	4370	PYRUVATE KINASE (EC 2.7.1.40)
81	82	RXA00682	GR00179	5299	3401	PHOSPHOENOLPYRUVATE SYNTHASE (EC 2.7.9.2)
83	84	RXA00683	GR00179	6440	5349	PHOSPHOENOLPYRUVATE SYNTHASE (EC 2.7.9.2)
85	86	RXN00635	VV0135	22708	20972	PYRUVATE DEHYDROGENASE (CYTOCHROME) (EC 1.2.2.2)
87	88	F RXA02807	GR00788	88	552	PYRUVATE DEHYDROGENASE (CYTOCHROME) (EC 1.2.2.2)
89	90	F RXA00635	GR00167	3	923	PYRUVATE DEHYDROGENASE (CYTOCHROME) (EC 1.2.2.2)
91	92	RXN03044	VV0019	1391	2221	PYRUVATE DEHYDROGENASE E1 COMPONENT (EC 1.2.4.1)
93	94	F RXA02852	GR00852	3	281	PYRUVATE DEHYDROGENASE E1 COMPONENT (EC 1.2.4.1)
95	96	F RXA00268	GR00041	125	955	PYRUVATE DEHYDROGENASE E1 COMPONENT (EC 1.2.4.1)
97	98	RXN03086	VV0049	2243	2650	PYRUVATE DEHYDROGENASE E1 COMPONENT (EC 1.2.4.1)
99	100	F RXA02887	GR10022	411	4	PYRUVATE DEHYDROGENASE E1 COMPONENT (EC 1.2.4.1)
101	102	RXN03043	VV0019	1	1362	PYRUVATE DEHYDROGENASE E1 COMPONENT (EC 1.2.4.1)
103	104	F RXA02897	GR10039	1291	5	DIHYDROLIPOAMIDE DEHYDROGENASE (EC 1.8.1.4)
105	106	RXN03083	VV0047	88	1110	DIHYDROLIPOAMIDE DEHYDROGENASE (EC 1.8.1.4)
107	108	F RXA02853	GR10001	89	1495	PHOSPHOENOLPYRUVATE CARBOXYLASE (EC 4.1.1.31)
109	110	RXA02259	GR00654	27401	30172	PHOSPHOENOLPYRUVATE CARBOXYLASE (EC 4.1.1.31)
111	112	RXN02326	VV0047	4500	5315	PYRUVATE CARBOXYLASE (EC 6.4.1.1)
113	114	F RXA02326	GR00668	5338	4523	PYRUVATE CARBOXYLASE (EC 6.4.1.1)
115	116	RXN02327	VV0047	3533	4492	PYRUVATE CARBOXYLASE (EC 6.4.1.1)
117	118	F RXA02327	GR00668	6305	5346	PYRUVATE CARBOXYLASE (EC 6.4.1.1)
119	120	RXN02328	VV0047	1842	3437	PYRUVATE CARBOXYLASE (EC 6.4.1.1)
121	122	F RXA02328	GR00668	7783	6401	PYRUVATE CARBOXYLASE (EC 6.4.1.1)
123	124	RXN01048	VV0079	12539	11316	MALIC ENZYME (EC 1.1.1.39)

Table 1 (continued)

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig.	NT Start	NT Stop	Function
125	126	F RXA01048	GR00296	3	290	MALIC ENZYME (EC 1.1.1.39)
127	128	F RXA00290	GR00046	4693	5655	MALIC ENZYME (EC 1.1.1.39)
129	130	RXA02694	GR00755	1879	2820	L-LACTATE DEHYDROGENASE (EC 1.1.1.27)
131	132	RXN00296	VW0176	35763	38606	D-LACTATE DEHYDROGENASE (CYTOCHROME) (EC 1.1.2.4)
133	134	F RXA00296	GR00048	3	2837	D-LACTATE DEHYDROGENASE (CYTOCHROME) (EC 1.1.2.3)
135	136	RXA01901	GR00544	4158	5417	L-LACTATE DEHYDROGENASE (EC 1.1.1.28)
137	138	RXN01952	VW0105	9954	11666	D-LACTATE DEHYDROGENASE (EC 1.1.1.28)
139	140	F RXA01952	GR00562	1	216	D-LACTATE DEHYDROGENASE (EC 1.1.1.28)
141	142	F RXA01955	GR00562	4611	6209	D-LACTATE DEHYDROGENASE (EC 1.1.1.28)
143	144	RXA00293	GR00047	2645	1734	D-3-PHOSPHOGLYCERATE DEHYDROGENASE (EC 1.1.1.95)
145	146	RXN01130	VW0157	6138	5536	D-3-PHOSPHOGLYCERATE DEHYDROGENASE (EC 1.1.1.95)
147	148	F RXA01130	GR00315	2	304	D-3-PHOSPHOGLYCERATE DEHYDROGENASE (EC 1.1.1.95)
149	150	RXN03112	VW0085	509	6	D-3-PHOSPHOGLYCERATE DEHYDROGENASE (EC 1.1.1.95)
151	152	F RXA01133	GR00316	568	1116	D-3-PHOSPHOGLYCERATE DEHYDROGENASE (EC 1.1.1.95)
153	154	RXN00871	VW0127	3127	2240	IOLB PROTEIN
155	156	F RXA00871	GR00239	2344	3207	IOLB PROTEIN: D-FRUCTOSE 1,6-BISPHOSPHATE = GLYCERONE-CC PHOSPHATE + D- GLYCERALDEHYDE 3-PHOSPHATE
157	158	RXN02829	VW0354	287	559	IOLS PROTEIN
159	160	F RXA02829	GR00816	287	562	IOLS PROTEIN
161	162	RXN01468	VW0019	7474	8298	NAGD PROTEIN
163	164	F RXA01468	GR00422	1250	2074	PUTATIVE N-GLYCERALDEHYDE-2-PHOSPHOTRANSFERASE
165	166	RXA00794	GR00211	3993	2989	GLPX PROTEIN
167	168	RXN02920	VW0213	6135	5224	D-3-PHOSPHOGLYCERATE DEHYDROGENASE (EC 1.1.1.95)
169	170	F RXA02379	GR00690	1390	686	D-3-PHOSPHOGLYCERATE DEHYDROGENASE (EC 1.1.1.95)
171	172	RXN02688	VW0098	59053	58385	PHOSPHOGLYCERATE MUTASE (EC 5.4.2.1)
173	174	RXN03087	VW0052	3216	3428	PYRUVATE CARBOXYLASE (EC 6.4.1.1)
175	176	RXN03186	VW0377	310	519	PYRUVATE DEHYDROGENASE E1 COMPONENT (EC 1.2.4.1)
177	178	RXN03187	VW0382	3	281	PYRUVATE DEHYDROGENASE E1 COMPONENT (EC 1.2.4.1)
179	180	RXN02591	VW0098	14370	12541	PHOSPHOENOLPYRUVATE CARBOXYKINASE [GTP] (EC 4.1.1.32)
181	182	RXS01260	VW0009	3477	2296	LIPAMIDE DEHYDROGENASE COMPONENT (E3) OF BRANCHED- CHAIN ALPHA-KETO ACID DEHYDROGENASE COMPLEX (EC 1.8.1.4)
183	184	RXS01261	VW0009	3703	3533	LIPAMIDE DEHYDROGENASE COMPONENT (E3) OF BRANCHED- CHAIN ALPHA-KETO ACID DEHYDROGENASE COMPLEX (EC 1.8.1.4)

Glycerol metabolism

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig.	NT Start	NT Stop	Function
185	186	RXA02640	GR00749	1400	2926	GLYCEROL KINASE (EC 2.7.1.30)
187	188	RXN01025	VW0143	5483	4488	GLYCEROL-3-PHOSPHATE DEHYDROGENASE (NAD(P) ⁺) (EC 1.1.1.94)
189	190	F RXA01025	GR00293	939	1853	GLYCEROL-3-PHOSPHATE DEHYDROGENASE (NAD(P) ⁺) (EC 1.1.1.94)
191	192	RXA01851	GR00525	3515	1830	AEROBIC GLYCEROL-3-PHOSPHATE DEHYDROGENASE (EC 1.1.99.5)
193	194	RXA01242	GR00359	1526	2302	GLYCEROL-3-PHOSPHATE REGULON REPRESSOR
195	196	RXA02288	GR00661	992	147	GLYCEROL-3-PHOSPHATE REGULON REPRESSOR

Table 1 (continued)

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig.	NT Start	NT Stop	Function
197	198	RXN01891	VV0122	24949	24086	GLYCEROL-3-PHOSPHATE-BINDING PERIPLASMIC PROTEIN PRECURSOR
199	200	F RXA01891	GR00541	1736	918	GLYCEROL-3-PHOSPHATE-BINDING PERIPLASMIC PROTEIN PRECURSOR
201	202	RXA02414	GR00703	3808	3062	Uncharacterized protein involved in glycerol metabolism (homolog of Drosophila rhomboid)
203	204	RXN01580	VV0122	22091	22807	Glycerophosphoryl diester phosphodiesterase

Acetate metabolism

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig.	NT Start	NT Stop	Function
205	206	RXA01436	GR00418	2547	1357	ACETATE KINASE (EC 2.7.2.1)
207	208	RXA00686	GR00179	8744	7941	ACETATE OPERON REPRESSOR
209	210	RXA00246	GR00037	4425	3391	ALCOHOL DEHYDROGENASE (EC 1.1.1.1)
211	212	RXA01571	GR00438	1360	1959	ALCOHOL DEHYDROGENASE (EC 1.1.1.1)
213	214	RXA01572	GR00438	1928	2419	ALCOHOL DEHYDROGENASE (EC 1.1.1.1)
215	216	RXA01758	GR00498	3961	2945	ALCOHOL DEHYDROGENASE (EC 1.1.1.1)
217	218	RXA02539	GR00726	11676	10159	ALDEHYDE DEHYDROGENASE (EC 1.1.1.1)
219	220	RXN03061	VV0034	108	437	ALDEHYDE DEHYDROGENASE (EC 1.2.1.3)
221	222	RXN03150	VV0155	10678	10055	ALDEHYDE DEHYDROGENASE (EC 1.2.1.3)
223	224	RXN01340	VV0033	3	860	ALDEHYDE DEHYDROGENASE (EC 1.2.1.3)
225	226	RXN01498	VV0008	1598	3160	ALDEHYDE DEHYDROGENASE (EC 1.2.1.3)
227	228	RXN02674	VV0315	15614	14163	ALDEHYDE DEHYDROGENASE (EC 1.2.1.3)
229	230	RXN00868	VV0127	2230	320	ACETOLACTATE SYNTHASE LARGE SUBUNIT (EC 4.1.3.18)
231	232	RXN01143	VV0077	9372	8254	ACETOLACTATE SYNTHASE LARGE SUBUNIT (EC 4.1.3.18)
233	234	RXN01146	VV0264	243	935	ACETOLACTATE SYNTHASE LARGE SUBUNIT (EC 4.1.3.18)
235	236	RXN01144	VV0077	8237	7722	ACETOLACTATE SYNTHASE SMALL SUBUNIT (EC 4.1.3.18)

Butanediol, diacetyl and acetoin formation

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig.	NT Start	NT Stop	Function
237	238	RXA02474	GR00715	8082	7309	(S,S)-butane-2,3-diol dehydrogenase (EC 1.1.1.176)
239	240	RXA02453	GR00710	6103	5351	ACETON(DIACETYL) REDUCTASE (EC 1.1.1.5)
241	242	RXS01758	VV0112	27383	28399	ALCOHOL DEHYDROGENASE (EC 1.1.1.1)

Table 1 (continued)

HMP-Cycl

<u>Nucleic Acid</u> <u>SEQ ID NO</u>	<u>Amino Acid</u> <u>SEQ ID NO</u>	<u>Identification Code</u>	<u>Contig.</u>	<u>NT Start</u>	<u>NT Stop</u>	<u>Function</u>
243	244	RXA02737	GR00763	3312	1771	GLUCOSE-6-PHOSPHATE 1-DEHYDROGENASE (EC 1.1.1.49)
245	246	RXA02738	GR00763	4499	3420	TRANSALDOLASE (EC 2.2.1.2)
247	248	RXA02739	GR00763	6769	4670	TRANSKETOLASE (EC 2.2.1.1)
249	250	RXA00965	GR00270	1232	510	6-PHOSPHOGLUCONATE DEHYDROGENASE, DECARBOXYLATING (EC 1.1.1.44)
251	252	RXN00999	VV0106	2817	1366	6-PHOSPHOGLUCONATE DEHYDROGENASE, DECARBOXYLATING (EC 1.1.1.44)
253	254	F RXA00999	GR00283	3012	4448	6-PHOSPHOGLUCONATE DEHYDROGENASE, DECARBOXYLATING (EC 1.1.1.44)

Nucleotide sugar conversion

<u>Nucleic Acid</u> <u>SEQ ID NO</u>	<u>Amino Acid</u> <u>SEQ ID NO</u>	<u>Identification Code</u>	<u>Contig.</u>	<u>NT Start</u>	<u>NT Stop</u>	<u>Function</u>
255	256	RXN02596	VV0098	48784	47582	UDP-GALACTOPYRANOSE MUTASE (EC 5.4.99.9)
257	258	F RXA02596	GR00742	1	489	UDP-GALACTOPYRANOSE MUTASE (EC 5.4.99.9)
259	260	F RXA02642	GR00749	5383	5880	UDP-GALACTOPYRANOSE MUTASE (EC 5.4.99.9)
261	262	RXA02572	GR00737	2	646	UDP-GLUCOSE 6-DEHYDROGENASE (EC 1.1.1.22)
263	264	RXA02485	GR00718	2345	3445	UDP-N-ACETYLENOLPYRUVOYLGLUCOSAMINE REDUCTASE (EC 1.1.1.158)
265	266	RXA01216	GR00352	2302	1202	UDP-N-ACETYLGLUCOSAMINE PYROPHOSPHORYLASE (EC 2.7.7.23)
267	268	RXA01259	GR00367	987	130	UTP-GLUCOSE-1-PHOSPHATE URIDYLTRANSFERASE (EC 2.7.7.9)
269	270	RXA02028	GR00616	573	998	UTP-GLUCOSE-1-PHOSPHATE URIDYLTRANSFERASE (EC 2.7.7.9)
271	272	RXA01262	GR00367	8351	7191	GDP-MANNOSE 6-DEHYDROGENASE (EC 1.1.1.132)
273	274	RXA01377	GR00400	3935	5020	MANNOSE-1-PHOSPHATE GUANYLTRANSFERASE (EC 2.7.7.13)
275	276	RXA02063	GR00626	3301	4527	GLUCOSE-1-PHOSPHATE ADENYLTRANSFERASE (EC 2.7.7.27)
277	278	RXN00014	VV0048	8848	9627	GLUCOSE-1-PHOSPHATE THYMIDYLTRANSFERASE (EC 2.7.7.24)
279	280	F RXA00014	GR00002	4448	5227	GLUCOSE-1-PHOSPHATE THYMIDYLTRANSFERASE (EC 2.7.7.24)
281	282	RXA01570	GR00438	427	1281	GLUCOSE-1-PHOSPHATE THYMIDYLTRANSFERASE (EC 2.7.7.24)
283	284	RXA02666	GR00753	7260	6493	GLUCOSE-1-PHOSPHATE THYMIDYLTRANSFERASE (EC 2.7.7.24)
285	286	RXA00825	GR00222	222	1154	D-RIBITOL-5-PHOSPHATE CYTIDYLTRANSFERASE (EC 2.7.7.40)
						DTDP-GLUCOSE 4,6-DEHYDRATASE (EC 4.2.1.46)

Inositol and ribitol metabolism

<u>Nucleic Acid</u> <u>SEQ ID NO</u>	<u>Amino Acid</u> <u>SEQ ID NO</u>	<u>Identification Code</u>	<u>Contig.</u>	<u>NT Start</u>	<u>NT Stop</u>	<u>Function</u>
287	288	RXA01887	GR00539	4219	3209	MYO-INOSITOL 2-DEHYDROGENASE (EC 1.1.1.18)

Table 1 (continued)

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig.	NT Start	NT Stop	Function
289	290	RXN00013	VW0048	7966	8838	MYO-INOSITOL-1(OR 4)-MONOPHOSPHATASE 1 (EC 3.1.3.25)
291	292	F RXA00013	GR00002	3566	4438	MYO-INOSITOL-1(OR 4)-MONOPHOSPHATASE 1 (EC 3.1.3.25)
293	294	RXA01099	GR00306	6328	5504	INOSITOL MONOPHOSPHATE PHOSPHATASE
295	296	RXN01332	VW0273	579	4	MYO-INOSITOL 2-DEHYDROGENASE (EC 1.1.1.18)
297	298	F RXA01332	GR00388	552	4	MYO-INOSITOL 2-DEHYDROGENASE (EC 1.1.1.18)
299	300	RXA01632	GR00454	2338	3342	MYO-INOSITOL 2-DEHYDROGENASE (EC 1.1.1.18)
301	302	RXA01633	GR00454	3380	4462	MYO-INOSITOL 2-DEHYDROGENASE (EC 1.1.1.18)
303	304	RXN01406	VW0278	2999	1977	MYO-INOSITOL 2-DEHYDROGENASE (EC 1.1.1.18)
305	306	RXN01630	VW0050	48113	47037	MYO-INOSITOL 2-DEHYDROGENASE (EC 1.1.1.18)
307	308	RXN00528	VW0079	23406	22318	MYO-INOSITOL-1-PHOSPHATE SYNTHASE (EC 5.5.1.4)
309	310	RXN03057	VW0028	7017	7688	MYO-INOSITOL 2-DEHYDROGENASE (EC 1.1.1.18)
311	312	F RXA02902	GR10040	10277	10948	GLUCOSE-FRUCTOSE OXIDOREDUCTASE PRECURSOR (EC 1.1.1.18)
313	314	RXA00251	GR00038	931	224	RIBITOL 2-DEHYDROGENASE (EC 1.1.1.56)

Utilization of sugars

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig.	NT Start	NT Stop	Function
315	316	RXN02654	VW0090	12206	13090	GLUCOSE 1-DEHYDROGENASE (EC 1.1.1.47)
317	318	F RXA02654	GR00752	7405	8289	GLUCOSE 1-DEHYDROGENASE II (EC 1.1.1.47)
319	320	RXN01049	VW0079	9633	11114	GLUCONOKINASE (EC 2.7.1.12)
321	322	F RXA01049	GR00296	1502	492	GLUCONOKINASE (EC 2.7.1.12)
323	324	F RXA01050	GR00296	1972	1499	GLUCONOKINASE (EC 2.7.1.12)
325	326	RXA00202	GR00032	1216	275	D-RIBOSE-BINDING PERIPLASMIC PROTEIN PRECURSOR
327	328	RXN00872	VW0127	6557	5604	FRUCTOKINASE (EC 2.7.1.4)
329	330	F RXA00872	GR00240	565	1086	FRUCTOKINASE (EC 2.7.1.4)
331	332	RXN00799	VW0009	58477	56834	PERIPLASMIC BETA-GLUCOSIDASE/BETA-XYLOSIDASE PRECURSOR (EC 3.2.1.21)
333	334	F RXA00799	GR00214	1	1584	PERIPLASMIC BETA-GLUCOSIDASE/BETA-XYLOSIDASE PRECURSOR (EC 3.2.1.21)
335	336	RXA00032	GR00003	12028	10520	MANNITOL 2-DEHYDROGENASE (EC 1.1.1.67)
337	338	RXA02528	GR00725	6880	7854	FRUCTOSE REPRESSOR
339	340	RXN00316	VW0006	7035	8180	Hypothetical Oxidoreductase (EC 1.1.1.1-)
341	342	F RXA00309	GR00053	316	5	GLUCOSE-FRUCTOSE OXIDOREDUCTASE PRECURSOR (EC 1.1.99.28)
343	344	RXN00310	VW0006	6616	7050	GLUCOSE-FRUCTOSE OXIDOREDUCTASE PRECURSOR (EC 1.1.99.28)
345	346	F RXA00310	GR00053	735	301	GLUCOSE-FRUCTOSE OXIDOREDUCTASE PRECURSOR (EC 1.1.99.28)
347	348	RXA00041	GR00007	1246	5	SUCROSE-6-PHOSPHATE HYDROLASE (EC 3.2.1.26)
349	350	RXA02026	GR00615	725	6	SUCROSE-6-PHOSPHATE HYDROLASE (EC 3.2.1.26)
351	352	RXA02061	GR00626	1842	349	SUCROSE-6-PHOSPHATE HYDROLASE (EC 3.2.1.26)

Table 1 (continued)

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig	NT Start	NT Stop	Function
353	354	RXN01369	VV0124	595	1776	MANNOSE-6-PHOSPHATE ISOMERASE (EC 5.3.1.8)
355	356	F RXA01369	GR00398	3	503	MANNOSE-6-PHOSPHATE ISOMERASE (EC 5.3.1.8)
357	358	F RXA01373	GR00399	595	1302	MANNOSE-6-PHOSPHATE ISOMERASE (EC 5.3.1.8)
359	360	RXA02611	GR00743	1	1752	1,4-ALPHA-GLUCAN BRANCHING ENZYME (EC 2.4.1.18)
361	362	RXA02612	GR00743	1793	3985	1,4-ALPHA-GLUCAN BRANCHING ENZYME (EC 2.4.1.18)
363	364	RXN01884	VV0184	1	1890	GLYCOGEN DEBRANCHING ENZYME (EC 2.4.1.18)
365	366	F RXA01884	GR00539	3	1475	GLYCOGEN DEBRANCHING ENZYME (EC 2.4.1.25) (EC 3.2.1.33)
367	368	RXA01111	GR00306	16981	17427	GLYCOGEN DEBRANCHING ENZYME (EC 2.4.1.25) (EC 3.2.1.33)
369	370	RXN01550	VV0143	14749	16260	GLYCOGEN OPERON PROTEIN GLGX (EC 3.2.1.-)
371	372	F RXA01550	GR00431	3	1346	GLYCOGEN PHOSPHORYLASE (EC 2.4.1.1)
373	374	RXN02100	VV0318	2	2326	GLYCOGEN PHOSPHORYLASE (EC 2.4.1.1)
375	376	F RXA02100	GR00631	3	920	GLYCOGEN PHOSPHORYLASE (EC 2.4.1.1)
377	378	F RXA02113	GR00633	2	1207	GLYCOGEN PHOSPHORYLASE (EC 2.4.1.1)
379	380	RXA02147	GR00639	15516	16532	ALPHA-AMYLASE (EC 3.2.1.1)
381	382	RXA01478	GR00422	10517	12352	GLUCOAMYLASE G1 AND G2 PRECURSOR (EC 3.2.1.3)
383	384	RXA01888	GR00539	4366	4923	GLUCOSE-RESISTANCE AMYLASE REGULATOR
385	386	RXN01927	VV0127	50623	49244	XYLULOSE KINASE (EC 2.7.1.17)
387	388	F RXA01927	GR00555	3	1118	XYLULOSE KINASE (EC 2.7.1.17)
389	390	RXA02729	GR00762	747	4	RIBOKINASE (EC 2.7.1.15)
391	392	RXA02797	GR00778	1739	2641	RIBOKINASE (EC 2.7.1.15)
393	394	RXA02730	GR00762	1768	731	RIBOSE OPERON REPRESSOR
395	396	RXA02551	GR00729	2193	2552	6-PHOSPHO-BETA-GLUCOSIDASE (EC 3.2.1.86)
397	398	RXA01325	GR00385	5676	5005	DEOXYRIBOSE-PHOSPHATE ALDOLASE (EC 4.1.2.4)
399	400	RXA00195	GR00030	543	1103	1-deoxy-D-xylulose 5-phosphate reductoisomerase (EC 1.1.1.-)
401	402	RXA00196	GR00030	1094	1708	1-deoxy-D-xylulose 5-phosphate reductoisomerase (EC 1.1.1.-)
403	404	RXN01562	VV0191	1230	3137	1-DEOXYXYLULOSE-5-PHOSPHATE SYNTHASE
405	406	F RXA01562	GR00436	2	1039	1-DEOXYXYLULOSE-5-PHOSPHATE SYNTHASE
407	408	F RXA01705	GR00480	971	1573	1-DEOXYXYLULOSE-5-PHOSPHATE SYNTHASE
409	410	RXN00879	VV0099	8763	6646	4-ALPHA-GLUCANOTRANSFERASE (EC 2.4.1.25)
411	412	F RXA00879	GR00242	5927	3828	4-ALPHA-GLUCANOTRANSFERASE (EC 2.4.1.25), amylomaltase
413	414	RXN00043	VV0119	3244	2081	N-ACETYLGLUCOSAMINE-6-PHOSPHATE DEACETYLASE (EC 3.5.1.25)
415	416	F RXA00043	GR00007	3244	2081	N-ACETYLGLUCOSAMINE-6-PHOSPHATE DEACETYLASE (EC 3.5.1.25)
417	418	RXN01752	VV0127	35265	33805	N-ACETYLGLUCOSAMINYLTRANSFERASE (EC 2.4.1.-)
419	420	F RXA01839	GR00520	1157	510	N-ACETYLGLUCOSAMINYLTRANSFERASE (EC 2.4.1.-)
421	422	RXA01859	GR00529	1473	547	N-ACETYLGLUCOSAMINYLTRANSFERASE (EC 2.4.1.-)
423	424	RXA00042	GR00007	2037	1279	GLUCOSAMINE-6-PHOSPHATE ISOMERASE (EC 5.3.1.10)
425	426	RXA01482	GR00422	17271	15397	GLUCOSAMINE-FRUCTOSE-6-PHOSPHATE AMINOTRANSFERASE (ISOMERIZING) (EC 2.6.1.16)
427	428	RXN03179	VV0336	2	667	URONATE ISOMERASE (EC 5.3.1.12)
429	430	F RXA02872	GR10013	675	4	URONATE ISOMERASE, Glucuronate isomerase (EC 5.3.1.12)
431	432	RXN03180	VV0337	672	163	URONATE ISOMERASE (EC 5.3.1.12)
433	434	F RXA02873	GR10014	672	163	URONATE ISOMERASE, Glucuronate isomerase (EC 5.3.1.12)
435	436	RXA02292	GR00662	1611	2285	GALACTOSIDE O-ACETYLTRANSFERASE (EC 2.3.1.18)
437	438	RXA02666	GR00753	7260	6493	D-RIBITOL-5-PHOSPHATE CYTIDYLTRANSFERASE (EC 2.7.7.40)
439	440	RXA00202	GR00032	1216	275	D-RIBOSE-BINDING PERIPLASMIC PROTEIN PRECURSOR
441	442	RXA02440	GR00709	5097	4258	D-RIBOSE-BINDING PERIPLASMIC PROTEIN PRECURSOR

Table 1 (continued)

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig.	NT Start	NT Stop	Function
443	444	RXN01569	VW0009	41086	42444	dTDP-4-DEHYDRORHAMNOSE REDUCTASE (EC 1.1.1.133)
445	446	F RXA01569	GR00438	2	427	DTDP-4-DEHYDRORHAMNOSE REDUCTASE (EC 1.1.1.133)
447	448	F RXA02055	GR00624	7122	8042	DTDP-4-DEHYDRORHAMNOSE REDUCTASE (EC 1.1.1.133)
449	450	RXA00825	GR00222	222	1154	DTDP-GLUCOSE 4,6-DEHYDRATASE (EC 4.2.1.46)
451	452	RXA02054	GR00624	6103	7119	DTDP-GLUCOSE 4,6-DEHYDRATASE (EC 4.2.1.46)
453	454	RXN00427	VW0112	7004	6219	dTDP-RHAMNOSYL TRANSFERASE RFBF (EC 2.---)
455	456	F RXA00427	GR00098	1591	2022	DTDP-RHAMNOSYL TRANSFERASE RFBF (EC 2.---)
457	458	RXA00327	GR00057	10263	9880	PROTEIN ARAJ
459	460	RXA00328	GR00057	11147	10656	PROTEIN ARAJ
461	462	RXA00329	GR00057	12390	11167	PROTEIN ARAJ
463	464	RXN01554	VW0135	28866	26545	GLUCAN ENDO-1,3-BETA-GLUCOSIDASE A1 PRECURSOR (EC 3.2.1.39)
465	466	RXN03015	VW0063	289	8	UDP-GLUCOSE 6-DEHYDROGENASE (EC 1.1.1.22)
467	468	RXN03056	VW0028	6258	6935	PUTATIVE HEXULOSE-6-PHOSPHATE ISOMERASE (EC 5.---)
469	470	RXN03030	VW0009	57006	56443	PERIPLASMIC BETA-GLUCOSIDASE/BETA-XYLOSIDASE PRECURSOR (EC 3.2.1.21) (EC 3.2.1.37)
471	472	RXN00401	VW0025	12427	11489	5-DEHYDRO-4-DEOXYGLUCARATE DEHYDRATASE (EC 4.2.1.41)
473	474	RXN02125	VW0102	23242	22442	ALDOSE REDUCTASE (EC 1.1.1.21)
475	476	RXN00200	VW0181	1679	5116	arabinosyl transferase subunit B (EC 2.4.2.-)
477	478	RXN01175	VW0017	39688	38303	PHOSPHO-2-DEHYDRO-3-DEOXYHEPTONATE ALDOLASE (EC 4.1.2.15)
479	480	RXN01376	VW0091	5610	4750	PUTATIVE GLYCOSYL TRANSFERASE WBIF
481	482	RXN01631	VW0050	47021	46143	PUTATIVE HEXULOSE-6-PHOSPHATE ISOMERASE (EC 5.---)
483	484	RXN01593	VW0229	13274	12408	NAGD PROTEIN
485	486	RXN00337	VW0197	20369	21418	GALACTOKINASE (EC 2.7.1.6)
487	488	RXS00584	VW0323	5516	6640	PHOSPHO-2-DEHYDRO-3-DEOXYHEPTONATE ALDOLASE (EC 4.1.2.15)
489	490	RXS02574				BETA-HEXOSAMINIDASE A PRECURSOR (EC 3.2.1.52)
491	492	RXS03215				GLUCOSE-FRUCTOSE OXIDOREDUCTASE PRECURSOR (EC 1.1.99.28)
493	494	F RXA01915	GR00549	1	1008	GLUCOSE-FRUCTOSE OXIDOREDUCTASE PRECURSOR (EC 1.1.99.28)
495	496	RXS03224				CYCLOMALTODEXTRINASE (EC 3.2.1.54)
497	498	F RXA00038	GR00006	1417	260	CYCLOMALTODEXTRINASE (EC 3.2.1.54)
499	500	RXC00233				protein involved in sugar metabolism
501	502	RXC00236				Membrane Lipoprotein involved in sugar metabolism
503	504	RXC00271				Exported Protein involved in ribose metabolism
505	506	RXC00338				protein involved in sugar metabolism
507	508	RXC00362				Membrane Spanning Protein involved in metabolism of diols
509	510	RXC00412				Amino Acid ABC Transporter ATP-Binding Protein involved in sugar metabolism
511	512	RXC00526				ABC Transporter ATP-Binding Protein involved in sugar metabolism
513	514	RXC01004				Membrane Spanning Protein involved in sugar metabolism
515	516	RXC01017				Cytosolic Protein involved in sugar metabolism
517	518	RXC01021				Cytosolic Kinase involved in metabolism of sugars and thiamin
519	520	RXC01212				ABC Transporter ATP-Binding Protein involved in sugar metabolism
521	522	RXC01306				Membrane Spanning Protein involved in sugar metabolism
523	524	RXC01366				Cytosolic Protein involved in sugar metabolism
525	526	RXC01372				Cytosolic Protein involved in sugar metabolism

Table 1 (continued)

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig.	NT Start	NT Stop	Function
527	528	RXC01659				protein involved in sugar metabolism
529	530	RXC01663				protein involved in sugar metabolism
531	532	RXC01693				protein involved in sugar metabolism
533	534	RXC01703				Cytosolic Protein involved in sugar metabolism
535	536	RXC02254				Membrane Associated Protein involved in sugar metabolism
537	538	RXC02255				Cytosolic Protein involved in sugar metabolism
539	540	RXC02435				protein involved in sugar metabolism
541	542	F RXA02435	GR00709	825	268	Uncharacterized protein involved in glycerol metabolism (homolog of Drosophila rhomboid)
543	544	RXC03216				protein involved in sugar metabolism

TCA-cycle

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig.	NT Start	NT Stop	Function
545	546	RXA02175	GR00641	10710	9418	CITRATE SYNTHASE (EC 4.1.3.7)
547	548	RXA02621	GR00746	2647	1829	CITRATE LYASE BETA CHAIN (EC 4.1.3.6)
549	550	RXN00519	VV0144	5585	3372	ISOCITRATE DEHYDROGENASE (NADP) (EC 1.1.1.42)
551	552	F RXA00521	GR00133	2	1060	ISOCITRATE DEHYDROGENASE [NADP] (EC 1.1.1.42)
553	554	RXN02209	VV0304	1	1671	ACONITATE HYDRATASE (EC 4.2.1.3)
555	556	F RXA02209	GR00648	3	1661	ACONITATE HYDRATASE (EC 4.2.1.3)
557	558	RXN02213	VV0305	1378	2151	ACONITATE HYDRATASE (EC 4.2.1.3)
559	560	F RXA02213	GR00649	1330	2046	ACONITATE HYDRATASE (EC 4.2.1.3)
561	562	RXA02056	GR00625	3	2870	2-OXOGLUTARATE DEHYDROGENASE E1 COMPONENT (EC 1.2.4.2)
563	564	RXA01745	GR00495	2	1495	2-OXOGLUTARATE DEHYDROGENASE COMPLEX (EC 2.3.1.61)
565	566	RXA00782	GR00206	3984	3103	SUCCINYL-COA SYNTHETASE ALPHA CHAIN (EC 6.2.1.5)
567	568	RXA00783	GR00206	5280	4009	SUCCINYL-COA SYNTHETASE BETA CHAIN (EC 6.2.1.5)
569	570	RXN01695	VV0139	11307	12806	L-MALATE DEHYDROGENASE (ACCEPTOR) (EC 1.1.99.16)
571	572	F RXA01615	GR00449	8608	9546	L-MALATE DEHYDROGENASE (ACCEPTOR) (EC 1.1.99.16)
573	574	F RXA01695	GR00474	4388	4179	L-MALATE DEHYDROGENASE (ACCEPTOR) (EC 1.1.99.16)
575	576	RXA00290	GR00046	4693	5655	MALIC ENZYME (EC 1.1.1.39)
577	578	RXN01048	VV0079	12539	11316	MALIC ENZYME (EC 1.1.1.39)
579	580	F RXA01048	GR00296	3	290	MALIC ENZYME (EC 1.1.1.39)
581	582	F RXA00290	GR00046	4693	5655	MALIC ENZYME (EC 1.1.1.39)
583	584	RXN03101	VV0066	2	583	MALIC ENZYME (EC 1.1.1.39)
585	586	RXN02046	VV0025	15056	14640	2-OXOGLUTARATE DEHYDROGENASE COMPLEX (EC 2.3.1.61)
587	588	RXN00389	VV0025	11481	9922	DIHYDROLIPOAMIDE SUCCINYLTRANSFERASE COMPONENT (E2) OF 2-OXOGLUTARATE DEHYDROGENASE COMPLEX (EC 2.3.1.61)

Table 1 (continued)

Glyoxylate bypass

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig.	NT Start	NT Stop	Function
589	590	RXN02399	VV0176	19708	18365	ISOCITRATE LYASE (EC 4.1.3.1)
591	592	F RXA02399	GR00699	478	1773	ISOCITRATE LYASE (EC 4.1.3.1)
593	594	RXN02404	VV0176	20259	22475	MALATE SYNTHASE (EC 4.1.3.2)
595	596	F RXA02404	GR00700	3798	1863	MALATE SYNTHASE (EC 4.1.3.2)
597	598	RXA01089	GR00304	3209	3958	GLYOXYLATE-INDUCED PROTEIN
599	600	RXA01886	GR00539	3203	2430	GLYOXYLATE-INDUCED PROTEIN

Methylcitrate-pathway

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig.	NT Start	NT Stop	Function
600	602	RXN03117	VV0092	3087	1576	2-methylisocitrate synthase (EC 5.3.3.-)
601	604	F RXA00406	GR00090	978	4	2-methylisocitrate synthase (EC 5.3.3.-)
603	606	F RXA00514	GR00130	1983	1576	2-methylisocitrate synthase (EC 5.3.3.-)
605	608	RXA00512	GR00130	621	4	2-methylcitrate synthase (EC 4.1.3.31)
607	610	RXA00518	GR00131	3069	2773	2-methylcitrate synthase (EC 4.1.3.31)
609	612	RXA01077	GR00300	4647	6017	2-methylisocitrate synthase (EC 5.3.3.-)
611	614	RXN03144	VV0141	2	901	2-methylisocitrate synthase (EC 5.3.3.-)
613	616	F RXA02322	GR00668	415	5	2-methylisocitrate synthase (EC 5.3.3.-)
615	618	RXA02329	GR00669	607	5	2-methylisocitrate synthase (EC 5.3.3.-)
617	620	RXA02332	GR00671	1906	764	2-methylcitrate synthase (EC 4.1.3.31)
619	622	RXN02333	VV0141	901	1815	methylisocitrate lyase (EC 4.1.3.30)
621	624	F RXA02333	GR00671	2120	1902	methylisocitrate lyase (EC 4.1.3.30)
623	626	RXA00030	GR00003	9590	9979	LACTOYLGLUTATHIONE LYASE (EC 4.4.1.5)

Methyl-Malonyl-CoA-Mutases

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig.	NT Start	NT Stop	Function
625	628	RXN00148	VV0167	9849	12059	METHYLMALONYL-COA MUTASE ALPHA-SUBUNIT (EC 5.4.99.2)
627	630	F RXA00148	GR00023	2002	5	METHYLMALONYL-COA MUTASE ALPHA-SUBUNIT (EC 5.4.99.2)
629	632	RXA00149	GR00023	3856	2009	METHYLMALONYL-COA MUTASE BETA-SUBUNIT (EC 5.4.99.2)

Table 1 (continued)

Others

<u>Nucleic Acid</u> <u>SEQ ID NO</u>	<u>Amino Acid</u> <u>SEQ ID NO</u>	<u>Identification Code</u>	<u>Contig.</u>	<u>NT Start</u>	<u>NT Stop</u>	<u>Function</u>
631	634	RXN00317	VV0197	26879	27532	PHOSPHOGLYCOLATE PHOSPHATASE (EC 3.1.3.18)
635	636	F RXA00317	GR00055	344	6	PHOSPHOGLYCOLATE PHOSPHATASE (EC 3.1.3.18)
637	638	RXA02196	GR00645	3956	3264	PHOSPHOGLYCOLATE PHOSPHATASE (EC 3.1.3.18)
639	640	RXN02461	VV0124	14236	14643	PHOSPHOGLYCOLATE PHOSPHATASE (EC 3.1.3.18)

Redox Chain

<u>Nucleic Acid</u> <u>SEQ ID NO</u>	<u>Amino Acid</u> <u>SEQ ID NO</u>	<u>Identification Code</u>	<u>Contig.</u>	<u>NT Start</u>	<u>NT Stop</u>	<u>Function</u>
641	642	RXN01744	VV0174	2350	812	CYTOCHROME D UBIQUINOL OXIDASE SUBUNIT I (EC 1.10.3.-)
643	644	F RXA00055	GR00008	11753	11890	CYTOCHROME D UBIQUINOL OXIDASE SUBUNIT I (EC 1.10.3.-)
645	646	F RXA01744	GR00494	2113	812	CYTOCHROME D UBIQUINOL OXIDASE SUBUNIT I (EC 1.10.3.-)
647	648	RXA00379	GR00082	212	6	CYTOCHROME C-TYPE BIOGENESIS PROTEIN CCDA
649	650	RXA00385	GR00083	773	435	CYTOCHROME C-TYPE BIOGENESIS PROTEIN CCDA
651	652	RXA01743	GR00494	806	6	CYTOCHROME D UBIQUINOL OXIDASE SUBUNIT II (EC 1.10.3.-)
653	654	RXN02480	VV0084	31222	29567	CYTOCHROME C OXIDASE POLYPEPTIDE I (EC 1.9.3.1)
655	656	F RXA01919	GR00550	288	4	CYTOCHROME C OXIDASE SUBUNIT I (EC 1.9.3.1)
657	658	F RXA02480	GR00717	1449	601	CYTOCHROME C OXIDASE POLYPEPTIDE I (EC 1.9.3.1)
659	660	F RXA02481	GR00717	1945	1334	CYTOCHROME C OXIDASE POLYPEPTIDE I (EC 1.9.3.1)
661	662	RXA02140	GR00639	7339	8415	CYTOCHROME C OXIDASE POLYPEPTIDE II (EC 1.9.3.1)
663	664	RXA02142	GR00639	9413	10063	CYTOCHROME C OXIDASE POLYPEPTIDE I (EC 1.9.3.1)
665	666	RXA02144	GR00639	11025	12248	RIESKE IRON-SULFUR PROTEIN
667	668	RXA02740	GR00763	7613	8542	PROBABLE CYTOCHROME C OXIDASE ASSEMBLY FACTOR
669	670	RXA02743	GR00763	13534	12497	CYTOCHROME AA3 CONTROLLING PROTEIN
671	672	RXA01227	GR00355	1199	1519	FERREDOXIN
673	674	RXA01865	GR00532	436	122	FERREDOXIN
675	676	RXA00680	GR00179	2632	2315	FERREDOXIN VI
677	678	RXA00679	GR00179	2302	1037	FERREDOXIN-NAD(+) REDUCTASE (EC 1.18.1.3)
679	680	RXA00224	GR00032	24965	24015	ELECTRON TRANSFER FLAVOPROTEIN ALPHA-SUBUNIT
681	682	RXA00225	GR00032	25783	24998	ELECTRON TRANSFER FLAVOPROTEIN BETA-SUBUNIT
683	684	RXN00606	VV0192	11299	9026	NADH DEHYDROGENASE I CHAIN L (EC 1.6.5.3)
685	686	F RXA00606	GR00160	121	1869	NADH DEHYDROGENASE I CHAIN L (EC 1.6.5.3)
687	688	RXN00595	VV0192	8842	7113	NADH DEHYDROGENASE I CHAIN M (EC 1.6.5.3)
689	690	F RXA00608	GR00160	2253	3017	NADH DEHYDROGENASE I CHAIN M (EC 1.6.5.3)
691	692	RXA00913	GR00249	3	2120	NADH DEHYDROGENASE I CHAIN L (EC 1.6.5.3)
693	694	RXA00909	GR00247	2552	3406	NADH DEHYDROGENASE I CHAIN L (EC 1.6.5.3)
695	696	RXA00700	GR00182	846	43	NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 2
697	698	RXN00483	VV0086	44824	46287	NADH-UBIQUINONE OXIDOREDUCTASE 39 KD SUBUNIT PRECURSOR (EC 1.6.5.3) (EC 1.6.99.3)

Table 1 (continued)

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig.	NT Start	NT Stop	Function
699	700	F RXA00483	GR00119	19106	20569	NADH-UBIQUINONE OXIDOREDUCTASE 39 KD SUBUNIT PRECURSOR (EC 1.6.5.3) (EC 1.6.99.3)
701	702	RXA01534	GR00427	1035	547	NADH-DEPENDENT FMN OXYDOREDUCTASE
703	704	RXA00288	GR00046	1636	1636	QUINONE OXIDOREDUCTASE (EC 1.6.5.5)
705	706	RXA02741	GR00763	9585	8620	QUINONE OXIDOREDUCTASE (EC 1.6.5.5)
707	708	RXN02560	VW0101	9922	10788	NADPH-FLAVIN OXIDOREDUCTASE (EC 1.6.99.-)
709	710	F RXA02560	GR00731	6339	7160	NADPH-FLAVIN OXIDOREDUCTASE (EC 1.6.99.-)
711	712	RXA01311	GR00380	1611	865	SUCCINATE DEHYDROGENASE IRON-SULFUR PROTEIN (EC 1.3.99.1)
713	714	RXN03014	VW0058	1273	368	NADH DEHYDROGENASE I CHAIN M (EC 1.6.5.3)
715	716	F RXA00910	GR00248	3	1259	Hydrogenase subunits
717	718	RXN01895	VW0117	955	5	NADH DEHYDROGENASE (EC 1.6.99.3)
719	720	F RXA01895	GR00543	2	817	DEHYDROGENASE
721	722	RXA00703	GR00183	2556	271	FORMATE DEHYDROGENASE ALPHA CHAIN (EC 1.2.1.2)
723	724	RXN00705	VW0005	6111	5197	FDHD PROTEIN
725	726	F RXA00705	GR00184	1291	407	FDHD PROTEIN
727	728	RXN00388	VW0025	2081	3091	CYTOCHROME C BIOGENESIS PROTEIN CCSA
729	730	F RXA00388	GR00085	969	667	essential protein similar to cytochrome c
731	732	F RXA00386	GR00084	514	5	RESC PROTEIN, essential protein similar to cytochrome c biogenesis protein
733	734	RXA00945	GR00259	1876	2847	putative cytochrome oxidase
735	736	RXN02556	VW0101	5602	6759	FLAVOHEMOPROTEIN / DIHYDROPTERIDINE REDUCTASE (EC 1.6.99.7)
737	738	F RXA02556	GR00731	2019	3176	FLAVOHEMOPROTEIN
739	740	RXA01392	GR00408	2297	3373	GLUTATHIONE S-TRANSFERASE (EC 2.5.1.18)
741	742	RXA00800	GR00214	2031	3134	GLUTATHIONE-DEPENDENT FORMALDEHYDE DEHYDROGENASE (EC 1.2.1.1)
743	744	RXA02143	GR00639	10138	11025	QCRC PROTEIN, menaquinol:cytochrome c oxidoreductase
745	746	RXN03096	VW0058	405	4	NADH DEHYDROGENASE I CHAIN M (EC 1.6.5.3)
747	748	RXN02036	VW0176	32683	33063	NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 4 (EC 1.6.5.3)
749	750	RXN02765	VW0317	3552	2784	Hypothetical Oxidoreductase
751	752	RXN02206	VW0302	1784	849	Hypothetical Oxidoreductase
753	754	RXN02554	VW0101	4633	4010	Hypothetical Oxidoreductase (EC 1.1.1.1.-)

ATP-Synthase

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig.	NT Start	NT Stop	Function
755	756	RXN01204	VW0121	1270	461	ATP SYNTHASE A CHAIN (EC 3.6.1.34)
757	758	F RXA01204	GR00345	394	1155	ATP SYNTHASE A CHAIN (EC 3.6.1.34)
759	760	RXA01201	GR00344	675	2315	ATP SYNTHASE ALPHA CHAIN (EC 3.6.1.34)
761	762	RXN01193	VW0175	5280	3832	ATP SYNTHASE BETA CHAIN (EC 3.6.1.34)
763	764	F RXA01193	GR00343	15	755	ATP SYNTHASE BETA CHAIN (EC 3.6.1.34)
765	766	F RXA01203	GR00344	3355	3993	ATP SYNTHASE BETA CHAIN (EC 3.6.1.34)

Table 1 (continued)

<u>Nucleic Acid</u> <u>SEQ ID NO</u>	<u>Amino Acid</u> <u>SEQ ID NO</u>	<u>Identification Code</u>	<u>Contig.</u>	<u>NT Start</u>	<u>NT Stop</u>	<u>Function</u>
767	768	RXN02821	VV0121	324	85	ATP SYNTHASE C CHAIN (EC 3.6.1.34)
769	770	F RXA02821	GR00802	139	318	ATP SYNTHASE C CHAIN (EC 3.6.1.34)
771	772	RXA01200	GR00344	2	610	ATP SYNTHASE DELTA CHAIN (EC 3.6.1.34)
773	774	RXA01194	GR00343	770	1141	ATP SYNTHASE EPSILON CHAIN (EC 3.6.1.34)
775	776	RXA01202	GR00344	2375	3349	ATP SYNTHASE GAMMA CHAIN (EC 3.6.1.34)
777	778	RXN02434	VV0090	4923	3274	ATP-BINDING PROTEIN

Cytochrome metabolism

<u>Nucleic Acid</u> <u>SEQ ID NO</u>	<u>Amino Acid</u> <u>SEQ ID NO</u>	<u>Identification Code</u>	<u>Contig.</u>	<u>NT Start</u>	<u>NT Stop</u>	<u>Function</u>
779	780	RXN00684	VV0005	29864	28581	CYTOCHROME P450 116 (EC 1.14.--)
781	782	RXN00387	VV0025	1150	2004	Hypothetical Cytochrome c Biogenesis Protein

TABLE 2 - Excluded Genes

GenBank™ Accession No.	Gene Name	Gene Function	Reference
A09073	ppg	Phosphoenol pyruvate carboxylase	Bachmann, B. et al. "DNA fragment coding for phosphoenolpyruvate carboxylase, recombinant DNA carrying said fragment, strains carrying the recombinant DNA and method for producing L-aminino acids using said strains," Patent: EP 0358940-A 3 03/21/90
A45579, A45581, A45583, A45585 A45587		Threonine dehydratase	Moockel, B. et al. "Production of L-isoleucine by means of recombinant micro-organisms with deregulated threonine dehydratase," Patent: WO 9519442-A 5 07/20/95
AB003132	murC; ftsQ; ftsZ		Kobayashi, M. et al. "Cloning, sequencing, and characterization of the ftsZ gene from coryneform bacteria," <i>Biochem. Biophys. Res. Commun.</i> , 236(2):383-388 (1997)
AB015023	murC; ftsQ		Wachi, M. et al. "A murC gene from Coryneform bacteria," <i>Appl. Microbiol. Biotechnol.</i> , 51(2):223-228 (1999)
AB018530	ftsR		Kimura, E. et al. "Molecular cloning of a novel gene, ftsR, which rescues the detergent sensitivity of a mutant derived from <i>Brevibacterium lactofermentum</i> ," <i>Biosci. Biotechnol. Biochem.</i> , 60(10):1565-1570 (1996)
AB018531	ftsR1; ftsR2		
AB020624	murI	D-glutamate racemase	
AB023377	tkt	transketolase	
AB024708	glbB; gltD	Glutamine 2-oxoglutarate aminotransferase large and small subunits	
AB025424	acn	aconitase	
AB027714	rep	Replication protein	
AB027715	rep; aad	Replication protein; aminoglycoside adenyltransferase	
AF005242	argC	N-acetylglutamate-5-semialdehyde dehydrogenase	
AF005635	glnA	Glutamine synthetase	
AF030405	hisF	cyclase	
AF030520	argG	Argininosuccinate synthetase	
AF031518	argF	Omithine carbamoyltransferase	
AF036932	aroD	3-dehydroquinate dehydratase	
AF038548	pyc	Pyruvate carboxylase	

Table 2 (continued)

	dcIAE; apt; rel	Dipeptide-binding protein; adenine phosphoribosyltransferase; GTP pyrophosphokinase	Wehmeier, L. et al. "The role of the Corynebacterium glutamicum rel gene in (p)ppGpp metabolism," <i>Microbiology</i> , 144:1853-1862 (1998)
AF038651			
AF041436	argR	Arginine repressor	
AF045998	impA	Inositol monophosphate phosphatase	
AF048764	argH	Argininosuccinate lyase	
AF049897	argC; argJ; argB; argD; argF; argR; argG; argH	N-acetylglutamyolphosphate reductase; ornithine acetyltransferase; N-acetylglutamate kinase; acetylornithine transaminase; ornithine carbamoyltransferase; arginine repressor; argininosuccinate synthase; argininosuccinate lyase	
AF050109	inhA	Enoyl-acyl carrier protein reductase	
AF050166	hisG	ATP phosphoribosyltransferase	
AF051846	hisA	Phosphoribosylformimino-5-amino-1-phosphoribosyl-4-imidazolecarboxamide isomerase	
AF052652	metA	Homoserine O-acetyltransferase	Park, S. et al. "Isolation and analysis of metA, a methionine biosynthetic gene encoding homoserine acetyltransferase in Corynebacterium glutamicum," <i>Mol. Cells</i> , 8(3):286-294 (1998)
AF053071	aroB	Dehydroquinase synthetase	
AF060558	hisH	Glutamine amidotransferase	
AF086704	hisE	Phosphoribosyl-ATP-pyrophosphohydrolase	
AF114233	aroA	5-enolpyruvylshikimate 3-phosphate synthase	
AF116184	panD	L-aspartate-alpha-decarboxylase precursor	Dusch, N. et al. "Expression of the Corynebacterium glutamicum panD gene encoding L-aspartate-alpha-decarboxylase leads to pantothenate overproduction in Escherichia coli," <i>Appl. Environ. Microbiol.</i> , 65(4):1530-1539 (1999)
AF124518	aroD; aroE	3-dehydroquinase; shikimate dehydrogenase	
AF124600	aroC; aroK; aroB; pepQ	Chorismate synthase; shikimate kinase; 3-dehydroquinase synthase; putative cytoplasmic peptidase	
AF145897	inhA		
AF145898	inhA		

Table 2 (continued)

AJ001436	ectP	Transport of ectoine, glycine betaine, proline	Peter, H. et al. "Corynebacterium glutamicum is equipped with four secondary carriers for compatible solutes: Identification, sequencing, and characterization of the proline/ectoine uptake system, ProP, and the ectoine/proline/glycine betaine carrier, EctP," <i>J. Bacteriol.</i> , 180(22):6005-6012 (1998)
AJ004934	dapD	Tetrahydrodipicolinate succinylase (incomplete)	Wehrmann, A. et al. "Different modes of diaminopimelate synthesis and their role in cell wall integrity: A study with <i>Corynebacterium glutamicum</i> ," <i>J. Bacteriol.</i> , 180(12):3159-3165 (1998)
AJ007732	ppc; secG; amt; ocd; soxA	Phosphoenolpyruvate-carboxylase; ?; high affinity ammonium uptake protein; putative ornithine-cyclodecarboxylase; sarcosine oxidase	
AJ010319	ftsY, glnB, glnD; srp; amtP	Involved in cell division; PII protein; uridylyltransferase (uridylyl-removing enzyme); signal recognition particle; low affinity ammonium uptake protein	Jakoby, M. et al. "Nitrogen regulation in <i>Corynebacterium glutamicum</i> ; Isolation of genes involved in biochemical characterization of corresponding proteins," <i>FEMS Microbiol.</i> , 173(2):303-310 (1999)
AJ132968	cat	Chloramphenicol acetyl transferase	
AJ224946	mgo	L-malate: quinone oxidoreductase	Molenaar, D. et al. "Biochemical and genetic characterization of the membrane-associated malate dehydrogenase (acceptor) from <i>Corynebacterium glutamicum</i> ," <i>Eur. J. Biochem.</i> , 254(2):395-403 (1998)
AJ238250	ndh	NADH dehydrogenase	
AJ238703	porA	Porin	Lichtinger, T. et al. "Biochemical and biophysical characterization of the cell wall porin of <i>Corynebacterium glutamicum</i> : The channel is formed by a low molecular mass polypeptide," <i>Biochemistry</i> , 37(43):15024-15032 (1998)
D17429		Transposable element IS31831	Vertes et al. "Isolation and characterization of IS31831, a transposable element from <i>Corynebacterium glutamicum</i> ," <i>Mol. Microbiol.</i> , 11(4):739-746 (1994)
D84102	odhA	2-oxoglutarate dehydrogenase	Usuda, Y. et al. "Molecular cloning of the <i>Corynebacterium glutamicum</i> (Brevibacterium lactofermentum AJ12036) odhA gene encoding a novel type of 2-oxoglutarate dehydrogenase," <i>Microbiology</i> , 142:3347-3354 (1996)
E01358	hdh; hk	Homoserine dehydrogenase; homoserine kinase	Katsumata, R. et al. "Production of L-threonine and L-isoleucine," Patent: JP 1987232392-A 1 10/12/87
E01359		Upstream of the start codon of homoserine kinase gene	Katsumata, R. et al. "Production of L-threonine and L-isoleucine," Patent: JP 1987232392-A 2 10/12/87
E01375		Tryptophan operon	
E01376	trpL; trpE	Leader peptide; anthranilate synthase	Matsui, K. et al. "Tryptophan operon, peptide and protein coded thereby, utilization of tryptophan operon gene expression and production of tryptophan," Patent: JP 1987244382-A 1 10/24/87

Table 2 (continued)

E01377	Promoter and operator regions of tryptophan operon	Matsui, K. et al. "Tryptophan operon, peptide and protein coded thereby, utilization of tryptophan operon gene expression and production of tryptophan," Patent: JP 1987244382-A 1 10/24/87
E03937	Biotin-synthase	Hatakeyama, K. et al. "DNA fragment containing gene capable of coding biotin synthetase and its utilization," Patent: JP 1992278088-A 1 10/02/92
E04040	Diamino pelargonic acid aminotransferase	Kohama, K. et al. "Gene coding diaminopelargonic acid aminotransferase and desthiobiotin synthetase and its utilization," Patent: JP 1992330284-A 1 11/18/92
E04041	Desthiobiotinsynthetase	Kohama, K. et al. "Gene coding diaminopelargonic acid aminotransferase and desthiobiotin synthetase and its utilization," Patent: JP 1992330284-A 1 11/18/92
E04307	Flavum aspartase	Kurusu, Y. et al. "Gene DNA coding aspartase and utilization thereof," Patent: JP 1993030977-A 1 02/09/93
E04376	Isocitric acid lyase	Katsumata, R. et al. "Gene manifestation controlling DNA," Patent: JP 1993056782-A 3 03/09/93
E04377	Isocitric acid lyase N-terminal fragment	Katsumata, R. et al. "Gene manifestation controlling DNA," Patent: JP 1993056782-A 3 03/09/93
E04484	Prephenate dehydratase	Sotouchi, N. et al. "Production of L-phenylalanine by fermentation," Patent: JP 1993076352-A 2 03/30/93
E05108	Aspartokinase	Fugono, N. et al. "Gene DNA coding Aspartokinase and its use," Patent: JP 1993184366-A 1 07/27/93
E05112	Dihydro-dipichorinate synthetase	Hatakeyama, K. et al. "Gene DNA coding dihydrodipicolinic acid synthetase and its use," Patent: JP 1993184371-A 1 07/27/93
E05776	Diaminopimelic acid dehydrogenase	Kobayashi, M. et al. "Gene DNA coding Diaminopimelic acid dehydrogenase and its use," Patent: JP 1993284970-A 1 11/02/93
E05779	Threonine synthase	Kohama, K. et al. "Gene DNA coding threonine synthase and its use," Patent: JP 1993284972-A 1 11/02/93
E06110	Prephenate dehydratase	Kikuchi, T. et al. "Production of L-phenylalanine by fermentation method," Patent: JP 1993344881-A 1 12/27/93
E06111	Mutated Prephenate dehydratase	Kikuchi, T. et al. "Production of L-phenylalanine by fermentation method," Patent: JP 1993344881-A 1 12/27/93
E06146	Acetohydroxy acid synthetase	Inui, M. et al. "Gene capable of coding Acetohydroxy acid synthetase and its use," Patent: JP 1993344893-A 1 12/27/93
E06825	Aspartokinase	Sugimoto, M. et al. "Mutant aspartokinase gene," patent: JP 1994062866-A 1 03/08/94
E06826	Mutated aspartokinase alpha subunit	Sugimoto, M. et al. "Mutant aspartokinase gene," patent: JP 1994062866-A 1 03/08/94

Table 2 (continued)

E06827		Mutated aspartokinase alpha subunit	Sugimoto, M. et al. "Mutant aspartokinase gene," patent: JP 1994062866-A I 03/08/94
E07701	secY		Honno, N. et al. "Gene DNA participating in integration of membraneous protein to membrane," Patent: JP 1994169780-A I 06/21/94
E08177		Aspartokinase	Sato, Y. et al. "Genetic DNA capable of coding Aspartokinase released from feedback inhibition and its utilization," Patent: JP 1994261766-A I 09/20/94
E08178, E08179, E08180, E08181, E08182		Feedback inhibition-released Aspartokinase	Sato, Y. et al. "Genetic DNA capable of coding Aspartokinase released from feedback inhibition and its utilization," Patent: JP 1994261766-A I 09/20/94
E08232		Acetohydroxy-acid isomeroreductase	Inui, M. et al. "Gene DNA coding acetohydroxy acid isomeroreductase," Patent: JP 1994277067-A I 10/04/94
E08234	secE		Asai, Y. et al. "Gene DNA coding for translocation machinery of protein," Patent: JP 1994277073-A I 10/04/94
E08643		FT aminotransferase and desthiobiotin synthetase promoter region	Hatakeyama, K. et al. "DNA fragment having promoter function in coryneform bacterium," Patent: JP 1995031476-A I 02/03/95
E08646		Biotin synthetase	Hatakeyama, K. et al. "DNA fragment having promoter function in coryneform bacterium," Patent: JP 1995031476-A I 02/03/95
E08649		Aspartase	Kohama, K. et al. "DNA fragment having promoter function in coryneform bacterium," Patent: JP 1995031478-A I 02/03/95
E08900		Dihydrodipicolinate reductase	Madori, M. et al. "DNA fragment containing gene coding Dihydrodipicolinate acid reductase and utilization thereof," Patent: JP 1995075578-A I 03/20/95
E08901		Diaminopimelic acid decarboxylase	Madori, M. et al. "DNA fragment containing gene coding Diaminopimelic acid decarboxylase and utilization thereof," Patent: JP 1995075579-A I 03/20/95
E12594		Serine hydroxymethyltransferase	Hatakeyama, K. et al. "Production of L-tryptophan," Patent: JP 1997028391-A I 02/04/97
E12760, E12759, E12758		transposase	Moriya, M. et al. "Amplification of gene using artificial transposon," Patent: JP 1997070291-A 03/18/97
E12764		Arginyl-tRNA synthetase; diaminopimelic acid decarboxylase	Moriya, M. et al. "Amplification of gene using artificial transposon," Patent: JP 1997070291-A 03/18/97
E12767		Dihydrodipicolinic acid synthetase	Moriya, M. et al. "Amplification of gene using artificial transposon," Patent: JP 1997070291-A 03/18/97
E12770		aspartokinase	Moriya, M. et al. "Amplification of gene using artificial transposon," Patent: JP 1997070291-A 03/18/97
E12773		Dihydrodipicolinic acid reductase	Moriya, M. et al. "Amplification of gene using artificial transposon," Patent: JP 1997070291-A 03/18/97

Table 2 (continued)

E13655		Glucose-6-phosphate dehydrogenase	Hatakeyama, K. et al. "Glucose-6-phosphate dehydrogenase and DNA capable of coding the same," Patent: JP 1997224661-A 1 09/02/97
L01508	ilvA	Threonine dehydratase	Moekkel, B. et al. "Functional and structural analysis of the threonine dehydratase of Corynebacterium glutamicum," <i>J. Bacteriol.</i> , 174:8065-8072 (1992)
L07603	EC 4.2.1.15	3-deoxy-D-arabinoheptulosonate-7-phosphate synthase	Chen, C. et al. "The cloning and nucleotide sequence of Corynebacterium glutamicum 3-deoxy-D-arabinoheptulosonate-7-phosphate synthase gene," <i>FEMS Microbiol. Lett.</i> , 107:223-230 (1993)
L09232	ilvB; ilvN; ilvC	Acetohydroxy acid synthase large subunit; Acetohydroxy acid synthase small subunit; Acetohydroxy acid isomeroreductase	Keilhauer, C. et al. "Isoleucine synthesis in Corynebacterium glutamicum: molecular analysis of the ilvB-ilvN-ilvC operon," <i>J. Bacteriol.</i> , 175(17):5595-5603 (1993)
L18874	PtsM	Phosphoenolpyruvate sugar phosphotransferase	Fouet, A. et al. "Bacillus subtilis sucrose-specific enzyme II of the phosphotransferase system: expression in Escherichia coli and homology to enzymes II from enteric bacteria," <i>PNAS USA</i> , 84(24):8773-8777 (1987); Lee, J.K. et al. "Nucleotide sequence of the gene encoding the Corynebacterium glutamicum mannose enzyme II and analyses of the deduced protein sequence," <i>FEMS Microbiol. Lett.</i> , 119(1-2):137-145 (1994)
L27123	aceB	Malate synthase	Lee, H.-S. et al. "Molecular characterization of aceB, a gene encoding malate synthase in Corynebacterium glutamicum," <i>J. Microbiol. Biotechnol.</i> , 4(4):256-263 (1994)
L27126		Pyruvate kinase	Jetten, M. S. et al. "Structural and functional analysis of pyruvate kinase from Corynebacterium glutamicum," <i>Appl. Environ. Microbiol.</i> , 60(7):2501-2507 (1994)
L28760	aceA	Isocitrate lyase	
L35906	dtxR	Diphtheria toxin repressor	Oguiza, J.A. et al. "Molecular cloning, DNA sequence analysis, and characterization of the Corynebacterium diphtheriae dtxR from Brevibacterium lactofermentum," <i>J. Bacteriol.</i> , 177(2):465-467 (1995)
M13774		Prephenate dehydratase	Follettie, M.T. et al. "Molecular cloning and nucleotide sequence of the Corynebacterium glutamicum pheA gene," <i>J. Bacteriol.</i> , 167:695-702 (1986)
M16175	5S rRNA		Park, Y.-H. et al. "Phylogenetic analysis of the coryneform bacteria by 5S rRNA sequences," <i>J. Bacteriol.</i> , 169:1801-1806 (1987)
M16663	trpE	Anthranilate synthase, 5' end	Sano, K. et al. "Structure and function of the trp operon control regions of Brevibacterium lactofermentum, a glutamic-acid-producing bacterium," <i>Gene</i> , 52:191-200 (1987)
M16664	trpA	Tryptophan synthase, 3' end	Sano, K. et al. "Structure and function of the trp operon control regions of Brevibacterium lactofermentum, a glutamic-acid-producing bacterium," <i>Gene</i> , 52:191-200 (1987)

Table 2 (continued)

		Phosphoenolpyruvate carboxylase	
M25819			O'Regan, M. et al. "Cloning and nucleotide sequence of the Phosphoenolpyruvate carboxylase-coding gene of <i>Corynebacterium glutamicum</i> ATCC13032," <i>Gene</i> , 77(2):237-251 (1989)
M85106		23S rRNA gene insertion sequence	Roller, C. et al. "Gram-positive bacteria with a high DNA G+C content are characterized by a common insertion within their 23S rRNA genes," <i>J. Gen. Microbiol.</i> , 138:1167-1175 (1992)
M85107, M85108		23S rRNA gene insertion sequence	Roller, C. et al. "Gram-positive bacteria with a high DNA G+C content are characterized by a common insertion within their 23S rRNA genes," <i>J. Gen. Microbiol.</i> , 138:1167-1175 (1992)
M89931	aecD; bmq; yhbw	Beta C-S lyase; branched-chain amino acid uptake carrier; hypothetical protein yhbw	Rossol, J. et al. "The <i>Corynebacterium glutamicum</i> aecD gene encodes a C-S lyase with alpha, beta-elimination activity that degrades aminoethylcysteine," <i>J. Bacteriol.</i> , 174(9):2968-2977 (1992); Tauch, A. et al. "Isoleucine uptake in <i>Corynebacterium glutamicum</i> ATCC 13032 is directed by the bmq gene product," <i>Arch. Microbiol.</i> , 169(4):303-312 (1998)
S59299	trp	Leader gene (promoter)	Herry, D.M. et al. "Cloning of the trp gene cluster from a tryptophan-hyperproducing strain of <i>Corynebacterium glutamicum</i> : identification of a mutation in the trp leader sequence," <i>Appl. Environ. Microbiol.</i> , 59(3):791-799 (1993)
U11545	trpD	Anthraniolate phosphoribosyltransferase	O'Gara, J.P. and Dunican, L.K. (1994) Complete nucleotide sequence of the <i>Corynebacterium glutamicum</i> ATCC 21850 trpD gene." Thesis, Microbiology Department, University College Galway, Ireland.
U13922	cglIM; cglIR; cglIIR	Putative type II 5-cytosine methyltransferase; putative type II restriction endonuclease; putative type I or type III restriction endonuclease	Schafer, A. et al. "Cloning and characterization of a DNA region encoding a stress-sensitive restriction system from <i>Corynebacterium glutamicum</i> ATCC 13032 and analysis of its role in intergeneric conjugation with <i>Escherichia coli</i> ," <i>J. Bacteriol.</i> , 176(23):7309-7319 (1994); Schafer, A. et al. "The <i>Corynebacterium glutamicum</i> cglIM gene encoding a 5-cytosine in an McrBC-deficient <i>Escherichia coli</i> strain," <i>Gene</i> , 203(2):95-101 (1997)
U14965	recA		
U31224	ppx		Ankri, S. et al. "Mutations in the <i>Corynebacterium glutamicum</i> proline biosynthetic pathway: A natural bypass of the proA step," <i>J. Bacteriol.</i> , 178(15):4412-4419 (1996)
U31225	proC	L-proline: NADP+ 5-oxidoreductase	Ankri, S. et al. "Mutations in the <i>Corynebacterium glutamicum</i> proline biosynthetic pathway: A natural bypass of the proA step," <i>J. Bacteriol.</i> , 178(15):4412-4419 (1996)
U31230	obg; proB; unkdh	?; gamma glutamyl kinase; similar to D-isomer specific 2-hydroxyacid dehydrogenases	Ankri, S. et al. "Mutations in the <i>Corynebacterium glutamicum</i> proline biosynthetic pathway: A natural bypass of the proA step," <i>J. Bacteriol.</i> , 178(15):4412-4419 (1996)

Table 2 (continued)

U31281	bioB	Biotin synthase	Serebriiskii, I.G., "Two new members of the bio B superfamily: Cloning, sequencing and expression of bio B genes of <i>Methylobacillus flagellatum</i> and <i>Corynebacterium glutamicum</i> ," <i>Gene</i> , 175:15-22 (1996)
U35023	thtR, accBC	Thiosulfate sulfurtransferase; acyl CoA carboxylase	Jager, W. et al. "A <i>Corynebacterium glutamicum</i> gene encoding a two-domain protein similar to biotin carboxylases and biotin-carboxyl-carrier proteins," <i>Arch. Microbiol.</i> , 166(2):76-82 (1996)
U43535	cmr	Multidrug resistance protein	Jager, W. et al. "A <i>Corynebacterium glutamicum</i> gene conferring multidrug resistance in the heterologous host <i>Escherichia coli</i> ," <i>J. Bacteriol.</i> , 179(7):2449-2451 (1997)
U43536	clpB	Heat shock ATP-binding protein	
U53587	aphA-3	3'5'-aminoglycoside phosphotransferase	
U89648		<i>Corynebacterium glutamicum</i> unidentified sequence involved in histidine biosynthesis, partial sequence	
X04960	trpA; trpB; trpC; trpD; trpE; trpG; trpL	Tryptophan operon	Matsui, K. et al. "Complete nucleotide and deduced amino acid sequences of the <i>Brevibacterium lactofermentum</i> tryptophan operon," <i>Nucleic Acids Res.</i> , 14(24):10113-10114 (1986)
X07563	lys A	DAP decarboxylase (meso-diaminopimelate decarboxylase, EC 4.1.1.20)	Yeh, P. et al. "Nucleic sequence of the lysA gene of <i>Corynebacterium glutamicum</i> and possible mechanisms for modulation of its expression," <i>Mol. Gen. Genet.</i> , 212(1):112-119 (1988)
X14234	EC 4.1.1.31	Phosphoenolpyruvate carboxylase	Elkmanns, B.J. et al. "The Phosphoenolpyruvate carboxylase gene of <i>Corynebacterium glutamicum</i> : Molecular cloning, nucleotide sequence, and expression," <i>Mol. Gen. Genet.</i> , 218(2):330-339 (1989); Lepiniec, L. et al. "Sorghum Phosphoenolpyruvate carboxylase gene family: structure, function and molecular evolution," <i>Plant. Mol. Biol.</i> , 21 (3):487-502 (1993)
X17313	fda	Fructose-bisphosphate aldolase	Von der Osten, C.H. et al. "Molecular cloning, nucleotide sequence and fine-structural analysis of the <i>Corynebacterium glutamicum</i> fda gene: structural comparison of <i>C. glutamicum</i> fructose-1, 6-bisphosphate aldolase to class I and class II aldolases," <i>Mol. Microbiol.</i>
X53993	dapA	L-2, 3-dihydrodipicolinate synthetase (EC 4.2.1.52)	Bonnassie, S. et al. "Nucleic sequence of the dapA gene from <i>Corynebacterium glutamicum</i> ," <i>Nucleic Acids Res.</i> , 18(21):6421 (1990)
X54223		AttB-related site	Ciancio, N. et al. "DNA sequence homology between att B-related sites of <i>Corynebacterium diphtheriae</i> , <i>Corynebacterium ulcerans</i> , <i>Corynebacterium glutamicum</i> , and the attP site of lambda corynebacteriophage," <i>FEMS. Microbiol. Lett.</i> , 66:299-302 (1990)
X54740	argS; lysA	Arginyl-tRNA synthetase; Diaminopimelate decarboxylase	Marcel, T. et al. "Nucleotide sequence and organization of the upstream region of the <i>Corynebacterium glutamicum</i> lysA gene," <i>Mol. Microbiol.</i> , 4(11):1819-1830 (1990)

Table 2 (continued)

X55994	trpL; trpE	Putative leader peptide; anthranilate synthase component I	Heery, D.M. et al. "Nucleotide sequence of the Corynebacterium glutamicum trpE gene," <i>Nucleic Acids Res.</i> , 18(23):7138 (1990)
X56037	thrC	Threonine synthase	Han, K.S. et al. "The molecular structure of the Corynebacterium glutamicum threonine synthase gene," <i>Mol. Microbiol.</i> , 4(10):1693-1702 (1990)
X56075	attB-related site	Attachment site	Cianciotto, N. et al. "DNA sequence homology between att B-related sites of Corynebacterium diphtheriae, Corynebacterium ulcerans, Corynebacterium glutamicum, and the attP site of lambdaCorynephage," <i>FEMS. Microbiol. Lett.</i> , 66:299-302 (1990)
X57226	lysC-alpha; lysC-beta; asd	Aspartokinase-alpha subunit; Aspartokinase-beta subunit; aspartate beta semialdehyde dehydrogenase	Kalinowski, J. et al. "Genetic and biochemical analysis of the Aspartokinase from Corynebacterium glutamicum," <i>Mol. Microbiol.</i> , 5(5):1197-1204 (1991); Kalinowski, J. et al. "Aspartokinase genes lysC alpha and lysC beta overlap and are adjacent to the aspartate beta-semialdehyde dehydrogenase gene asd in Corynebacterium glutamicum," <i>Mol. Gen. Genet.</i> , 224(3):317-324 (1990)
X59403	gap;pgk; tpi	Glyceraldehyde-3-phosphate; phosphoglycerate kinase; triosephosphate isomerase	Eikmanns, B.J. "Identification, sequence analysis, and expression of a Corynebacterium glutamicum gene cluster encoding the three glycolytic enzymes glyceraldehyde-3-phosphate dehydrogenase, 3-phosphoglycerate kinase, and triosephosphate isomerase," <i>J. Bacteriol.</i> , 174(19):6076-6086 (1992)
X59404	gdh	Glutamate dehydrogenase	Bormann, E.R. et al. "Molecular analysis of the Corynebacterium glutamicum gdh gene encoding glutamate dehydrogenase," <i>Mol. Microbiol.</i> , 6(3):317-326 (1992)
X60312	lysI	L-lysine permease	Seep-Feldhaus, A.H. et al. "Molecular analysis of the Corynebacterium glutamicum lysI gene involved in lysine uptake," <i>Mol. Microbiol.</i> , 5(12):2995-3005 (1991)
X66078	copI	Psl protein	Joliff, G. et al. "Cloning and nucleotide sequence of the cspI gene encoding Psl, one of the two major secreted proteins of Corynebacterium glutamicum: The deduced N-terminal region of Psl is similar to the Mycobacterium antigen 85 complex," <i>Mol. Microbiol.</i> , 6(16):2349-2362 (1992)
X66112	glt	Citrate synthase	Eikmanns, B.J. et al. "Cloning sequence, expression and transcriptional analysis of the Corynebacterium glutamicum gltA gene encoding citrate synthase," <i>Microbiol.</i> , 140:1817-1828 (1994)
X67737	dapB	Dihydrodipicolinate reductase	
X69103	csp2	Surface layer protein PS2	Peyret, J.L. et al. "Characterization of the cspB gene encoding PS2, an ordered surface-layer protein in Corynebacterium glutamicum," <i>Mol. Microbiol.</i> , 9(1):97-109 (1993)
X69104		IS3 related insertion element	Bonamy, C. et al. "Identification of IS1206, a Corynebacterium glutamicum IS3-related insertion sequence and phylogenetic analysis," <i>Mol. Microbiol.</i> , 14(3):571-581 (1994)

Table 2 (continued)

X70959	leuA	Isopropylmalate synthase	Patek, M. et al. "Leucine synthesis in <i>Corynebacterium glutamicum</i> : enzyme activities, structure of leuA, and effect of leuA inactivation on lysine synthesis," <i>Appl. Environ. Microbiol.</i> , 60(1):133-140 (1994)
X71489	icd	Isocitrate dehydrogenase (NADP+)	Eikmanns, B.J. et al. "Cloning sequence analysis, expression, and inactivation of the <i>Corynebacterium glutamicum</i> icd gene encoding isocitrate dehydrogenase and biochemical characterization of the enzyme," <i>J. Bacteriol.</i> , 177(3):774-782 (1995)
X72855	GDHA	Glutamate dehydrogenase (NADP+)	
X75083, X70584	mitrA	5-methyltryptophan resistance	Heery, D.M. et al. "A sequence from a tryptophan-hyperproducing strain of <i>Corynebacterium glutamicum</i> encoding resistance to 5-methyltryptophan," <i>Biochem. Biophys. Res. Commun.</i> , 201(3):1255-1262 (1994)
X75085	recA		Fitzpatrick, R. et al. "Construction and characterization of recA mutant strains of <i>Corynebacterium glutamicum</i> and <i>Brevibacterium lactofermentum</i> ," <i>Appl. Microbiol. Biotechnol.</i> , 42(4):575-580 (1994)
X75504	aceA; thiX	Partial Isocitrate lyase; ?	Reinscheid, D.J. et al. "Characterization of the isocitrate lyase gene from <i>Corynebacterium glutamicum</i> and biochemical analysis of the enzyme," <i>J. Bacteriol.</i> , 176(12):3474-3483 (1994)
X76875		ATPase beta-subunit	Ludwig, W. et al. "Phylogenetic relationships of bacteria based on comparative sequence analysis of elongation factor Tu and ATP-synthase beta-subunit genes," <i>Antonie Van Leeuwenhoek</i> , 64:285-305 (1993)
X77034	tuf	Elongation factor Tu	Ludwig, W. et al. "Phylogenetic relationships of bacteria based on comparative sequence analysis of elongation factor Tu and ATP-synthase beta-subunit genes," <i>Antonie Van Leeuwenhoek</i> , 64:285-305 (1993)
X77384	recA		Billman-Jacobe, H. "Nucleotide sequence of a recA gene from <i>Corynebacterium glutamicum</i> ," <i>DNA Seq.</i> , 4(6):403-404 (1994)
X78491	aceB	Malate synthase	Reinscheid, D.J. et al. "Malate synthase from <i>Corynebacterium glutamicum</i> pia-ack operon encoding phosphotransacetylase: sequence analysis," <i>Microbiology</i> , 140:3099-3108 (1994)
X80629	16S rDNA	16S ribosomal RNA	Rainey, F.A. et al. "Phylogenetic analysis of the genera <i>Rhodococcus</i> and <i>Norcardia</i> and evidence for the evolutionary origin of the genus <i>Norcardia</i> from within the radiation of <i>Rhodococcus</i> species," <i>Microbiol.</i> , 141:523-528 (1995)
X81191	gluA; gluB; gluC; gluD	Glutamate uptake system	Kronmeyer, W. et al. "Structure of the gluABCD cluster encoding the glutamate uptake system of <i>Corynebacterium glutamicum</i> ," <i>J. Bacteriol.</i> , 177(5):1152-1158 (1995)
X81379	dapE	Succinyl/diaminopimelate desuccinylase	Wehrmann, A. et al. "Analysis of different DNA fragments of <i>Corynebacterium glutamicum</i> complementing dapE of <i>Escherichia coli</i> ," <i>Microbiology</i> , 40:3349-56 (1994)

Table 2 (continued)

X82061	16S rDNA	16S ribosomal RNA	Ruimy, R. et al. "Phylogeny of the genus <i>Corynebacterium</i> deduced from analyses of small-subunit ribosomal DNA sequences," <i>Int. J. Syst. Bacteriol.</i> , 45(4):740-746 (1995)
X82928	asd; lysC	Aspartate-semialdehyde dehydrogenase; ?	Serebrijski, I. et al. "Multicopy suppression by asd gene and osmotic stress-dependent complementation by heterologous proA in proA mutants," <i>J. Bacteriol.</i> , 177(24):7255-7260 (1995)
X82929	proA	Gamma-glutamyl phosphate reductase	Serebrijski, I. et al. "Multicopy suppression by asd gene and osmotic stress-dependent complementation by heterologous proA in proA mutants," <i>J. Bacteriol.</i> , 177(24):7255-7260 (1995)
X84257	16S rDNA	16S ribosomal RNA	Pascual, C. et al. "Phylogenetic analysis of the genus <i>Corynebacterium</i> based on 16S rRNA gene sequences," <i>Int. J. Syst. Bacteriol.</i> , 45(4):724-728 (1995)
X85965	aroP; dapE	Aromatic amino acid permease; ?	Wehrmann et al. "Functional analysis of sequences adjacent to dapE of <i>C. glutamicum</i> proline reveals the presence of aroP, which encodes the aromatic amino acid transporter," <i>J. Bacteriol.</i> , 177(20):5991-5993 (1995)
X86157	argB; argC; argD; argF; argJ	Acetylglutamate kinase; N-acetyl-gamma-glutamyl-phosphate reductase; acetylornithine aminotransferase; ornithine carbamoyltransferase; glutamate N-acetyltransferase	Sakanyan, V. et al. "Genes and enzymes of the acetyl cycle of arginine biosynthesis in <i>Corynebacterium glutamicum</i> : enzyme evolution in the early steps of the arginine pathway," <i>Microbiology</i> , 142:99-108 (1996)
X89084	pta; ackA	Phosphate acetyltransferase; acetate kinase	Reinscheid, D.J. et al. "Cloning, sequence analysis, expression and inactivation of the <i>Corynebacterium glutamicum</i> pta-ack operon encoding phosphotransacetylase and acetate kinase," <i>Microbiology</i> , 145:503-513 (1999)
X89850	attB	Attachment site	Le Marrec, C. et al. "Genetic characterization of site-specific integration functions of phi AAU2 infecting <i>Arthrobacter aureus</i> C70," <i>J. Bacteriol.</i> , 178(7):1996-2004 (1996)
X90356		Promoter fragment F1	Patek, M. et al. "Promoters from <i>Corynebacterium glutamicum</i> : cloning, molecular analysis and search for a consensus motif," <i>Microbiology</i> , 142:1297-1309 (1996)
X90357		Promoter fragment F2	Patek, M. et al. "Promoters from <i>Corynebacterium glutamicum</i> : cloning, molecular analysis and search for a consensus motif," <i>Microbiology</i> , 142:1297-1309 (1996)
X90358		Promoter fragment F10	Patek, M. et al. "Promoters from <i>Corynebacterium glutamicum</i> : cloning, molecular analysis and search for a consensus motif," <i>Microbiology</i> , 142:1297-1309 (1996)
X90359		Promoter fragment F13	Patek, M. et al. "Promoters from <i>Corynebacterium glutamicum</i> : cloning, molecular analysis and search for a consensus motif," <i>Microbiology</i> , 142:1297-1309 (1996)

Table 2 (continued)

X90360		Promoter fragment F22	Patek, M. et al. "Promoters from <i>Corynebacterium glutamicum</i> : cloning, molecular analysis and search for a consensus motif," <i>Microbiology</i> , 142:1297-1309 (1996)
X90361		Promoter fragment F34	Patek, M. et al. "Promoters from <i>Corynebacterium glutamicum</i> : cloning, molecular analysis and search for a consensus motif," <i>Microbiology</i> , 142:1297-1309 (1996)
X90362		Promoter fragment F37	Patek, M. et al. "Promoters from <i>C. glutamicum</i> : cloning, molecular analysis and search for a consensus motif," <i>Microbiology</i> , 142:1297-1309 (1996)
X90363		Promoter fragment F45	Patek, M. et al. "Promoters from <i>Corynebacterium glutamicum</i> : cloning, molecular analysis and search for a consensus motif," <i>Microbiology</i> , 142:1297-1309 (1996)
X90364		Promoter fragment F64	Patek, M. et al. "Promoters from <i>Corynebacterium glutamicum</i> : cloning, molecular analysis and search for a consensus motif," <i>Microbiology</i> , 142:1297-1309 (1996)
X90365		Promoter fragment F75	Patek, M. et al. "Promoters from <i>Corynebacterium glutamicum</i> : cloning, molecular analysis and search for a consensus motif," <i>Microbiology</i> , 142:1297-1309 (1996)
X90366		Promoter fragment PF101	Patek, M. et al. "Promoters from <i>Corynebacterium glutamicum</i> : cloning, molecular analysis and search for a consensus motif," <i>Microbiology</i> , 142:1297-1309 (1996)
X90367		Promoter fragment PF104	Patek, M. et al. "Promoters from <i>Corynebacterium glutamicum</i> : cloning, molecular analysis and search for a consensus motif," <i>Microbiology</i> , 142:1297-1309 (1996)
X90368		Promoter fragment PF109	Patek, M. et al. "Promoters from <i>Corynebacterium glutamicum</i> : cloning, molecular analysis and search for a consensus motif," <i>Microbiology</i> , 142:1297-1309 (1996)
X93513	amt	Ammonium transport system	Siewe, R.M. et al. "Functional and genetic characterization of the (methyl) ammonium uptake carrier of <i>Corynebacterium glutamicum</i> ," <i>J. Biol. Chem.</i> , 271(10):5398-5403 (1996)
X93514	betP	Glycine betaine transport system	Peter, H. et al. "Isolation, characterization, and expression of the <i>Corynebacterium glutamicum</i> betP gene, encoding the transport system for the compatible solute glycine betaine," <i>J. Bacteriol.</i> , 178(17):5229-5234 (1996)
X95649	orf4		Patek, M. et al. "Identification and transcriptional analysis of the dapB-ORF2-dapA-ORF4 operon of <i>Corynebacterium glutamicum</i> , encoding two enzymes involved in L-lysine synthesis," <i>Biotechnol. Lett.</i> , 19:1113-1117 (1997)
X96471	lysE; lysG	Lysine exporter protein; Lysine export regulator protein	Vrljic, M. et al. "A new type of transporter with a new type of cellular function: L-lysine export from <i>Corynebacterium glutamicum</i> ," <i>Mol. Microbiol.</i> , 22(5):815-826 (1996)

Table 2 (continued)

X96580	panB; panC; xylB	3-methyl-2-oxobutanoate hydroxymethyltransferase; pantoate-beta-alanine ligase; xylulokinase	Sahm, H. et al. "D-pantothenate synthesis in Corynebacterium glutamicum and use of panBC and genes encoding L-valine synthesis for D-pantothenate overproduction," <i>Appl. Environ. Microbiol.</i> , 65(5):1973-1979 (1999)
X96962		Insertion sequence IS1207 and transposase	
X99289		Elongation factor P	Ramos, A. et al. "Cloning, sequencing and expression of the gene encoding elongation factor P in the amino-acid producer Brevibacterium lactofermentum (Corynebacterium glutamicum ATCC 13869)," <i>Gene</i> , 198:217-222 (1997)
Y00140	thrB	Homoserine kinase	Mateos, L.M. et al. "Nucleotide sequence of the homoserine kinase (thrB) gene of the Brevibacterium lactofermentum," <i>Nucleic Acids Res.</i> , 15(9):3922 (1987)
Y00151	ddh	Meso-diaminopimelate D-dehydrogenase (EC 1.4.1.16)	Ishino, S. et al. "Nucleotide sequence of the meso-diaminopimelate D-dehydrogenase gene from Corynebacterium glutamicum," <i>Nucleic Acids Res.</i> , 15(9):3917 (1987)
Y00476	thrA	Homoserine dehydrogenase	Mateos, L.M. et al. "Nucleotide sequence of the homoserine dehydrogenase (thrA) gene of the Brevibacterium lactofermentum," <i>Nucleic Acids Res.</i> , 15(24):10598 (1987)
Y00546	hom; thrB	Homoserine dehydrogenase; homoserine kinase	Peoples, O.P. et al. "Nucleotide sequence and fine structural analysis of the Corynebacterium glutamicum hom-thrB operon," <i>Mol. Microbiol.</i> , 2(1):63-72 (1988)
Y08964	murC; ftsQ/divD; ftsZ	UPD-N-acetylmuramate-alanine ligase; division initiation protein or cell division protein; cell division protein	Honrubia, M.P. et al. "Identification, characterization, and chromosomal organization of the ftsZ gene from Brevibacterium lactofermentum," <i>Mol. Gen. Genet.</i> , 259(1):97-104 (1998)
Y09163	putP	High affinity proline transport system	Peter, H. et al. "Isolation of the putP gene of Corynebacterium glutamicumproline and characterization of a low-affinity uptake system for compatible solutes," <i>Arch. Microbiol.</i> , 168(2):143-151 (1997)
Y09548	pyc	Pyruvate carboxylase	Peters-Wendisch, P.G. et al. "Pyruvate carboxylase from Corynebacterium glutamicum: characterization, expression and inactivation of the pyc gene," <i>Microbiology</i> , 144:915-927 (1998)
Y09578	leuB	3-isopropylmalate dehydrogenase	Patek, M. et al. "Analysis of the leuB gene from Corynebacterium glutamicum," <i>Appl. Microbiol. Biotechnol.</i> , 50(1):42-47 (1998)
Y12472		Attachment site bacteriophage Phi-16	Moreau, S. et al. "Site-specific integration of corynebacteriophage Phi-16: The construction of an integration vector," <i>Microbiol.</i> , 145:539-548 (1999)
Y12537	proP	Proline/ectoine uptake system protein	Peter, H. et al. "Corynebacterium glutamicum is equipped with four secondary carriers for compatible solutes: Identification, sequencing, and characterization of the proline/ectoine uptake system, ProP, and the ectoine/proline/glycine betaine carrier, EctP," <i>J. Bacteriol.</i> , 180(22):6005-6012 (1998)

Table 2 (continued)

	glnA	Glutamine synthetase I	
Y13221			Jakoby, M. et al. "Isolation of <i>Corynebacterium glutamicum</i> glnA gene encoding glutamine synthetase I," <i>FEMS Microbiol. Lett.</i> , 154(1):81-88 (1997)
Y16642	lpd	Dihydrolipoamide dehydrogenase	
Y18059		Attachment site <i>Corynebacterium</i> 304L	Moreau, S. et al. "Analysis of the integration functions of ϕ 304L: An integrase module among corynebacteriophages," <i>Virology</i> , 255(1):150-159 (1999)
Z21501	argS; lysA	Arginyl-tRNA synthetase; diaminopimelate decarboxylase (partial)	Oguiza, J.A. et al. "A gene encoding arginyl-tRNA synthetase is located in the upstream region of the lysA gene in <i>Brevibacterium lactofermentum</i> : Regulation of argS-lysA cluster expression by arginine," <i>J. Bacteriol.</i> , 175(22):7356-7362 (1993)
Z21502	dapA; dapB	Dihydrodipicolinate synthase; dihydrodipicolinate reductase	Pisabarro, A. et al. "A cluster of three genes (dapA, orf2, and dapB) of <i>Brevibacterium lactofermentum</i> encodes dihydrodipicolinate reductase, and a third polypeptide of unknown function," <i>J. Bacteriol.</i> , 175(9):2743-2749 (1993)
Z29563	thrC	Threonine synthase	Malumbres, M. et al. "Analysis and expression of the thrC gene of the encoded threonine synthase," <i>Appl. Environ. Microbiol.</i> , 60(7):2209-2219 (1994)
Z46753	16S rDNA	Gene for 16S ribosomal RNA	
Z49822	sigA	SigA sigma factor	Oguiza, J.A. et al. "Multiple sigma factor genes in <i>Brevibacterium lactofermentum</i> : Characterization of sigA and sigB," <i>J. Bacteriol.</i> , 178(2):550-553 (1996)
Z49823	galE; dtxR	Catalytic activity UDP-galactose 4-epimerase; diphtheria toxin regulatory protein	Oguiza, J.A. et al. "The galE gene encoding the UDP-galactose 4-epimerase of <i>Brevibacterium lactofermentum</i> is coupled transcriptionally to the dmdR gene," <i>Gene</i> , 177:103-107 (1996)
Z49824	orf1; sigB	?; SigB sigma factor	Oguiza, J.A. et al. "Multiple sigma factor genes in <i>Brevibacterium lactofermentum</i> : Characterization of sigA and sigB," <i>J. Bacteriol.</i> , 178(2):550-553 (1996)
Z66534		Transposase	Correia, A. et al. "Cloning and characterization of an IS-like element present in the genome of <i>Brevibacterium lactofermentum</i> ATCC 13869," <i>Gene</i> , 170(1):91-94 (1996)
A sequence for this gene was published in the indicated reference. However, the sequence obtained by the inventors of the present application is significantly longer than the published version. It is believed that the published version relied on an incorrect start codon, and thus represents only a fragment of the actual coding region.			

TABLE 3: *Corynebacterium* and *Brevibacterium* Strains Which May be Used in the Practice of the Invention

Genus	species	ATCC	FERM	NRRL	CECT	NCIMB	CBS	NCTC	DSMZ
<i>Brevibacterium</i>	<i>ammoniagenes</i>	21054							
<i>Brevibacterium</i>	<i>ammoniagenes</i>	19350							
<i>Brevibacterium</i>	<i>ammoniagenes</i>	19351							
<i>Brevibacterium</i>	<i>ammoniagenes</i>	19352							
<i>Brevibacterium</i>	<i>ammoniagenes</i>	19353							
<i>Brevibacterium</i>	<i>ammoniagenes</i>	19354							
<i>Brevibacterium</i>	<i>ammoniagenes</i>	19355							
<i>Brevibacterium</i>	<i>ammoniagenes</i>	19356							
<i>Brevibacterium</i>	<i>ammoniagenes</i>	21055							
<i>Brevibacterium</i>	<i>ammoniagenes</i>	21077							
<i>Brevibacterium</i>	<i>ammoniagenes</i>	21553							
<i>Brevibacterium</i>	<i>ammoniagenes</i>	21580							
<i>Brevibacterium</i>	<i>ammoniagenes</i>	39101							
<i>Brevibacterium</i>	<i>butanicum</i>	21196							
<i>Brevibacterium</i>	<i>divaricatum</i>	21792	P928						
<i>Brevibacterium</i>	<i>flavum</i>	21474							
<i>Brevibacterium</i>	<i>flavum</i>	21129							
<i>Brevibacterium</i>	<i>flavum</i>	21518							
<i>Brevibacterium</i>	<i>flavum</i>			B11474					
<i>Brevibacterium</i>	<i>flavum</i>			B11472					
<i>Brevibacterium</i>	<i>flavum</i>	21127							
<i>Brevibacterium</i>	<i>flavum</i>	21128							
<i>Brevibacterium</i>	<i>flavum</i>	21427							
<i>Brevibacterium</i>	<i>flavum</i>	21475							
<i>Brevibacterium</i>	<i>flavum</i>	21517							
<i>Brevibacterium</i>	<i>flavum</i>	21528							
<i>Brevibacterium</i>	<i>flavum</i>	21529							
<i>Brevibacterium</i>	<i>flavum</i>			B11477					
<i>Brevibacterium</i>	<i>flavum</i>			B11478					
<i>Brevibacterium</i>	<i>flavum</i>	21127							
<i>Brevibacterium</i>	<i>flavum</i>			B11474					
<i>Brevibacterium</i>	<i>healii</i>	15527							
<i>Brevibacterium</i>	<i>ketoglutamicum</i>	21004							
<i>Brevibacterium</i>	<i>ketoglutamicum</i>	21089							
<i>Brevibacterium</i>	<i>ketosoreductum</i>	21914							
<i>Brevibacterium</i>	<i>lactofermentum</i>				70				
<i>Brevibacterium</i>	<i>lactofermentum</i>				74				
<i>Brevibacterium</i>	<i>lactofermentum</i>				77				
<i>Brevibacterium</i>	<i>lactofermentum</i>	21798							
<i>Brevibacterium</i>	<i>lactofermentum</i>	21799							
<i>Brevibacterium</i>	<i>lactofermentum</i>	21800							
<i>Brevibacterium</i>	<i>lactofermentum</i>	21801							
<i>Brevibacterium</i>	<i>lactofermentum</i>			B11470					
<i>Brevibacterium</i>	<i>lactofermentum</i>			B11471					

Genus	species	ATCC	FERM	NRRL	CECT	NCIMB	CBS	NCTC	DSMZ
Brevibacterium	lactofermentum	21086							
Brevibacterium	lactofermentum	21420							
Brevibacterium	lactofermentum	21086							
Brevibacterium	lactofermentum	31269							
Brevibacterium	linens	9174							
Brevibacterium	linens	19391							
Brevibacterium	linens	8377							
Brevibacterium	paraffinolyticum					11160			
Brevibacterium	spec.						717.73		
Brevibacterium	spec.						717.73		
Brevibacterium	spec.	14604							
Brevibacterium	spec.	21860							
Brevibacterium	spec.	21864							
Brevibacterium	spec.	21865							
Brevibacterium	spec.	21866							
Brevibacterium	spec.	19240							
Corynebacterium	acetoacidophilum	21476							
Corynebacterium	acetoacidophilum	13870							
Corynebacterium	acetoglutamicum			B11473					
Corynebacterium	acetoglutamicum			B11475					
Corynebacterium	acetoglutamicum	15806							
Corynebacterium	acetoglutamicum	21491							
Corynebacterium	acetoglutamicum	31270							
Corynebacterium	acetophilum			B3671					
Corynebacterium	ammoniagenes	6872						2399	
Corynebacterium	ammoniagenes	15511							
Corynebacterium	fujikense	21496							
Corynebacterium	glutamicum	14067							
Corynebacterium	glutamicum	39137							
Corynebacterium	glutamicum	21254							
Corynebacterium	glutamicum	21255							
Corynebacterium	glutamicum	31830							
Corynebacterium	glutamicum	13032							
Corynebacterium	glutamicum	14305							
Corynebacterium	glutamicum	15455							
Corynebacterium	glutamicum	13058							
Corynebacterium	glutamicum	13059							
Corynebacterium	glutamicum	13060							
Corynebacterium	glutamicum	21492							
Corynebacterium	glutamicum	21513							
Corynebacterium	glutamicum	21526							
Corynebacterium	glutamicum	21543							
Corynebacterium	glutamicum	13287							
Corynebacterium	glutamicum	21851							
Corynebacterium	glutamicum	21253							
Corynebacterium	glutamicum	21514							
Corynebacterium	glutamicum	21516							
Corynebacterium	glutamicum	21299							

Genus	species	ATCC	FERM	NRRL	CECT	NCIMB	CBS	NCTC	DSMZ
Corynebacterium	glutamicum	21300							
Corynebacterium	glutamicum	39684							
Corynebacterium	glutamicum	21488							
Corynebacterium	glutamicum	21649							
Corynebacterium	glutamicum	21650							
Corynebacterium	glutamicum	19223							
Corynebacterium	glutamicum	13869							
Corynebacterium	glutamicum	21157							
Corynebacterium	glutamicum	21158							
Corynebacterium	glutamicum	21159							
Corynebacterium	glutamicum	21355							
Corynebacterium	glutamicum	31808							
Corynebacterium	glutamicum	21674							
Corynebacterium	glutamicum	21562							
Corynebacterium	glutamicum	21563							
Corynebacterium	glutamicum	21564							
Corynebacterium	glutamicum	21565							
Corynebacterium	glutamicum	21566							
Corynebacterium	glutamicum	21567							
Corynebacterium	glutamicum	21568							
Corynebacterium	glutamicum	21569							
Corynebacterium	glutamicum	21570							
Corynebacterium	glutamicum	21571							
Corynebacterium	glutamicum	21572							
Corynebacterium	glutamicum	21573							
Corynebacterium	glutamicum	21579							
Corynebacterium	glutamicum	19049							
Corynebacterium	glutamicum	19050							
Corynebacterium	glutamicum	19051							
Corynebacterium	glutamicum	19052							
Corynebacterium	glutamicum	19053							
Corynebacterium	glutamicum	19054							
Corynebacterium	glutamicum	19055							
Corynebacterium	glutamicum	19056							
Corynebacterium	glutamicum	19057							
Corynebacterium	glutamicum	19058							
Corynebacterium	glutamicum	19059							
Corynebacterium	glutamicum	19060							
Corynebacterium	glutamicum	19185							
Corynebacterium	glutamicum	13286							
Corynebacterium	glutamicum	21515							
Corynebacterium	glutamicum	21527							
Corynebacterium	glutamicum	21544							
Corynebacterium	glutamicum	21492							
Corynebacterium	glutamicum			B8183					
Corynebacterium	glutamicum			B8182					
Corynebacterium	glutamicum			B12416					
Corynebacterium	glutamicum			B12417					

Genus	species	ATCC	FERM	NRRL	CECT	NCIMB	CBS	NCTC	DSMZ
Corynebacterium	glutamicum			B12418					
Corynebacterium	glutamicum			B11476					
Corynebacterium	glutamicum	21608							
Corynebacterium	lilium		P973						
Corynebacterium	nitrilophilus	21419				11594			
Corynebacterium	spec.		P4445						
Corynebacterium	spec.		P4446						
Corynebacterium	spec.	31088							
Corynebacterium	spec.	31089							
Corynebacterium	spec.	31090							
Corynebacterium	spec.	31090							
Corynebacterium	spec.	31090							
Corynebacterium	spec.	15954							20145
Corynebacterium	spec.	21857							
Corynebacterium	spec.	21862							
Corynebacterium	spec.	21863							

ATCC: American Type Culture Collection, Rockville, MD, USA

FERM: Fermentation Research Institute, Chiba, Japan

NRRL: ARS Culture Collection, Northern Regional Research Laboratory, Peoria, IL, USA

CECT: Coleccion Espanola de Cultivos Tipo, Valencia, Spain

NCIMB: National Collection of Industrial and Marine Bacteria Ltd., Aberdeen, UK

CBS: Centraalbureau voor Schimmelcultures, Baarn, NL

NCTC: National Collection of Type Cultures, London, UK

DSMZ: Deutsche Sammlung von Mikroorganismen und Zellkulturen, Braunschweig, Germany

For reference see Sugawara, H. et al. (1993) World directory of collections of cultures of microorganisms: Bacteria, fungi and yeasts (4th edn), World federation for culture collections world data center on microorganisms, Saimata, Japan.

Table 4: Alignment Results

ID #	length (NT)	Genbank Hit	Length	Accession	Name of Genbank Hit	Source of Genbank Hit	% homology (GAP)	Date of Deposit
rx00013 996		GB_GSS4:AQ713475	581	AQ713475	HS_5402_B2_A12_T7A RPCI-11 Human Male BAC Library Homo sapiens genomic clone Plate=978 Col=24 Row=B, genomic survey sequence.	Homo sapiens	37,148	13-Jul-99
		GB_HTG3:AC007420	130583	AC007420	Drosophila melanogaster chromosome 2 clone BACR07M10 (D630) RPCI-98 07.M.10 map 24A-24D strain y; cn bw sp, *** SEQUENCING IN PROGRESS ***. 83 unordered pieces.	Drosophila melanogaster	34,568	20-Sep-99
		GB_HTG3:AC007420	130583	AC007420	Drosophila melanogaster chromosome 2 clone BACR07M10 (D630) RPCI-98 07.M.10 map 24A-24D strain y; cn bw sp, *** SEQUENCING IN PROGRESS ***. 83 unordered pieces.	Drosophila melanogaster	34,568	20-Sep-99
rx00014 903		GB_BA1:MTCY3A2	25830	Z83867	Mycobacterium tuberculosis H37Rv complete genome; segment 136/162.	Mycobacterium tuberculosis	58,140	17-Jun-98
		GB_BA1:MLCB1779	43254	Z98271	Mycobacterium leprae cosmid B1779.	Mycobacterium leprae	57,589	8-Aug-97
		GB_BA1:SAPURCLUS	9120	X92429	S.alboniger naph, pur7, pur10, pur6, pur4, pur5 and pur3 genes.	Streptomyces anulatus	55,667	28-Feb-96
rx00030 513		GB_EST21:C89713	767	C89713	C89713 Dictyostelium discoideum SS (H.Urushiara) Dictyostelium discoideum cDNA clone SSG229, mRNA sequence.	Dictyostelium discoideum	45,283	20-Apr-98
		GB_EST28:AI497294	484	AI497294	fb3g03.y1 Zebrafish WashU MPIMG EST Danio rerio cDNA 5' similar to SW:AFP4_MYOC P80961 ANTIFREEZE PROTEIN LS-12.; mRNA sequence.	Danio rerio	42,991	11-MAR-1999
		GB_EST21:C92167	637	C92167	C92167 Dictyostelium discoideum SS (H.Urushiara) Dictyostelium discoideum cDNA clone SSD179, mRNA sequence.	Dictyostelium discoideum	44,444	12-Jul-99
rx00032 1632		GB_BA2:AF010496	189370	AF010496	Rhodobacter capsulatus strain SB1003, partial genome.	Rhodobacter capsulatus	39,689	12-MAY-1998
		GB_BA2:AF018073	9810	AF018073	Rhodobacter sphaeroides operon regulator (smoC), periplasmic sorbitol-binding protein (smoE), sorbitol/mannitol transport inner membrane protein (smoF), sorbitol/mannitol transport inner membrane protein (smoG), sorbitol/mannitol transport ATP-binding transport protein (smoK), sorbitol dehydrogenase (smoS), mannitol dehydrogenase (mtlK), and periplasmic mannitol-binding protein (smoM) genes, complete cds.	Rhodobacter sphaeroides	48,045	22-OCT-1997
		GB_BA2:AF045245	5930	AF045245	Klebsiella pneumoniae D-arabinol transporter (dalT), D-arabinol kinase (dalK), D-arabinol dehydrogenase (dalD), and repressor (dalR) genes, complete cds.	Klebsiella pneumoniae	38,514	16-Jul-98
rx00041 1342		EM_PAT:E11760	6911	E11760	Base sequence of sucrose gene.	Corynebacterium glutamicum	99,031	08-OCT-1997 (Rel. 52, Created)
		GB_PAT:126124	6911	126124	Sequence 4 from patent US 5556776.	Unknown.	99,031	07-OCT-1996
		GB_IN1:LMFL5883	31934	AL117384	Leishmania major Friedlin chromosome 23 cosmid L5883, complete sequence.	Leishmania major	43,663	21-OCT-1999
rx00042 882		EM_PAT:E11760	6911	E11760	Base sequence of sucrose gene.	Corynebacterium glutamicum	94,767	08-OCT-1997 (Rel. 52, Created)
		GB_PAT:126124	6911	126124	Sequence 4 from patent US 5556776.	Unknown.	94,767	07-OCT-1996

Table 4 (continued)

rxa00043	1287	GB_IN1:CEU33051 GB_PAT:126124 EM_PAT:E11760	4899 6911 6911	U33051 126124 E11760	Caenorhabditis elegans sur-2 mRNA, complete cds. Sequence 4 from patent US 5556776. Base sequence of sucrase gene.	40,276 97,591 97,591	Caenorhabditis elegans Unknown. Corynebacterium glutamicum	23-Jan-96 07-OCT-1996 08-OCT-1997 (Rel. 52, Created)
rxa00098	1743	GB_PR3:AC005174 GB_BA1:MSU88433	39769 1928	AC005174 U88433	Homo sapiens clone UWGC:g1564a012 from 7p14-15, complete sequence. Mycobacterium smegmatis phosphoglucose isomerase gene, complete cds.	35,879 62,658	Homo sapiens Mycobacterium smegmatis	24-Jun-98 19-Apr-97
rxa00148	2334	GB_BA1:SCSA7 GB_BA1:MTCY10D7	40337 39800	AL031107 Z79700	Streptomyces coelicolor cosmid 5A7. Mycobacterium tuberculosis H37Rv complete genome; segment 44/162.	37,638 36,784	Streptomyces coelicolor Mycobacterium tuberculosis	27-Jul-98 17-Jun-98
rxa00148	2334	GB_BA1:MTCY277	38300	Z79701	Mycobacterium tuberculosis H37Rv complete genome; segment 65/162.	67,457	Mycobacterium tuberculosis	17-Jun-98
rxa00149	1971	GB_BA1:MSGY456	37316	AD000001	Mycobacterium tuberculosis sequence from clone y456.	40,883	Mycobacterium tuberculosis	03-DEC-1996
rxa00149	1971	GB_BA1:MSGY175	18106	AD000015	Mycobacterium tuberculosis sequence from clone y175.	67,457	Mycobacterium tuberculosis	10-DEC-1996
rxa00149	1971	GB_BA1:MSGY456	37316	AD000001	Mycobacterium tuberculosis sequence from clone y456.	35,883	Mycobacterium tuberculosis	03-DEC-1996
rxa00149	1971	GB_BA1:MSGY175	18106	AD000015	Mycobacterium tuberculosis sequence from clone y175.	51,001	Mycobacterium tuberculosis	10-DEC-1996
rxa00195	684	GB_BA1:MTCY277	38300	Z79701	Mycobacterium tuberculosis H37Rv complete genome; segment 65/162.	51,001	Mycobacterium tuberculosis	17-Jun-98
rxa00195	684	GB_BA1:MTCY274	39991	Z74024	Mycobacterium tuberculosis H37Rv complete genome; segment 126/162.	35,735	Mycobacterium tuberculosis	19-Jun-98
rxa00196	738	GB_BA1:MTCY274	39991	Z74024	Mycobacterium tuberculosis H37Rv complete genome; segment 126/162.	57,014 41,892	Mycobacterium leprae Mycobacterium tuberculosis	15-Jun-96 19-Jun-98
rxa00196	738	GB_BA1:MTCY274	39991	Z74024	Mycobacterium tuberculosis H37Rv complete genome; segment 126/162.	41,841	Mycobacterium tuberculosis	19-Jun-98
rxa00202	1065	GB_RO:RATCBRQ GB_EST11:AA253618 GB_EST26:AI390284	10752 313 490	M55532 AA253618 AI390284	Rat carbohydrate binding receptor gene, complete cds. mw95c10.r1 Soares mouse NML Mus musculus cDNA clone IMAGE:678450 5', Mus musculus mRNA sequence. mw96a03.y1 Soares mouse NML Mus musculus cDNA clone IMAGE:678508 5', Mus musculus mRNA sequence. METHYLTRANSFERASE; mRNA sequence.	36,212 38,816 42,239	Rattus norvegicus Mus musculus	27-Apr-93 13-MAR-1997 2-Feb-99
rxa00206	1161	GB_BA1:MLCB637 GB_BA1:MTV012	44882 70287	Z99263 AL021287	mw95c10.y1 Soares mouse NML Mus musculus cDNA clone IMAGE:678450 5', mRNA sequence. Mycobacterium leprae cosmid B637. Mycobacterium tuberculosis H37Rv complete genome; segment 132/162.	37,307 58,312 36,632	Mus musculus Mycobacterium leprae Mycobacterium tuberculosis	2-Feb-99 17-Sep-97 23-Jun-99

Table 4 (continued)

GB_BA1:SC6E10	23990	AL109661	Streptomyces coelicolor cosmid 6E10.	Streptomyces coelicolor A3(2)	38,616	5-Aug-99
rx00224 1074	1769	U32230	Bradyrhizobium japonicum electron transfer flavoprotein small subunit (etfS) nd large subunit (etfL) genes, complete cds.	Bradyrhizobium japonicum	48,038	25-MAY-1996
GB_BA1:PDEETFAB	2440	L14864	Paracoccus denitrificans electron transfer flavoprotein alpha and beta subunit genes, complete cds's.	Paracoccus denitrificans	48,351	27-OCT-1993
GB_HTG3:AC009689	177954	AC009689	Homo sapiens chromosome 4 clone 104_F_7 map 4, LOW-PASS SEQUENCE SAMPLING.	Homo sapiens	38,756	28-Aug-99
GB_RO:AF060178	2057	AF060178	Mus musculus heparan sulfate 2-sulfotransferase (Hs2st) mRNA, complete cds.	Mus musculus	39,506	18-Jun-98
GB_GSS11:AQ325043	734	AQ325043	mgxb0020J01r CUGI Rice Blast Library Magnaporthe grisea genomic clone mgxb0020J01r, genomic survey sequence.	Magnaporthe grisea	38,333	8-Jan-99
GB_EST31:A1676413	551	A1676413	etmEST0167 Eimeria tenella cDNA clone etmc074 5', mRNA sequence.	Eimeria tenella	35,542	19-MAY-1999
GB_BA1:MTCY10G2	38970	Z92539	Mycobacterium tuberculosis H37Rv complete genome; segment 47/162.	Mycobacterium tuberculosis	65,759	17-Jun-98
GB_BA2:AF061753	3721	AF061753	Nitrosomonas europaea CTP synthase (pyrG) gene, partial cds; and enolase (eno) gene, complete cds.	Nitrosomonas europaea	58,941	31-Aug-98
GB_BA2:AF086791	37867	AF086791	Zymomonas mobilis strain ZM4 clone 67E10 carbamoylphosphate synthetase small subunit (carA), carbamoylphosphate synthetase large subunit (carB), transcription elongation factor (greA), enolase (eno), pyruvate dehydrogenase alpha subunit (pdhA), pyruvate dehydrogenase beta subunit (pdhB), ribonuclease H (rnh), homoserine kinase homolog, alcohol dehydrogenase II (adhB), and excinuclease ABC subunit A (uvrA) genes, complete cds; and unknown genes.	Zymomonas mobilis	61,239	4-Nov-98
GB_BA2:AF012550	2690	AF012550	Acinetobacter sp. BD413 ComP (comp) gene, complete cds.	Acinetobacter sp. BD413	53,726	27-Sep-99
GB_PAT:E03856	1506	E03856	gDNA encoding alcohol dehydrogenase.	Bacillus	51,688	29-Sep-97
GB_BA1:BACADHT	1688	D90421	B. stearothermophilus adhT gene for alcohol dehydrogenase.	stearothermophilus Bacillus	51,602	7-Feb-99
GB_BA1:MTCY20G9	37218	Z77162	Mycobacterium tuberculosis H37Rv complete genome; segment 25/162.	stearothermophilus Mycobacterium tuberculosis	42,875	17-Jun-98
GB_BA1:MTV004	69350	AL009198	Mycobacterium tuberculosis H37Rv complete genome; segment 144/162.	Mycobacterium tuberculosis	40,380	18-Jun-98
GB_BA1:MTV004	69350	AL009198	Mycobacterium tuberculosis H37Rv complete genome; segment 144/162.	Mycobacterium tuberculosis	41,789	18-Jun-98
GB_BA2:AF050114	1038	AF050114	Pseudomonas sp. W7 alginate lyase gene, complete cds.	Mycobacterium tuberculosis Pseudomonas sp. W7	49,898	03-MAR-1999
GB_GSS3:B16984	469	B16984	344A14.TVC C1T978SKA1 Homo sapiens genomic clone A-344A14, genomic survey sequence.	Homo sapiens	39,355	4-Jun-98
GB_IN2:AF144549	7887	AF144549	Aedes albopictus ribosomal protein L34 (pl34) gene, complete cds.	Aedes albopictus	36,509	3-Jun-99
GB_EST1:T28483	313	T28483	EST46182 Human Kidney Homo sapiens cDNA 3' end similar to flavin-containing monooxygenase 1 (HT:1956), mRNA sequence.	Homo sapiens	42,997	6-Sep-95

Table 4 (continued)

GB_PR1:HUMFMO1	2134	M64082	Human flavin-containing monooxygenase (FMO1) mRNA, complete cds.	Homo sapiens	37,915	8-Nov-94
GB_EST32:AI734238	512	AI734238	zb73c05.y5 Soares_fetal_lung_NbHL19W Homo sapiens cDNA clone IMAGE:309224 5' similar to gb:M64082 DIMETHYLANILINE MONOOXYGENASE (HUMAN); mRNA sequence.	Homo sapiens	41,502	14-Jun-99
GB_HTG6:AC011069	168266	AC011069	Drosophila melanogaster chromosome X clone BACR11H20 (D881) RPCI-98 11.H.20 map 12B-12C strain y; cn bw sp, *** SEQUENCING IN PROGRESS ***; 92 unordered pieces.	Drosophila melanogaster	33,890	02-DEC-1999
GB_EST15:AA531468	414	AA531468	np63d12.s1 NCI_CGAP_Prt10 Homo sapiens cDNA clone IMAGE:997175, mRNA sequence.	Homo sapiens	40,821	20-Aug-97
GB_HTG6:AC011069	168266	AC011069	Drosophila melanogaster chromosome X clone BACR11H20 (D881) RPCI-98 11.H.20 map 12B-12C strain y; cn bw sp, *** SEQUENCING IN PROGRESS ***; 92 unordered pieces.	Drosophila melanogaster	30,963	02-DEC-1999
GB_VI:VMVY16780	186986	Y16780	variola minor virus complete genome.	variola minor virus	35,883	2-Sep-99
GB_VI:VARCG	186103	L22579	Variola major virus (strain Bangladesh-1975) complete genome.	Variola major virus	34,664	12-Jan-95
GB_VI:VVCAGAA	185578	X69198	Variola virus DNA complete genome.	Variola virus	36,000	13-DEC-1996
GB_HTG3:AC009571	159648	AC009571	Homo sapiens chromosome 4 clone 57_A_22 map 4, *** SEQUENCING IN PROGRESS ***; 8 unordered pieces.	Homo sapiens	36,988	29-Sep-99
GB_HTG3:AC009571	159648	AC009571	Homo sapiens chromosome 4 clone 57_A_22 map 4, *** SEQUENCING IN PROGRESS ***; 8 unordered pieces.	Homo sapiens	36,988	29-Sep-99
GB_PR3:AC005697	174503	AC005697	Homo sapiens chromosome 17, clone hRPK.138_P_22, complete sequence.	Homo sapiens	36,340	09-OCT-1998
GB_BA1:LCATPASEB	1514	X64542	L.casei gene for ATPase beta-subunit.	Lactobacillus casei	34,664	11-DEC-1992
GB_BA1:LCATPASEB	1514	X64542	L.casei gene for ATPase beta-subunit.	Lactobacillus casei	39,308	11-DEC-1992
GB_BA1:STYPUTPE	1887	L01138	Salmonella (S2980) proline permease (putP) gene, 5' end.	Salmonella sp.	39,623	09-MAY-1996
GB_BA1:STYPUTPF	1887	L01139	Salmonella (S2983) proline permease (putP) gene, 5' end.	Salmonella sp.	39,623	09-MAY-1996
GB_BA1:STYPUTPI	1889	L01142	Salmonella (S3015) proline permease (putP) gene, 5' end.	Salmonella sp.	42,906	09-MAY-1996
GB_PR3:AC004691	141990	AC004691	Homo sapiens PAC clone DJ0740D02 from 7p14-p15, complete sequence.	Homo sapiens	38,142	16-MAY-1998
GB_PR4:AC004916	129014	AC004916	Homo sapiens clone DJ0891L14, complete sequence.	Homo sapiens	38,549	17-Jul-99
GB_PR3:AC004691	141990	AC004691	Homo sapiens PAC clone DJ0740D02 from 7p14-p15, complete sequence.	Homo sapiens	35,865	16-MAY-1998
GB_BA1:MTCY427	38110	Z70692	Mycobacterium tuberculosis H37Rv complete genome; segment 99/162.	Mycobacterium tuberculosis	38,940	24-Jun-99
GB_GSS12:AQ412290	238	AQ412290	RPCI-11-195H2.TV RPCI-11 Homo sapiens genomic clone RPCI-11-195H2, genomic survey sequence.	Homo sapiens	36,555	23-MAR-1999
GB_PL2:AF112871	2394	AF112871	Astasia longa small subunit ribosomal RNA gene, complete sequence.	Astasia longa	36,465	28-Jun-99
GB_HTG1:CEY56A3	224746	AL022280	Caenorhabditis elegans chromosome III clone Y56A3, *** SEQUENCING IN PROGRESS ***; in unordered pieces.	Caenorhabditis elegans	35,179	6-Sep-99
GB_HTG1:CEY56A3	224746	AL022280	Caenorhabditis elegans chromosome III clone Y56A3, *** SEQUENCING IN PROGRESS ***; in unordered pieces.	Caenorhabditis elegans	35,179	6-Sep-99

Table 4 (continued)

rx00381	729	GB_PR2:HS134O19	86897	AL034555	Human DNA sequence from clone 134O19 on chromosome 1p36.11-36.33, complete sequence.	Homo sapiens	40,604	23-Nov-99
		GB_GSS4:AQ730532	416	AQ730532	HS_2149_A1_C06_TTC CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2149 Col=11 Row=E, genomic survey sequence.	Homo sapiens	35,766	15-Jul-99
		GB_EST23:AI120939	561	AI120939	ub74f05.r1 Soares mouse mammary gland NMLMG Mus musculus cDNA clone Mus musculus IMAGE:1383489 5' similar to gb:J04046 CALMODULIN (HUMAN); gb:M19381 Mouse calmodulin (MOUSE);, mRNA sequence.		41,113	2-Sep-98
		GB_EST23:AI120939	561	AI120939	ub74f05.r1 Soares mouse mammary gland NMLMG Mus musculus cDNA clone Mus musculus IMAGE:1383489 5' similar to gb:J04046 CALMODULIN (HUMAN); gb:M19381 Mouse calmodulin (MOUSE);, mRNA sequence.		41,113	2-Sep-98
rx00385	362	GB_EST32:AI726450	565	AI726450	BNLGH15857 Six-day Cotton fiber Gossypium hirsutum cDNA 5' similar to (AF015913) Skb1Hs [Homo sapiens], mRNA sequence.	Gossypium hirsutum	41,152	11-Jun-99
		GB_GSS4:AQ740856	768	AQ740856	HS_2274_A2_A07_TTC CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2274 Col=14 Row=A, genomic survey sequence.	Homo sapiens	41,360	16-Jul-99
		GB_PR1:HSPAIP	1587	X91809	H.sapiens mRNA for GAIP protein.	Homo sapiens	36,792	29-MAR-1996
rx00388	1134	GB_BA1:MTY25D10	40838	Z95558	Mycobacterium tuberculosis H37Rv complete genome; segment 28/162.	Mycobacterium tuberculosis	51,852	17-Jun-98
		GB_BA1:MSGY224	40051	AD000004	Mycobacterium tuberculosis sequence from clone y224.	Mycobacterium tuberculosis	51,852	03-DEC-1996
rx00427	909	GB_HTG1:AP000471	72466	AP000471	Homo sapiens chromosome 21 clone B2308H15 map 21q22.3, *** SEQUENCING IN PROGRESS ***, in unordered pieces.	Homo sapiens	36,875	13-Sep-99
		GB_BA1:MSGY126	37164	AD000012	Mycobacterium tuberculosis sequence from clone y126.	Mycobacterium tuberculosis	60,022	10-DEC-1996
		GB_BA1:MTY13D12	37085	Z80343	Mycobacterium tuberculosis H37Rv complete genome; segment 156/162.	Mycobacterium tuberculosis	60,022	17-Jun-98
rx00483	1587	GB_HTG1:CEY48C3	270193	Z92855	Caenorhabditis elegans chromosome II clone Y48C3, *** SEQUENCING IN PROGRESS ***, in unordered pieces.	Caenorhabditis elegans	28,013	29-MAY-1999
		GB_PR2:HSAF001550	173882	AF001550	Homo sapiens chromosome 16 BAC clone CIT987SK-334D11 complete sequence.	Homo sapiens	38,226	22-Aug-97
		GB_BA1:LLCPJW565	12828	Y12736	Lactococcus lactis cremoris plasmid pJW565 DNA, abliR genes and orfX.	Lactococcus lactis subsp. cremoris	37,492	01-MAR-1999
		GB_HTG2:AC006754	206217	AC006754	Caenorhabditis elegans clone Y40B10, *** SEQUENCING IN PROGRESS ***, 5 unordered pieces.	Caenorhabditis elegans	36,648	23-Feb-99
rx00511	615	GB_PR3:HSE127C11	38423	Z74581	Human DNA sequence from cosmid E127C11 on chromosome 22q11.2-qter contains STS.	Homo sapiens	39,831	23-Nov-99
		GB_PR3:HSE127C11	38423	Z74581	Human DNA sequence from cosmid E127C11 on chromosome 22q11.2-qter contains STS.	Homo sapiens	36,409	23-Nov-99
rx00512	718	GB_BA1:MTCY22G8	22550	Z95585	Mycobacterium tuberculosis H37Rv complete genome; segment 49/162.	Mycobacterium tuberculosis	56,232	17-Jun-98

Table 4 (continued)

	GB_BA1:MSGLTA	1776	X60513	M. smegmatis gltA gene for citrate synthase.	Mycobacterium smegmatis	56,143	20-Sep-91
	GB_BA2:ECU73857	128824	U73857	Escherichia coli chromosome minutes 6-8.	Escherichia coli	48,563	14-Jul-99
rx00517 1164	GB_HTG2:AC006911	298804	AC006911	Caenorhabditis elegans clone Y94H6x, *** SEQUENCING IN PROGRESS ***	Caenorhabditis elegans	37,889	24-Feb-99
	GB_HTG2:AC006911	298804	AC006911	15 unordered pieces.			
	GB_HTG2:AC006911	298804	AC006911	Caenorhabditis elegans clone Y94H6x, *** SEQUENCING IN PROGRESS ***	Caenorhabditis elegans	37,889	24-Feb-99
	GB_EST29:AI602158	481	AI602158	15 unordered pieces.			
	GB_EST29:AI602158	481	AI602158	UI-R-AB0-vy-a-01-0-UI.s2 UI-R-AB0 Rattus norvegicus cDNA clone UI-R-AB0-vy-a-01-0-UI 3', mRNA sequence.	Rattus norvegicus	40,833	21-Apr-99
rx00518 320	GB_BA2:ECU73857	128824	U73857	Escherichia coli chromosome minutes 6-8.	Escherichia coli	49,688	14-Jul-99
	GB_BA2:STU51879	8371	U51879	Salmonella typhimurium propionate catabolism operon: RpoN activator protein homolog (prpR), carboxyphosphoenolpyruvate phosphonmutase homolog (prpB), citrate synthase homolog (prpC), prpD and prpE genes, complete cds.	Salmonella typhimurium	50,313	5-Aug-99
	GB_BA2:AE000140	12498	AE000140	Escherichia coli K-12 MG1655 section 30 of 400 of the complete genome.	Escherichia coli	49,688	12-Nov-98
rx00606 2378	GB_EST32:AU068253	376	AU068253	AU068253 Rice callus Oryza sativa cDNA clone C12658_9A, mRNA sequence.	Oryza sativa	41,333	7-Jun-99
	GB_EST13:AA363046	329	AA363046	EST72922 Ovary II Homo sapiens cDNA 5' end, mRNA sequence.	Homo sapiens	34,347	21-Apr-97
	GB_EST32:AU068253	376	AU068253	AU068253 Rice callus Oryza sativa cDNA clone C12658_9A, mRNA sequence.	Oryza sativa	41,899	7-Jun-99
rx00635 1860	GB_BA1:PAORF1	1440	X13378	Pseudomonas amyloclavata DNA for ORF 1.	Pseudomonas amyloclavata	53,912	14-Jul-95
	GB_BA1:PAORF1	1440	X13378	Pseudomonas amyloclavata DNA for ORF 1.	Pseudomonas amyloclavata	54,422	14-Jul-95
rx00679 1389	GB_PL2:AC010871	80381	AC010871	Arabidopsis thaliana chromosome III BAC T16011 genomic sequence, complete sequence.	Arabidopsis thaliana	38,244	13-Nov-99
	GB_PL1:AT81KBGEN	81493	X98130	A.thaliana 81kb genomic sequence.	Arabidopsis thaliana	36,091	12-MAR-1997
	GB_PL2:AC010871	80381	AC010871	Arabidopsis thaliana chromosome III BAC T16011 genomic sequence, complete sequence.	Arabidopsis thaliana	37,135	13-Nov-99
rx00680 441	GB_PR3:AC004058	38400	AC004058	Homo sapiens chromosome 4 clone B241P19 map 4q25, complete sequence.	Homo sapiens	36,165	30-Sep-98
	GB_PL1:AT81KBGEN	81493	X98130	A.thaliana 81kb genomic sequence.	Arabidopsis thaliana	38,732	12-MAR-1997
	GB_PL1:AB026648	43481	AB026648	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MLJ15, complete sequence.	Arabidopsis thaliana	38,732	07-MAY-1999
rx00682 2022	GB_HTG3:AC010325	197110	AC010325	Homo sapiens chromosome 19 clone CITB-E1_2568A17, *** SEQUENCING IN PROGRESS ***	Homo sapiens	37,976	15-Sep-99
	GB_HTG3:AC010325	197110	AC010325	40 unordered pieces.			
	GB_HTG3:AC010325	197110	AC010325	Homo sapiens chromosome 19 clone CITB-E1_2568A17, *** SEQUENCING IN PROGRESS ***	Homo sapiens	37,976	15-Sep-99
	GB_PR4:AC008179	181745	AC008179	40 unordered pieces.			
	GB_PR4:AC008179	181745	AC008179	Homo sapiens clone NH0576F01, complete sequence.	Homo sapiens	37,143	28-Sep-99

Table 4 (continued)

rx00683 1215	GB_BA2:AE000896	10707	AE000896	Methanobacterium thermoautotrophicum from bases 1189349 to 1200055 (section 102 of 148) of the complete genome.	Methanobacterium thermoautotrophicum	38,429	15-Nov-97
	GB_IN1:DMBR7A4	212734	AL109630	Drosophila melanogaster clone BACR7A4.	Drosophila melanogaster	36,454	30-Jul-99
	GB_EST35:AV163010	273	AV163010	AV163010 Mus musculus head C57BL/6J 13-day embryo Mus musculus cDNA clone 3110006J22, mRNA sequence.	Mus musculus	41,758	8-Jul-99
rx00686 927	GB_HTG2:HSDJ137K2	190223	AL049820	Homo sapiens chromosome 6 clone RP1-137K2 map q25.1-25.3, *** SEQUENCING IN PROGRESS ***. In unordered pieces.	Homo sapiens	38,031	03-DEC-1999
	GB_HTG2:HSDJ137K2	190223	AL049820	Homo sapiens chromosome 6 clone RP1-137K2 map q25.1-25.3, *** SEQUENCING IN PROGRESS ***. In unordered pieces.	Homo sapiens	38,031	03-DEC-1999
	GB_EST12:AA284399	431	AA284399	zs57b04.t1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:701551 5', mRNA sequence.	Homo sapiens	39,205	14-Aug-97
rx00700 927	GB_EST34:AI785570	454	AI785570	uj44d03.x1 Sugano mouse liver mlia Mus musculus cDNA clone IMAGE:1922789 3' similar to gb:Z28407 60S RIBOSOMAL PROTEIN L8 (HUMAN); mRNA sequence.	Mus musculus	41,943	2-Jul-99
	GB_EST25:AI256147	684	AI256147	uj95e12.x1 Sugano mouse liver mlia Mus musculus cDNA clone IMAGE:1890190 3' similar to gb:Z28407 60S RIBOSOMAL PROTEIN L8 (HUMAN); mRNA sequence.	Mus musculus	40,791	12-Nov-98
rx00703 2409	GB_BA1:CARCG12	2079	X14979	C. aurantiacus reaction center genes 1 and 2.	Chloroflexus aurantiacus	37,721	23-Apr-91
	GB_BA1:SC7H2	42655	AL109732	Streptomyces coelicolor cosmid 7H2.	Streptomyces coelicolor A3(2)	56,646	2-Aug-99
	GB_BA1:MTCY274	39991	Z74024	Mycobacterium tuberculosis H37Rv complete genome; segment 126/162.	Mycobacterium tuberculosis	37,369	19-Jun-98
rx00705 1038	GB_BA2:REU60056	2520	U60056	Ralstonia eutropha formate dehydrogenase-like protein (cbbBc) gene, complete cds.	Ralstonia eutropha	51,087	16-OCT-1996
	GB_GSS15:AQ604477	505	AQ604477	HS_2116_B1_G07_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2116 Col=13 Row=N, genomic survey sequence.	Homo sapiens	39,617	10-Jun-99
	GB_EST11:AA224340	443	AA224340	zr14e07.s1 Stralagene hNT neuron (#937233) Homo sapiens cDNA clone IMAGE:648804 3', mRNA sequence.	Homo sapiens	35,129	11-MAR-1998
	GB_EST5:N30648	291	N30648	yw77b02.s1 Soares_placenta_8to9weeks_2NbHP8to9W Homo sapiens cDNA clone IMAGE:258219 3', mRNA sequence.	Homo sapiens	43,986	5-Jan-96
rx00782 1005	GB_BA1:MTCY10D7	39800	Z79700	Mycobacterium tuberculosis H37Rv complete genome; segment 44/162.	Mycobacterium tuberculosis	63,327	17-Jun-98
	GB_BA1:MLCL373	37304	AL035500	Mycobacterium leprae cosmid L373.	Mycobacterium leprae	62,300	27-Aug-99
	GB_BA2:AF128399	2642	AF128399	Pseudomonas aeruginosa succinyl-CoA synthetase beta subunit (sucC) and succinyl-CoA synthetase alpha subunit (sucD) genes, complete cds.	Pseudomonas aeruginosa	53,698	25-MAR-1999
rx00783 1395	GB_HTG2:AC008158	118792	AC008158	Homo sapiens chromosome 17 clone hRPK.42_F_20 map 17, *** SEQUENCING IN PROGRESS ***. 14 unordered pieces.	Homo sapiens	35,135	28-Jul-99
	GB_HTG2:AC008158	118792	AC008158	Homo sapiens chromosome 17 clone hRPK.42_F_20 map 17, *** SEQUENCING IN PROGRESS ***. 14 unordered pieces.	Homo sapiens	35,135	28-Jul-99
rx00794 1128	GB_PR3:AC005017	137176	AC005017	Homo sapiens BAC clone GS214N13 from 7p14-p15, complete sequence.	Homo sapiens	35,864	8-Aug-98
	GB_BA1:MTV017	67200	AL021897	Mycobacterium tuberculosis H37Rv complete genome; segment 48/162.	Mycobacterium tuberculosis	40,331	24-Jun-99

Table 4 (continued)

GB_BA1:MLCB1222	34714	AL049491	Mycobacterium leprae cosmid B1222.	Mycobacterium leprae	61,170	27-Aug-99
GB_PR2:HS151B14	128942	Z82188	Human DNA sequence from clone 151B14 on chromosome 22 Contains SOMATOSTATIN RECEPTOR TYPE 3 (SS3R) gene, pseudogene similar to ribosomal protein L39, RAC2 (RAS-RELATED C3 BOTULINUM TOXIN SUBSTRATE 2 (P21-RAC2)) gene ESTs, STSs, GSSs and CpG islands, complete sequence.	Homo sapiens	37,455	16-Jun-99
rx000799 1767						
GB_PL2:AF016327	616	AF016327	Hordeum vulgare Barperm1 (permi1) mRNA, partial cds.	Hordeum vulgare	41,311	01-OCT-1997
GB_HTG2:HSDJ319M7	128208	AL079341	Homo sapiens chromosome 6 clone RP1-319M7 map p21.1-21.3, *** SEQUENCING IN PROGRESS ***, in unordered pieces.	Homo sapiens	36,845	30-Nov-99
GB_HTG2:HSDJ319M7	128208	AL079341	Homo sapiens chromosome 6 clone RP1-319M7 map p21.1-21.3, *** SEQUENCING IN PROGRESS ***, in unordered pieces.	Homo sapiens	36,845	30-Nov-99
rx000800 1227						
GB_BA1:MTV022	13025	AL021925	Mycobacterium tuberculosis H37Rv complete genome; segment 100/162.	Mycobacterium tuberculosis	63,101	17-Jun-98
GB_BA1:AB019513	4417	AB019513	Streptomyces coelicolor genes for alcohol dehydrogenase and ABC transporter, complete cds.	Streptomyces coelicolor	41,312	13-Nov-98
GB_PL1:SCSFAARP	7008	X68020	S. cerevisiae SFA and ARP genes.	Saccharomyces cerevisiae	36,288	29-Nov-94
rx000825 1056						
GB_BA1:MTY15C10	33050	Z95436	Mycobacterium tuberculosis H37Rv complete genome; segment 154/162.	Mycobacterium tuberculosis	39,980	17-Jun-98
GB_BA1:MLCB2548	38916	AL023093	Mycobacterium leprae cosmid B2548.	Mycobacterium leprae	39,435	27-Aug-99
GB_BA2:AF169031	1141	AF169031	Xanthomonas oryzae pv. oryzae putative sugar nucleotide epimerase/dehydratase gene, partial cds.	Xanthomonas oryzae pv. oryzae	46,232	14-Sep-99
rx000871						
rx000872 1077						
GB_IN1:CEF23H12	35564	Z74472	Caenorhabditis elegans cosmid F23H12, complete sequence.	Caenorhabditis elegans	34,502	08-OCT-1999
GB_HTG2:AC007263	167390	AC007263	Homo sapiens chromosome 14 clone BAC 79J20 map 14q31, *** SEQUENCING IN PROGRESS ***, 5 ordered pieces.	Homo sapiens	35,714	24-MAY-1999
GB_HTG2:AC007263	167390	AC007263	Homo sapiens chromosome 14 clone BAC 79J20 map 14q31, *** SEQUENCING IN PROGRESS ***, 5 ordered pieces.	Homo sapiens	35,714	24-MAY-1999
rx000879 2241						
GB_BA1:MTV049	40360	AL022021	Mycobacterium tuberculosis H37Rv complete genome; segment 61/162.	Mycobacterium tuberculosis	36,981	19-Jun-98
GB_PL2:CDU236897	1827	AJ236897	Candida dubliniensis ACT1 gene, exons 1-2.	Candida dubliniensis	38,716	1-Sep-99
GB_PL1:CAACT1A	3206	X16377	Candida albicans act1 gene for actin.	Candida albicans	36,610	10-Apr-93
rx000909 955						
GB_BA2:AF010496	189370	AF010496	Rhodobacter capsulatus strain SB1003, partial genome.	Rhodobacter capsulatus	51,586	12-MAY-1998
GB_BA1:RMPHA	7888	X93358	Rhizobium meliloti pha[A,B,C,D,E,F,G] genes.	Sinorhizobium meliloti	48,367	12-MAR-1999
GB_EST16:C23528	317	C23528	C23528 Japanese flounder spleen Paralicthys olivaceus cDNA clone HB5(2), mRNA sequence.	Paralicthys olivaceus	41,640	28-Sep-99
rx000913 2118						
GB_HTG2:AC007734	188267	AC007734	Homo sapiens chromosome 18 clone hRPK.44_O_1 map 18, *** SEQUENCING IN PROGRESS ***, 18 unordered pieces.	Homo sapiens	34,457	5-Jun-99

Table 4 (continued)

GB_HTG2:AC007734	188267	AC007734	188267	AC007734	Homo sapiens chromosome 18 clone hRPK.44_O_1 map 18, *** SEQUENCING IN PROGRESS ***; 18 unordered pieces.	Homo sapiens	34,457	5-Jun-99
GB_EST18:AA709478	406	AA709478	406	AA709478	IMAGE:1224272 5', mRNA sequence.	Mus musculus	42,065	24-DEC-1997
GB_HTG4:AC010351	220710	AC010351	220710	AC010351	Homo sapiens chromosome 5 clone CITB-H1_2022B6, *** SEQUENCING IN PROGRESS ***; 68 unordered pieces.	Homo sapiens	36,448	31-OCT-1999
GB_HTG4:AC010351	220710	AC010351	220710	AC010351	Homo sapiens chromosome 5 clone CITB-H1_2022B6, *** SEQUENCING IN PROGRESS ***; 68 unordered pieces.	Homo sapiens	36,448	31-OCT-1999
GB_BA1:MTCY05A6	38631	Z96072	38631	Z96072	Mycobacterium tuberculosis H37Rv complete genome; segment 120/162.	Mycobacterium tuberculosis	36,218	17-Jun-98
rx00965								
GB_PAT:E13660	1916	E13660	1916	E13660	gDNA encoding 6-phosphogluconate dehydrogenase.	Corynebacterium glutamicum	98,349	24-Jun-98
GB_BA1:MTCY359	36021	Z83859	36021	Z83859	Mycobacterium tuberculosis H37Rv complete genome; segment 84/162.	Mycobacterium tuberculosis	38,520	17-Jun-98
GB_BA1:MLCB1788	39228	AL008609	39228	AL008609	Mycobacterium leprae cosmid B1788.	Mycobacterium leprae	64,355	27-Aug-99
GB_BA1:MTV008	63033	AL021246	63033	AL021246	Mycobacterium tuberculosis H37Rv complete genome; segment 108/162.	Mycobacterium tuberculosis	39,860	17-Jun-98
GB_BA1:MTV008	63033	AL021246	63033	AL021246	Mycobacterium tuberculosis H37Rv complete genome; segment 108/162.	Mycobacterium tuberculosis	39,120	17-Jun-98
rx01025 1119								
GB_BA1:SC7A1	32039	AL034447	32039	AL034447	Streptomyces coelicolor cosmid 7A1.	Streptomyces coelicolor	55,287	15-DEC-1998
GB_BA1:MSG1723CS	38477	L78825	38477	L78825	Mycobacterium leprae cosmid B1723 DNA sequence.	Mycobacterium leprae	56,847	15-Jun-96
GB_BA1:MLCB637	44882	Z99263	44882	Z99263	Mycobacterium leprae cosmid B637.	Mycobacterium leprae	56,676	17-Sep-97
GB_BA2:AF017444	3067	AF017444	3067	AF017444	Sinorhizobium meliloti NADP-dependent malic enzyme (tme) gene, complete cds.	Sinorhizobium meliloti	53,660	2-Nov-97
GB_BA1:BSUB0013	218470	Z99116	218470	Z99116	Bacillus subtilis complete genome (section 13 of 21); from 2395261 to 2613730.	Bacillus subtilis	37,255	26-Nov-97
GB_VI:HSV2HG52	154746	Z86099	154746	Z86099	Herpes simplex virus type 2 (strain HG52), complete genome.	human herpesvirus 2	38,081	04-DEC-1998
GB_HTG2:AC002518	131855	AC002518	131855	AC002518	Homo sapiens chromosome X clone bWXD20, *** SEQUENCING IN PROGRESS ***; 11 unordered pieces.	Homo sapiens	35,647	2-Sep-97
GB_HTG2:AC002518	131855	AC002518	131855	AC002518	Homo sapiens chromosome X clone bWXD20, *** SEQUENCING IN PROGRESS ***; 11 unordered pieces.	Homo sapiens	35,647	2-Sep-97
GB_HTG2:AC002518	131855	AC002518	131855	AC002518	Homo sapiens chromosome X clone bWXD20, *** SEQUENCING IN PROGRESS ***; 11 unordered pieces.	Homo sapiens	26,180	2-Sep-97
GB_PR3:HSDJ653C5	85237	AL049743	85237	AL049743	Human DNA sequence from clone 653C5 on chromosome 1p21.3:22.3 Contains CA repeat(D1S435), STSs and GSSs, complete sequence.	Homo sapiens	36,462	23-Nov-99
GB_BA1:ECU29579	72221	U29579	72221	U29579	Escherichia coli K-12 genome; approximately 61 to 62 minutes.	Escherichia coli	41,808	1-Jul-95
GB_BA1:ECU29579	72221	U29579	72221	U29579	Escherichia coli K-12 genome; approximately 61 to 62 minutes.	Escherichia coli	36,130	1-Jul-95
GB_GSS8:AQ044021	387	AQ044021	387	AQ044021	CIT-HSP-2318C18. TR CIT-HSP Homo sapiens genomic clone 2318C18, genomic survey sequence.	Homo sapiens	36,528	14-Jul-98

Table 4 (continued)

GB_GSS8:AQ042907	392	AQ042907	CIT-HSP-2318D17:TR CIT-HSP Homo sapiens genomic clone 2318D17, genomic survey sequence.	Homo sapiens	35,969	14-Jul-98
GB_GSS8:AQ044021	387	AQ044021	CIT-HSP-2318C18:TR CIT-HSP Homo sapiens genomic clone 2318C18, genomic survey sequence.	Homo sapiens	44,545	14-Jul-98
GB_BA1:CORPYK1	2795	L27126	Corynebacterium pyruvate kinase gene, complete cds.	Corynebacterium glutamicum	100,000	07-DEC-1994
GB_BA1:MTCY01B2	35938	Z95554	Mycobacterium tuberculosis H37Rv complete genome; segment 72/162.	Mycobacterium tuberculosis	63,771	17-Jun-98
GB_BA1:MIU65430	1439	U65430	Mycobacterium intracellulare pyruvate kinase (pykF) gene, complete cds.	Mycobacterium intracellulare	67,061	23-DEC-1996
GB_BA2:AF045998	780	AF045998	Corynebacterium glutamicum inositol monophosphate phosphatase (impA) gene, complete cds.	Corynebacterium glutamicum	99,615	19-Feb-98
GB_BA2:AF051846	738	AF051846	Corynebacterium glutamicum phosphoribosylformimino-5-amino-1-phosphoribosyl-4-imidazolecarboxamide isomerase (hisA) gene, complete cds.	Corynebacterium glutamicum	100,000	12-MAR-1998
GB_GSS1:FR0005503	619	Z89313	F. rubripes GSS sequence, clone 079B16aE8, genomic survey sequence.	Fugu rubripes	37,785	01-MAR-1997
GB_PR3:AC004063	177014	AC004063	Homo sapiens chromosome 4 clone B3218, complete sequence.	Homo sapiens	35,835	10-Jul-98
GB_PR3:HS1178121	62268	AL109852	Human DNA sequence from clone RP5-1178121 on chromosome X, complete sequence.	Homo sapiens	37,873	01-DEC-1999
GB_HTG3:AC009301	163369	AC009301	Homo sapiens clone NH0062F14, *** SEQUENCING IN PROGRESS ***, 5 unordered pieces.	Homo sapiens	37,240	13-Aug-99
GB_HTG3:AC009444	164587	AC009444	Homo sapiens clone 1_O_3, *** SEQUENCING IN PROGRESS ***, 8 unordered pieces.	Homo sapiens	38,416	22-Aug-99
GB_HTG3:AC009444	164587	AC009444	Homo sapiens clone 1_O_3, *** SEQUENCING IN PROGRESS ***, 8 unordered pieces.	Homo sapiens	38,416	22-Aug-99
GB_IN1:DMC66A1	34127	AL031227	Drosophila melanogaster cosmid 66A1.	Drosophila melanogaster	38,416	05-OCT-1998
GB_BA1:CGASO19	1452	X76875	C. glutamicum (ASO 19) ATPase beta-subunit gene.	Corynebacterium glutamicum	99,931	27-OCT-1994
EM_PAT:E09634	1452	E09634	Brevibacterium flavum UncD gene whose gene product is involved in	Corynebacterium glutamicum	99,242	07-OCT-1997 (Rel. 52, Created)
GB_BA1:MLU15186	36241	U15186	Mycobacterium leprae cosmid L471.	Mycobacterium leprae	39,153	09-MAR-1995
EM_PAT:E09634	1452	E09634	Brevibacterium flavum UncD gene whose gene product is involved in	Corynebacterium glutamicum	100,000	07-OCT-1997 (Rel. 52, Created)
GB_BA1:CGASO19	1452	X76875	C. glutamicum (ASO 19) ATPase beta-subunit gene.	Corynebacterium glutamicum	100,000	27-OCT-1994
GB_VI:HEPCRE4B	414	X60570	Hepatitis C genomic RNA for putative envelope protein (RE4B isolate).	Hepatitis C virus	36,769	5-Apr-92

Table 4 (continued)

rx01201 1764	GB_BA1:SLATPSYNA	8560	Z22606	S. lividans i protein and ATP synthase genes.	Streptomyces lividans	66,269	01-MAY-1995
	GB_BA1:MTCV373	35516	Z73419	Mycobacterium tuberculosis H37Rv complete genome; segment 57/162.	Mycobacterium tuberculosis	65,437	17-Jun-98
	GB_BA1:MLU15186	36241	U15186	Mycobacterium leprae cosmid L471.	Mycobacterium leprae	39,302	09-MAR-1995
rx01202 1098	GB_BA1:SLATPSYNA	8560	Z22606	S. lividans i protein and ATP synthase genes.	Streptomyces lividans	57,087	01-MAY-1995
	GB_BA1:SLATPSYNA	8560	Z22606	S. lividans i protein and ATP synthase genes.	Streptomyces lividans	38,298	01-MAY-1995
	GB_BA1:MCSQSSHC	5538	Y09978	M. capsulatus orfz, orfz, sqs and shc genes.	Methylococcus capsulatus	37,626	26-MAY-1998
rx01204 933	GB_PL1:AP000423	154478	AP000423	Arabidopsis thaliana chloroplast genomic DNA, complete sequence, strain: Columbia.	Chloroplast Arabidopsis thaliana	38,395	15-Sep-99
	GB_HTG6:AC009762	164070	AC009762	Homo sapiens clone RP11-114116, *** SEQUENCING IN PROGRESS ***	Homo sapiens	35,459	04-DEC-1999
	GB_HTG6:AC009762	164070	AC009762	unordered pieces.			
	GB_HTG6:AC009762	164070	AC009762	Homo sapiens clone RP11-114116, *** SEQUENCING IN PROGRESS ***	Homo sapiens	36,117	04-DEC-1999
	GB_HTG6:AC009762	164070	AC009762	unordered pieces.			
rx01216 1124	GB_BA1:MTCY10G2	38970	Z92639	Mycobacterium tuberculosis H37Rv complete genome; segment 47/162.	Mycobacterium tuberculosis	39,064	17-Jun-98
	GB_BA2:AF017435	4301	AF017435	Methylobacterium extorquens methanol oxidation genes, glmU-like gene, partial cds, and orfL2, orfL1, orfR genes, complete cds.	Methylobacterium extorquens	42,671	10-MAR-1998
	GB_BA1:CCRFLBDBA	4424	M69228	C. crescentus flagellar gene promoter region.	Caulobacter crescentus	41,054	26-Apr-93
rx01225 1563	GB_BA2:AF058302	25306	AF058302	Streptomyces roseofulvus frenolicin biosynthetic gene cluster, complete sequence.	Streptomyces roseofulvus	36,205	2-Jun-98
	GB_HTG3:AC007301	165741	AC007301	Drosophila melanogaster chromosome 2 clone BACR04B09 (D576) RPCI-98	Drosophila melanogaster	39,922	17-Aug-99
	GB_HTG3:AC007301	165741	AC007301	04.B.9 map 43E12-44F1 strain y; cn bw sp. *** SEQUENCING IN PROGRESS ***			
	GB_HTG3:AC007301	165741	AC007301	150 unordered pieces.			
	GB_HTG3:AC007301	165741	AC007301	Drosophila melanogaster chromosome 2 clone BACR04B09 (D576) RPCI-98	Drosophila melanogaster	39,922	17-Aug-99
	GB_HTG3:AC007301	165741	AC007301	04.B.9 map 43E12-44F1 strain y; cn bw sp. *** SEQUENCING IN PROGRESS ***			
	GB_HTG3:AC007301	165741	AC007301	150 unordered pieces.			
rx01227 444	GB_BA1:SERFDXA	3869	M61119	Saccharopolyspora erythraea ferredoxin (fdxA) gene, complete cds.	Saccharopolyspora erythraea	64,908	13-MAR-1996
	GB_BA1:MTV005	37840	AL010186	Mycobacterium tuberculosis H37Rv complete genome; segment 51/162.	Mycobacterium tuberculosis	62,838	17-Jun-98
	GB_BA1:MSGY348	40056	AD000020	Mycobacterium tuberculosis sequence from clone y348.	Mycobacterium tuberculosis	61,712	10-DEC-1996
rx01242 900	GB_PR3:AC005697	174503	AC005697	Homo sapiens chromosome 17, clone hRPK.138_P_22, complete sequence.	Homo sapiens	35,373	09-OCT-1998
	GB_HTG3:AC010722	160723	AC010722	Homo sapiens clone NH0122L09, *** SEQUENCING IN PROGRESS ***	Homo sapiens	39,863	25-Sep-99
	GB_HTG3:AC010722	160723	AC010722	unordered pieces.			
	GB_HTG3:AC010722	160723	AC010722	Homo sapiens clone NH0122L09, *** SEQUENCING IN PROGRESS ***	Homo sapiens	39,863	25-Sep-99
	GB_HTG3:AC010722	160723	AC010722	unordered pieces.			

Table 4 (continued)

rx01243 1083	GB_GSS10:AO255057	583	AO255057	mgxb008N01r CUGI Rice Blast BAC Library Magnaporthe grisea genomic clone mgxb008N01r, genomic survey sequence.	Magnaporthe grisea	38,722	23-OCT-1998
	GB_IN1:CEK05D4	19000	Z92804	Caenorhabditis elegans cosmid K05D4, complete sequence.	Caenorhabditis elegans	35,448	23-Nov-98
	GB_IN1:CEK05D4	19000	Z92804	Caenorhabditis elegans cosmid K05D4, complete sequence.	Caenorhabditis elegans	35,694	23-Nov-98
rx01259 981	GB_BA1:CGLPD	1800	Y16642	Corynebacterium glutamicum lpd gene, complete CDS.	Corynebacterium glutamicum	100,000	1-Feb-99
	GB_HTG4:AC010567	143287	AC010567	Drosophila melanogaster chromosome 3L/69C1 clone RPC198-11N6, *** SEQUENCING IN PROGRESS ***; 70 unordered pieces.	Drosophila melanogaster	37,178	16-OCT-1999
	GB_HTG4:AC010567	143287	AC010567	Drosophila melanogaster chromosome 3L/69C1 clone RPC198-11N6, ***SEQUENCING IN PROGRESS ***; 70 unordered pieces.	Drosophila melanogaster	37,178	16-OCT-1999
rx01262 1284	GB_BA2:AF172324	14263	AF172324	Escherichia coli GalF (galF) gene, partial cds; O-antigen repeat unit transporter Wzx (wzx), WbnA (wbnA), O-antigen polymerase Wzy (wzy), WbnB (wbnB), WbnC (wbnC), WbnD (wbnD), WbnE (wbnE), UDP-Glc-4-epimerase GalE (galE), 6-phosphogluconate dehydrogenase Gnd (gnd), UDP-Glc-6-dehydrogenase Ugd (ugd), and WbnF (wbnF) genes, complete cds; and chain length determinant Wzz (wzz) gene, partial cds.	Escherichia coli	59,719	29-OCT-1999
	GB_BA2:ECU78086	4759	U78086	Escherichia coli hypothetical uridine-5'-diphosphoglucose dehydrogenase (ugd) and O-chain length regulator (wzz) genes, complete cds.	Escherichia coli	59,735	5-Nov-97
	GB_BA1:D90841	20226	D90841	E. coli genomic DNA, Kohara clone #351(45.1-45.5 min.).	Escherichia coli	37,904	21-MAR-1997
rx01311 870	GB_PR3:AC004103	144368	AC004103	Homo sapiens Xp22 BAC GS-619J3 (Genome Systems Human BAC library) complete sequence.	Homo sapiens	37,340	18-Apr-98
	GB_HTG3:AC007383	215529	AC007383	Homo sapiens clone NH0310K15, *** SEQUENCING IN PROGRESS ***; 4 unordered pieces.	Homo sapiens	36,385	25-Sep-99
	GB_HTG3:AC007383	215529	AC007383	Homo sapiens clone NH0310K15, *** SEQUENCING IN PROGRESS ***; 4 unordered pieces.	Homo sapiens	36,385	25-Sep-99
rx01312 2142	GB_BA2:AE000487	13889	AE000487	Escherichia coli K-12 MG1655 section 377 of 400 of the complete genome.	Escherichia coli	39,494	12-Nov-98
	GB_BA1:MTV016	53662	AL021841	Mycobacterium tuberculosis H37Rv complete genome; segment 143/162.	Mycobacterium tuberculosis	46,252	23-Jun-99
	GB_BA1:U00022	36411	U00022	Mycobacterium leprae cosmid L308.	Mycobacterium leprae	46,368	01-MAR-1994
rx01325 795	GB_HTG4:AC009245	215767	AC009245	Homo sapiens chromosome 7, *** SEQUENCING IN PROGRESS ***; 24 unordered pieces.	Homo sapiens	36,016	2-Nov-99
	GB_HTG4:AC009245	215767	AC009245	Homo sapiens chromosome 7, *** SEQUENCING IN PROGRESS ***; 24 unordered pieces.	Homo sapiens	36,016	2-Nov-99
	GB_HTG4:AC009245	215767	AC009245	Homo sapiens chromosome 7, *** SEQUENCING IN PROGRESS ***; 24 unordered pieces.	Homo sapiens	39,618	2-Nov-99
rx01332 576	GB_HTG6:AC007186	225851	AC007186	Drosophila melanogaster chromosome 2 clone BACR03D06 (D569) RPC1-98 03.D.6 map 32A-32A strain y; cn bw sp. *** SEQUENCING IN PROGRESS***; 91 unordered pieces.	Drosophila melanogaster	35,366	07-DEC-1999
	GB_HTG6:AC007147	202291	AC007147	Drosophila melanogaster chromosome 2 clone BACR19N18 (D572) RPC1-98 19.N.18 map 32A-32A strain y; cn bw sp. *** SEQUENCING IN PROGRESS ***; 22 unordered pieces.	Drosophila melanogaster	35,366	07-DEC-1999

Table 4 (continued)

GB_HTG3:AC010207	207890	AC010207	Homo sapiens clone RPC111-375120, *** SEQUENCING IN PROGRESS ***; 25 Homo sapiens unordered pieces.	34,821	16-Sep-99
GB_BA2:AF109682	990	AF109682	Aquaspirillum arcticum malate dehydrogenase (MDH) gene, complete cds.	58,487	19-OCT-1999
GB_HTG2:AC006759	103725	AC006759	Caenorhabditis elegans clone Y40G12, *** SEQUENCING IN PROGRESS ***; 8 unordered pieces.	37,963	25-Feb-99
GB_HTG2:AC006759	103725	AC006759	Caenorhabditis elegans clone Y40G12, *** SEQUENCING IN PROGRESS ***; 8 unordered pieces.	37,963	25-Feb-99
GB_BA1:MTY20B11	36330	Z95121	Mycobacterium tuberculosis H37Rv complete genome; segment 139/162.	38,011	17-Jun-98
GB_BA1:XANXANAB	3410	M83231	Xanthomonas campestris phosphoglucosyltransferase and phosphomannomutase (xanA) and phosphomannose isomerase and GDP-mannose pyrophosphorylase (xanB) genes, complete cds.	47,726	25-Apr-93
GB_GSS10:QA194038	697	AQ194038	RPC111-47D24, TJ RPC11-11 Homo sapiens genomic clone RPC11-11-47D24, genomic survey sequence.	36,599	20-Apr-99
GB_BA1:MTY20B11	36330	Z95121	Mycobacterium tuberculosis H37Rv complete genome; segment 139/162.	36,940	17-Jun-98
GB_GSS3:B10037	974	B10037	T27A19-T7 TAMU Arabidopsis thaliana genomic clone T27A19, genomic survey sequence.	35,284	14-MAY-1997
GB_GSS3:B09549	1097	B09549	T21A19-T7.1 TAMU Arabidopsis thaliana genomic clone T21A19, genomic survey sequence.	38,324	14-MAY-1997
GB_BA1:MTY71	42729	Z92771	Mycobacterium tuberculosis H37Rv complete genome; segment 141/162.	39,778	10-Feb-99
GB_HTG5:AC007547	262181	AC007547	Homo sapiens clone RP11-252O18, WORKING DRAFT SEQUENCE, 121 unordered pieces.	32,658	16-Nov-99
GB_HTG5:AC007547	262181	AC007547	Homo sapiens clone RP11-252O18, WORKING DRAFT SEQUENCE, 121 unordered pieces.	38,395	16-Nov-99
GB_BA2:AF072709	8366	AF072709	Streptomyces lividans amplifiable element AUD4: putative transcriptional regulator, putative ferredoxin, putative cytochrome oxidoreductase, and putative oxidoreductase genes, complete cds; and unknown genes.	55,221	8-Jul-98
GB_BA1:CGLYSEG	2374	X96471	C. glutamicum lysE and lysG genes.	100,000	24-Feb-97
GB_PR4:AC005906	185952	AC005906	Homo sapiens 12p13.3 BAC RPC111-429A20 (Roswell Park Cancer Institute Human BAC Library) complete sequence.	36,756	30-Jan-99
GB_BA1:CGPTAACKA	3657	X89084	C. glutamicum pta gene and ackA gene.	100,000	23-MAR-1999
GB_BA1:D90861	14839	D90861	E. coli genomic DNA, Kohara clone #405(52.0-52.3 min.).	53,041	29-MAY-1997
GB_PAT:ED0287	1200	E02087	DNA encoding acetate kinase protein from Escherichia coli.	54,461	29-Sep-97
GB_GSS1:HPU06027	280	U06027	Helicobacter pylori feoB-like DNA sequence; genomic survey sequence.	39,286	9-Apr-97
GB_EST31:A1701691	349	A1701691	IMAGE:2347494 3' similar to gb:L19686_ma1 MACROPHAGE MIGRATION INHIBITORY FACTOR (HUMAN); mRNA sequence.	39,412	3-Jun-99

Table 4 (continued)

GB_EST15:AA480256	389	AA480256	ne31f04.s1 NCI_CGAP_Co3 Homo sapiens cDNA clone IMAGE:898975 3' similar to gb:L19686_rna1 MACROPHAGE MIGRATION INHIBITORY FACTOR (HUMAN); mRNA sequence.	Homo sapiens	39,574	14-Aug-97
GB_BA1:SCJ51	40745	AL109848	Streptomyces coelicolor cosmid I51.	Streptomyces coelicolor A3(2)	54,141	16-Aug-99
GB_BA1:SCE36	12581	AL049763	Streptomyces coelicolor cosmid E36.	Streptomyces coelicolor	38,126	05-MAY-1999
GB_BA1:CGU43535	2531	U43535	Corynebacterium glutamicum multidrug resistance protein (cmr) gene, complete cds.	Corynebacterium glutamicum	41,852	9-Apr-97
GB_BA1:SC6G4	41055	AL031317	Streptomyces coelicolor cosmid 6G4.	Streptomyces coelicolor	62,149	20-Aug-98
GB_BA1:U00020	36947	U00020	Mycobacterium leprae cosmid B229.	Mycobacterium leprae	38,303	01-MAR-1994
GB_BA1:MTCY77	22255	Z95389	Mycobacterium tuberculosis H37Rv complete genome; segment 146/162.	Mycobacterium tuberculosis	38,179	18-Jun-98
GB_BA1:MLCB1222	34714	AL049491	Mycobacterium leprae cosmid B1222.	Mycobacterium leprae	66,208	27-Aug-99
GB_BA1:MTV017	67200	AL021897	Mycobacterium tuberculosis H37Rv complete genome; segment 48/162.	Mycobacterium tuberculosis	38,553	24-Jun-99
GB_BA1:PAU72494	4368	U72494	Pseudomonas aeruginosa fumarase (fumC) and Mn superoxide dismutase (sodA) genes, complete cds.	Pseudomonas aeruginosa	52,690	23-OCT-1996
GB_BA1:D90907	132419	D90907	Synechocystis sp. PCC6803 complete genome, 9/27, 1056467-1188885.	Synechocystis sp.	56,487	7-Feb-99
GB_IN2:AF073177	9534	AF073177	Drosophila melanogaster glycogen phosphorylase (GlyP) gene, complete cds.	Drosophila melanogaster	55,100	1-Jul-99
GB_IN2:AF073179	3159	AF073179	Drosophila melanogaster glycogen phosphorylase (GlyP) mRNA, complete cds.	Drosophila melanogaster	56,708	27-Apr-99
GB_BA1:D78182	7836	D78182	Streptococcus mutans DNA for dTDP-rhamnose synthesis pathway, complete cds.	Streptococcus mutans	44,050	5-Feb-99
GB_BA2:AF079139	4342	AF079139	Streptomyces venezuelae pikCD operon, complete sequence.	Streptomyces venezuelae	38,587	28-OCT-1998
GB_BA2:AF087022	1470	AF087022	Streptomyces venezuelae cytochrome P450 monooxygenase (pick) gene, complete cds.	Streptomyces venezuelae	38,621	15-OCT-1998
GB_BA1:MTCY63	38900	Z96800	Mycobacterium tuberculosis H37Rv complete genome; segment 16/162.	Mycobacterium tuberculosis	59,035	17-Jun-98
GB_BA2:AF097519	4594	AF097519	Klebsiella pneumoniae dTDP-D-glucose 4,6 dehydratase (mlb), glucose-1-phosphate thymidyl transferase (mia), dTDP-4-keo-L-rhamnose reductase (mlD), dTDP-4-keo-6-deoxy-D-glucose 3,5-epimerase (mlC), and rhamnosyl transferase (wbbL) genes, complete cds.	Klebsiella pneumoniae	59,714	4-Nov-98

Table 4 (continued)

			GB_BA2:NGOCPSPS	8905	L09189	Neisseria meningitidis dTDP-D-glucose 4,6-dehydratase (rfbB), glucose-1-phosphate thymidyl transferase (rfbA) and rfbC genes, complete cds and UPD-glucose-4-epimerase (galE) pseudogene.	Neisseria meningitidis	58,384	30-Jul-96
rx01571	723		GB_BA1:AB011413	12070	AB011413	Streptomyces griseus genes for Orf2, Orf3, Orf4, Orf5, AfsA, Orf8, partial and complete cds.	Streptomyces griseus	57,500	7-Aug-98
			GB_BA1:AB011413	12070	AB011413	Streptomyces griseus genes for Orf2, Orf3, Orf4, Orf5, AfsA, Orf8, partial and complete cds.	Streptomyces griseus	35,655	7-Aug-98
rx01572	615		GB_BA1:AB011413	12070	AB011413	Streptomyces griseus genes for Orf2, Orf3, Orf4, Orf5, AfsA, Orf8, partial and complete cds.	Streptomyces griseus	57,843	7-Aug-98
			GB_BA1:AB011413	12070	AB011413	Streptomyces griseus genes for Orf2, Orf3, Orf4, Orf5, AfsA, Orf8, partial and complete cds.	Streptomyces griseus	38,119	7-Aug-98
rx01606	2799		GB_VI:CFU72240	4783	U72240	Choristoneura fumiferana nuclear polyhedrosis virus ETM protein homolog, 79 kDa protein homolog, 15 kDa protein homolog and GTA protein homolog genes, complete cds.	Choristoneura fumiferana nucleopolyhedrovirus	37,115	29-Jan-99
			GB_GSS10:AQ213248	408	AQ213248	HS_3249_B1_A02_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3249 Col=3 Row=B, genomic survey sequence.	Homo sapiens	34,559	18-Sep-98
			GB_GSS8:AQ070145	285	AQ070145	HS_3027_B1_H02_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3027 Col=3 Row=P, genomic survey sequence.	Homo sapiens	40,351	5-Aug-98
rx01626	468		GB_PR4:AF152510	2490	AF152510	Homo sapiens protocadherin gamma A3 short form protein (PCDH-gamma-A3) variable region sequence, complete cds.	Homo sapiens	34,298	14-Jul-99
			GB_PR4:AF152323	4605	AF152323	Homo sapiens protocadherin gamma A3 (PCDH-gamma-A3) mRNA, complete cds.	Homo sapiens	34,298	22-Jul-99
rx01632	1128		GB_PR4:AF152509	2712	AF152509	Homo sapiens PCDH-gamma-A3 gene, aberrantly spliced, mRNA sequence.	Homo sapiens	34,298	14-Jul-99
			GB_HTG4:AC006590	127171	AC006590	Drosophila melanogaster chromosome 2 clone BACR13N02 (D543) RPCI-98 13.N.2 map 36E-36E strain y; cn bw sp, *** SEQUENCING IN PROGRESS***, 101 unordered pieces.	Drosophila melanogaster	33,812	19-OCT-1999
			GB_HTG4:AC006590	127171	AC006590	Drosophila melanogaster chromosome 2 clone BACR13N02 (D543) RPCI-98 13.N.2 map 36E-36E strain y; cn bw sp, *** SEQUENCING IN PROGRESS***, 101 unordered pieces.	Drosophila melanogaster	33,812	19-OCT-1999
			GB_GSS8:B99182	415	B99182	CIT-HSP-2280113.TR CIT-HSP Homo sapiens genomic clone 2280113, genomic survey sequence.	Homo sapiens	36,111	26-Jun-98
rx01633	1206		GB_BA1:BSUB0009	208780	Z99112	Bacillus subtilis complete genome (section 9 of 21): from 1598421 to 1807200.	Bacillus subtilis	36,591	26-Nov-97
			GB_BA1:BSUB0009	208780	Z99112	Bacillus subtilis complete genome (section 9 of 21): from 1598421 to 1807200.	Bacillus subtilis	34,941	26-Nov-97
			GB_HTG2:AC006247	174368	AC006247	Drosophila melanogaster chromosome 2 clone BACR48I10 (D505) RPCI-98 48.I.10 map 49E6-49F8 strain y; cn bw sp, *** SEQUENCING IN PROGRESS***, 17 unordered pieces.	Drosophila melanogaster	37,037	2-Aug-99

Table 4 (continued)

αa01695 1623	GB_BA1:CGA224946	2408	AJ224946	Corynebacterium glutamicum DNA for L-Malate:quinone oxidoreductase.	Corynebacterium glutamicum	100,000	11-Aug-98
	GB_BA1:MTCY24A1	20270	Z95207	Mycobacterium tuberculosis H37Rv complete genome; segment 124/162.	Mycobacterium tuberculosis	38,626	17-Jun-98
αa01702 1155	GB_IN1:DMU15974	2994	U15974	Drosophila melanogaster kinesin-like protein (klp68d) mRNA, complete cds.	Drosophila melanogaster	36,783	18-Jul-95
	GB_BA1:CGFDA	3371	X17313	Corynebacterium glutamicum fda gene for fructose-bisphosphate aldolase (EC 4.1.2.13).	Corynebacterium glutamicum	99,913	12-Sep-93
	GB_BA1:MTY13E10	35019	Z95324	Mycobacterium tuberculosis H37Rv complete genome; segment 18/162.	Mycobacterium tuberculosis	38,786	17-Jun-98
αa01743 901	GB_BA1:MLCB4	36310	AL023514	Mycobacterium leprae cosmid B4.	Mycobacterium leprae	38,238	27-Aug-99
	GB_IN2:CELC27H5	35840	U14635	Caenorhabditis elegans cosmid C27H5.	Caenorhabditis elegans	35,334	13-Jul-95
	GB_EST24:AI167112	579	AI167112	xylem.est.878 Poplar xylem Lambda ZAPI library Populus balsamifera subsp. trichocarpa cDNA 5' mRNA sequence.	Populus balsamifera subsp. trichocarpa	39,222	03-DEC-1998
	GB_GSS9:AQ102635	347	AQ102635	HS_3048_B1_F08_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3048 Col=15 Row=L, genomic survey sequence.	Homo sapiens	40,653	27-Aug-98
αa01744 1662	GB_BA1:MTCY01B2	35938	Z95554	Mycobacterium tuberculosis H37Rv complete genome; segment 72/162.	Mycobacterium tuberculosis	36,650	17-Jun-98
	GB_GSS1:AF009226	665	AF009226	Mycobacterium tuberculosis cytochrome D oxidase subunit I (appC) gene, partial sequence, genomic survey sequence.	Mycobacterium tuberculosis	63,438	31-Jul-97
αa01745 836	GB_BA1:SCD78	36224	AL034355	Streptomyces coelicolor cosmid D78.	Streptomyces coelicolor	53,088	26-Nov-98
	GB_BA1:MTCY190	34150	Z70283	Mycobacterium tuberculosis H37Rv complete genome; segment 98/162.	Mycobacterium tuberculosis	62,081	17-Jun-98
	GB_BA1:MLCB22	40281	Z98741	Mycobacterium leprae cosmid B22.	Mycobacterium leprae	61,364	22-Aug-97
αa01758 1140	GB_BA2:AE000175	15067	AE000175	Escherichia coli K-12 MG1655 section 65 of 400 of the complete genome.	Escherichia coli	52,323	12-Nov-98
	GB_PR3:HS57G9	113872	Z95116	Human DNA sequence from BAC 57G9 on chromosome 22q12.1 Contains ESTs, CA repeat, GSS.	Homo sapiens	39,209	23-Nov-99
	GB_PL2:YSCH9666	39057	U10397	Saccharomyces cerevisiae chromosome VIII cosmid 9666.	Saccharomyces cerevisiae	40,021	5-Sep-97
	GB_PL2:YSCH9986	41664	U00027	Saccharomyces cerevisiae chromosome VIII cosmid 9986.	Saccharomyces cerevisiae	34,375	29-Aug-97
αa01814 1785	GB_BA1:ABCCELB	2058	L24077	Acetobacter xylinum phosphoglucosyltransferase (celB) gene, complete cds.	Acetobacter xylinus	62,173	21-Sep-94
	GB_BA1:MTCY22D7	31859	Z83866	Mycobacterium tuberculosis H37Rv complete genome; segment 133/162.	Mycobacterium tuberculosis	39,749	17-Jun-98
	GB_BA1:MTCY22D7	31859	Z83866	Mycobacterium tuberculosis H37Rv complete genome; segment 133/162.	Mycobacterium tuberculosis	40,034	17-Jun-98
αa01851 1809	GB_GSS9:AQ142579	529	AQ142579	HS_2222_B1_H03_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2222 Col=5 Row=P, genomic survey sequence.	Homo sapiens	38,068	24-Sep-98
	GB_IN2:AC005689	108924	AC005689	Drosophila melanogaster, chromosome 2L, region 30A3-30A6, P1 clones DS06958 and DS03097, complete sequence.	Drosophila melanogaster	36,557	30-OCT-1998
	GB_GSS1:AG008814	637	AG008814	Homo sapiens genomic DNA, 21q region, clone: B137B7BB68, genomic survey sequence.	Homo sapiens	35,316	7-Feb-99

Table 4 (continued)

rx01859 1050	GB_BA2:AF183408	63626	AF183408	Microcystis aeruginosa DNA polymerase III beta subunit (dnaN) gene, partial cds; microcystin synthetase gene cluster, complete sequence; Uma1 (uma1), Uma2 (uma2), Uma3 (uma3), Uma4 (uma4), and Uma5 (uma5) genes, complete cds; and Uma6 (uma6) gene, partial cds.	Microcystis aeruginosa	36,364	03-OCT-1999
	GB_HTG5:AC008031	158889	AC008031	Trypanosoma brucei chromosome II clone RPC193-25N14, *** SEQUENCING IN PROGRESS ***; 2 unordered pieces.	Trypanosoma brucei	35,334	15-Nov-99
	GB_BA2:AF183408	63626	AF183408	Microcystis aeruginosa DNA polymerase III beta subunit (dnaN) gene, partial cds; microcystin synthetase gene cluster, complete sequence; Uma1 (uma1), Uma2 (uma2), Uma3 (uma3), Uma4 (uma4), and Uma5 (uma5) genes, complete cds; and Uma6 (uma6) gene, partial cds.	Microcystis aeruginosa	36,529	03-OCT-1999
rx01865 438	GB_BA1:SERFDXA	3869	M61119	Saccharopolyspora erythraea ferredoxin (fdxA) gene, complete cds.	Saccharopolyspora erythraea	59,862	13-MAR-1996
	GB_BA1:MTV005	37840	AL010186	Mycobacterium tuberculosis H37Rv complete genome; segment 51/162.	Mycobacterium tuberculosis	61,949	17-Jun-98
	GB_BA1:MSGY348	40056	AD000020	Mycobacterium tuberculosis sequence from clone y348.	Mycobacterium tuberculosis	59,908	10-DEC-1996
rx01882 1113	GB_PR1:HUMADRA2C	1491	J03853	Human kidney alpha-2-adrenergic receptor mRNA, complete cds.	Homo sapiens	36,899	27-Apr-93
	GB_PR4:HSU72648	4850	U72648	Homo sapiens alpha2-C4-adrenergic receptor gene, complete cds.	Homo sapiens	36,899	23-Nov-98
	GB_GSS3:B42200	387	B42200	HS-1055-B1-A03-MR.abi CIT Human Genomic Sperm Library C Homo sapiens genomic clone Plate=CT 777 Col=5 Row=B, genomic survey sequence.	Homo sapiens	34,805	18-OCT-1997
rx01884 1913	GB_BA1:MTCY48	35377	Z74020	Mycobacterium tuberculosis H37Rv complete genome; segment 69/162.	Mycobacterium tuberculosis	37,892	17-Jun-98
	GB_BA1:SCO001206	9184	AJ001206	Streptomyces coelicolor A3(2), glycogen metabolism cluster II.	Streptomyces coelicolor	40,413	29-MAR-1999
rx01886 897	GB_BA1:D90908	122349	D90908	Synechocystis sp. PCC6803 complete genome, 10/27, 1188886-1311234.	Synechocystis sp.	47,792	7-Feb-99
	GB_GSS9:AQ116291	572	AQ116291	RPCL11-49P6.TK.1 RPCL11 Homo sapiens genomic clone RPCL11-49P6, genomic survey sequence.	Homo sapiens	43,231	20-Apr-99
	GB_BA2:AE001721	17632	AE001721	Thermotoga maritima section 33 of 136 of the complete genome.	Thermotoga maritima	39,306	2-Jun-99
	GB_EST16:AA567090	596	AA567090	GM01044.5prime GM Drosophila melanogaster ovary BlueScript Drosophila melanogaster cDNA clone GM01044 5prime, mRNA sequence.	Drosophila melanogaster	42,807	28-Nov-98
rx01887 1134	GB_HTG6:AC008147	303147	AC008147	Homo sapiens clone RP3-405.110, *** SEQUENCING IN PROGRESS ***; 102 unordered pieces.	Homo sapiens	36,417	03-DEC-1999
	GB_HTG6:AC008147	303147	AC008147	Homo sapiens clone RP3-405.110, *** SEQUENCING IN PROGRESS ***; 102 unordered pieces.	Homo sapiens	37,667	03-DEC-1999
	GB_BA2:ALW243431	26953	AJ243431	Acinetobacter lwofii wzc, wzb, wza, weeA, weeB, weeC, wzc, wzy, weeD, weeE, weeF, weeG, weeH, weeI, weeJ, weeK, galU, ugd, pgi, galE, pgm (partial) and mip (partial) genes (emulsan biosynthetic gene cluster), strain RAG-1.	Acinetobacter lwofii	39,640	01-OCT-1999
rx01888 658	GB_HTG2:AC008197	125235	AC008197	Drosophila melanogaster chromosome 3 clone BACR02L12 (D753) RPCL-98 02.L.12 map 94B-94C strain y; cn bw sp, *** SEQUENCING IN PROGRESS***, 113 unordered pieces.	Drosophila melanogaster	32,969	2-Aug-99

Table 4 (continued)

GB_HTG2:AC008197	125235	AC008197	Drosophila melanogaster chromosome 3 clone BACR02L12 (D753) RPCI-98 02.L.12 map 94B-94C strain y; cn bw sp. *** SEQUENCING IN PROGRESS ***. 113 unordered pieces.	Drosophila melanogaster	32,969	2-Aug-99
GB_EST36:AI881527	598	AI881527	606070C09.y1 606 - Ear tissue cDNA library from Schmidt lab Zea mays cDNA, Zea mays mRNA sequence.	Zea mays	43,617	21-Jul-99
GB_VI:HIV232971	621	AJ232971	Human immunodeficiency virus type 1 subtype C nef gene, patient MP83.	Human immunodeficiency virus type 1	40,040	05-MAR-1999
GB_PL1:AFCHSE	6158	Y09542	A.fumigatus chsE gene.	Aspergillus fumigatus	37,844	1-Apr-97
GB_PR3:AF064858	193387	AF064858	Homo sapiens chromosome 21q22.3 BAC 28F9, complete sequence.	Homo sapiens	37,136	2-Jun-98
GB_BA1:CGL238250	1593	AJ238250	Corynebacterium glutamicum ndh gene.	Corynebacterium glutamicum	100,000	24-Apr-99
GB_BA2:AF038423	1376	AF038423	Mycobacterium smegmatis NADH dehydrogenase (ndh) gene, complete cds.	Mycobacterium smegmatis	65,254	05-MAY-1998
GB_BA1:MTCY359	36021	Z83859	Mycobacterium tuberculosis H37Rv complete genome; segment 84/162.	Mycobacterium tuberculosis	40,058	17-Jun-98
GB_BA1:MSGB38COS	37114	L01095	M. leprae genomic DNA sequence, cosmid B38 bfr gene, complete cds.	Mycobacterium leprae	59,551	6-Sep-94
GB_BA1:SCE63	37200	AL035640	Streptomyces coelicolor cosmid E63.	Streptomyces coelicolor	39,468	17-MAR-1999
GB_PR3:AF093117	147216	AF093117	Homo sapiens chromosome 7qtel0 BAC E3, complete sequence.	Homo sapiens	39,291	02-OCT-1998
GB_BA1:CGPAN	2164	X96580	C.glutamicum panB, panC & xylB genes.	Corynebacterium glutamicum	38,384	11-MAY-1999
GB_BA1:ASXYLA	1905	X59466	Arthrobacter Sp. N.R.L. B3728 xylA gene for D-xylose(D-glucose) isomerase. Arthrobacter sp.	Arthrobacter sp.	56,283	04-MAY-1992
GB_HTG3:AC009500	176060	AC009500	Homo sapiens clone NH0511A20, *** SEQUENCING IN PROGRESS ***. 6 unordered pieces.	Homo sapiens	37,593	24-Aug-99
GB_BA2:AE000739	13335	AE000739	Aquifex aeolicus section 71 of 109 of the complete genome.	Aquifex aeolicus	36,309	25-MAR-1998
GB_EST28:AI519629	612	AI519629	LD39282.5prime LD Drosophila melanogaster embryo pOT2 Drosophila melanogaster cDNA clone LD39282 5prime, mRNA sequence.	Drosophila melanogaster	41,941	16-MAR-1999
GB_EST21:AA949396	767	AA949396	LD28277.5prime LD Drosophila melanogaster embryo pOT2 Drosophila melanogaster cDNA clone LD28277 5prime, mRNA sequence.	Drosophila melanogaster	39,855	25-Nov-98
GB_BA1:BSPGIA	1822	X16639	Bacillus stearothermophilus pgIA gene for phosphoglucosyltransferase isoenzyme A (EC 5.3.1.9).	Bacillus stearothermophilus	66,292	20-Apr-95
GB_BA1:BSUB0017	217420	Z99120	Bacillus subtilis complete genome (section 17 of 21): from 3197001 to 3414420.	Bacillus subtilis	37,255	26-Nov-97
GB_BA2:AF132127	8452	AF132127	Streptococcus mutans sorbitol phosphoenolpyruvate:sugar phosphotransferase operon, complete sequence and unknown gene.	Streptococcus mutans	63,607	28-Sep-99
GB_BA1:SXSCRBA	3161	X67744	S.xylosus scrB and scrR genes.	Staphylococcus xylosus	67,778	28-Nov-96
GB_BA1:BSUB0020	212150	Z99123	Bacillus subtilis complete genome (section 20 of 21): from 3798401 to 4010550.	Bacillus subtilis	35,574	26-Nov-97
GB_BA1:BSGENR	97015	X73124	B.subtilis genomic region (325 to 333).	Bacillus subtilis	51,826	2-Nov-93
GB_BA1:MTCI237	27030	Z94752	Mycobacterium tuberculosis H37Rv complete genome; segment 46/162.	Mycobacterium tuberculosis	54,476	17-Jun-98

Table 4 (continued)

	GB_PL2:SCE9537	66030	U18778	Saccharomyces cerevisiae chromosome V cosmids 9537, 9581, 9495, 9867, and lambda clone 5898.	Saccharomyces cerevisiae	36,100	1-Aug-97
	GB_GSS13:AQ501177	767	AQ501177	V26G9 mTrn-3xHA/lacZ Insertion Library Saccharomyces cerevisiae genomic 5'.	Saccharomyces cerevisiae	32,039	29-Apr-99
rxa02054	1140			genomic survey sequence.			
		34714	AL049491	Mycobacterium leprae cosmid B1222.	Mycobacterium leprae	61,896	27-Aug-99
		43401	Z95390	Mycobacterium tuberculosis H37Rv complete genome; segment 147/162.	Mycobacterium tuberculosis	59,964	17-Jun-98
rxa02056	2891						
		3453	U43540	Mycobacterium tuberculosis rfbA, rhamnose biosynthesis protein (rfbA), and rmlC genes, complete cds.	Mycobacterium tuberculosis	59,659	14-Aug-97
		4394	E14601	Brevibacterium lactofermentum gene for alpha-ketoglutaric acid dehydrogenase.	Corynebacterium glutamicum	98,928	28-Jul-99
		4394	D84102	Corynebacterium glutamicum DNA for 2-oxoglutarate dehydrogenase, complete cds.	Corynebacterium glutamicum	98,928	6-Feb-99
rxa02061	1617						
		22440	AL021006	Mycobacterium tuberculosis H37Rv complete genome; segment 54/162.	Mycobacterium tuberculosis	39,265	18-Jun-98
		211682	AC005883	Homo sapiens chromosome 17 clone RP11-958E11 map 17, *** SEQUENCING IN PROGRESS ***; 2 ordered pieces.	Homo sapiens	37,453	08-DEC-1999
		84254	AC003033	Arabidopsis thaliana chromosome II BAC T21L14 genomic sequence, complete sequence.	Arabidopsis thaliana	37,711	19-DEC-1997
rxa02063	1350						
		75050	AC002334	Arabidopsis thaliana chromosome II BAC F25118 genomic sequence, complete sequence.	Arabidopsis thaliana	37,711	04-MAR-1998
		1518	X89733	S. coelicolor DNA for glgC gene.	Streptomyces coelicolor	56,972	12-Jul-99
		786	AQ687350	nbxb0074H11r CUGI Rice BAC Library Oryza sativa genomic clone nbxb0074H11r, genomic survey sequence.	Oryza sativa	40,696	1-Jul-99
rxa02100	2348						
		444	AW028530	wv27110.x1 NCI CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2530795 3' similar to WP:T03G11.6 CE04874 ; mRNA sequence.	Homo sapiens	36,795	27-OCT-1999
		37036	AD000018	Mycobacterium tuberculosis sequence from clone y151.	Mycobacterium tuberculosis	40,156	10-DEC-1996
		32514	Z73902	Mycobacterium tuberculosis H37Rv complete genome; segment 59/162.	Mycobacterium tuberculosis	55,218	17-Jun-98
rxa02122	822						
		9589	AJ001205	Streptomyces coelicolor A3(2) glycogen metabolism cluster.	Streptomyces coelicolor	38,475	29-MAR-1999
		13548	D90858	E. coli genomic DNA, Kohara clone #401(51.3-51.6 min.).	Escherichia coli	38,586	29-MAY-1997
		469	A1948595	wq07d12.x1 NCI CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2470583 3' mRNA sequence.	Homo sapiens	37,259	6-Sep-99
rxa02140	1200						
		220665	AC010387	Homo sapiens chromosome 5 clone CITB-H1_2074D8, *** SEQUENCING IN PROGRESS ***; 77 unordered pieces.	Homo sapiens	38,868	15-Sep-99
		36548	L78813	Mycobacterium leprae cosmid B1551 DNA sequence.	Mycobacterium leprae	51,399	15-Jun-96
		36548	L78814	Mycobacterium leprae cosmid B1554 DNA sequence.	Mycobacterium leprae	51,399	15-Jun-96
rxa02142	774						
		2482	AF093099	Mus musculus transcription factor TBLYM (Tblym) mRNA, complete cds.	Mus musculus	36,683	01-OCT-1999
		34150	Z70283	Mycobacterium tuberculosis H37Rv complete genome; segment 98/162.	Mycobacterium tuberculosis	57,292	17-Jun-98

Table 4 (continued)

GB_BA1:SCG10	36734	AL049497	Streptomyces coelicolor cosmid 6G10.	Streptomyces coelicolor	35,058	24-MAR-1999
GB_BA1:AB016787	5550	AB016787	Pseudomonas putida genes for cytochrome o ubiquinol oxidase A-E and 2 ORFs, complete cds.	Pseudomonas putida	47,403	5-Aug-99
GB_BA1:MTCY190	34150	Z70283	Mycobacterium tuberculosis H37Rv complete genome; segment 98/162.	Mycobacterium tuberculosis	57,317	17-Jun-98
GB_BA1:MSGB1551CS	36548	L78813	Mycobacterium leprae cosmid B1551 DNA sequence.	Mycobacterium leprae	38,159	15-Jun-96
GB_BA1:MSGB1554CS	36548	L78814	Mycobacterium leprae cosmid B1554 DNA sequence.	Mycobacterium leprae	38,159	15-Jun-96
GB_BA1:MTCY190	34150	Z70283	Mycobacterium tuberculosis H37Rv complete genome; segment 98/162.	Mycobacterium tuberculosis	55,530	17-Jun-98
GB_HTG3:AC011500_0	300851	AC011500	Homo sapiens chromosome 19 clone CIT978SKB_60E11, *** SEQUENCING IN PROGRESS ***, 246 unordered pieces.	Homo sapiens	39,659	18-Feb-00
GB_HTG3:AC011500_0	300851	AC011500	Homo sapiens chromosome 19 clone CIT978SKB_60E11, *** SEQUENCING IN PROGRESS ***, 246 unordered pieces.	Homo sapiens	39,659	18-Feb-00
GB_EST28:AI492095	485	AI492095	tg07a01.x1 NCI_CGAP_CLL1 Homo sapiens cDNA clone IMAGE:2108040 3'; mRNA sequence.	Homo sapiens	39,798	30-MAR-1999
GB_EST10:AA157467	376	AA157467	zo50e01.r1 Stratagene endothelial cell 937223 Homo sapiens cDNA clone IMAGE:590328 5'; mRNA sequence.	Homo sapiens	36,436	11-DEC-1996
GB_EST10:AA157467	376	AA157467	zo50e01.r1 Stratagene endothelial cell 937223 Homo sapiens cDNA clone IMAGE:590328 5'; mRNA sequence.	Homo sapiens	36,436	11-DEC-1996
GB_PR3:HSBK277P6	61698	AL117347	Human DNA sequence from clone 277P6 on chromosome 1q25.3-31.2, complete sequence.	Homo sapiens	36,872	23-Nov-99
GB_BA2:EMB065R075	360	AF116423	Rhizobium etli mutant MB045 RosR-transcriptionally regulated sequence.	Rhizobium etli	43,175	06-DEC-1999
GB_EST34:AI789323	574	AI789323	uk53g05.y1 Sugano mouse kidney mKia Mus musculus cDNA clone IMAGE:1972760 5' similar to WP:K11H12.8 CE12160 ; mRNA sequence.	Mus musculus	39,715	2-Jul-99
GB_BA1:CGGLTG	3013	X66112	C.glutamicum glt gene for citrate synthase and ORF.	Corynebacterium glutamicum	100,000	17-Feb-95
GB_BA1:MTCY31	37630	Z73101	Mycobacterium tuberculosis H37Rv complete genome; segment 41/162.	Mycobacterium tuberculosis	64,331	17-Jun-98
GB_BA1:MLCB57	38029	Z99494	Mycobacterium leprae cosmid B57.	Mycobacterium leprae	62,491	10-Feb-99
GB_RO:RATDAPRP	2819	M76426	Rattus norvegicus dipeptidyl aminopeptidase-related protein (dpp6) mRNA, complete cds.	Rattus norvegicus	38,791	31-MAY-1995
GB_GSS8:AQ012162	763	AQ012162	127PB037070197 Cosmid library of chromosome II Rhodobacter sphaeroides genomic clone 127PB037070197, genomic survey sequence.	Rhodobacter sphaeroides	40,044	4-Jun-98
GB_RO:RATDAPRP	2819	M76426	Rattus norvegicus dipeptidyl aminopeptidase-related protein (dpp6) mRNA, complete cds.	Rattus norvegicus	37,312	31-MAY-1995
GB_BA1:AB025424	2995	AB025424	Corynebacterium glutamicum gene for aconitase, partial cds.	Corynebacterium glutamicum	99,173	3-Apr-99
GB_BA2:AF002133	15437	AF002133	Mycobacterium avium strain GIR10 transcriptional regulator (mav81) gene, partial cds, aconitase (acn), invasin 1 (inv1), invasin 2 (inv2), transcriptional regulator (moxR), ketoacyl-reductase (fabG), enoyl-reductase (inhA) and ferrochelatase (mav272) genes, complete cds.	Mycobacterium avium	40,219	26-MAR-1998

Table 4 (continued)

na02213 874	GB_BA1:MTV007	32806	AL021184	Mycobacterium tuberculosis H37Rv complete genome; segment 64/162.	Mycobacterium tuberculosis	38,253	17-Jun-98
	GB_BA1:AB025424	2995	AB025424	Corynebacterium glutamicum gene for aconitase, partial cds.	Corynebacterium glutamicum	99,096	3-Apr-99
	GB_BA1:MTV007	32806	AL021184	Mycobacterium tuberculosis H37Rv complete genome; segment 64/162.	Mycobacterium tuberculosis	34,937	17-Jun-98
	GB_BA2:AF002133	15437	AF002133	Mycobacterium avium strain GIR10 transcriptional regulator (mav81) gene, partial cds, aconitase (acn), invasin 1 (inv1), invasin 2 (inv2), transcriptional regulator (moxR), ketoacyl-reductase (fabG), enoyl-reductase (inhA) and ferrochelatase (mav272) genes, complete cds.	Mycobacterium avium	36,885	26-MAR-1998
na02245 780	GB_BA2:RCU23145	5960	U23145	Rhodobacter capsulatus Calvin cycle carbon dioxide fixation operon: fructose-1,6-bisphosphate-1,7-bisphosphate aldolase (cbbA) gene, partial cds; Form II ribulose-1,5-bisphosphate carboxylase/oxygenase (cbbM) gene, complete cds, and Calvin cycle operon: pentose-5-phosphate-3-epimerase (cbbE), phosphoglycerate phosphatase (cbbZ), and cbbY genes, complete cds.	Rhodobacter capsulatus	48,701	28-OCT-1997
	GB_BA1:ECU82664	139818	U82664	Escherichia coli minutes 9 to 11 genomic sequence.	Escherichia coli	39,119	11-Jan-97
	GB_HTG2:AC007922	158858	AC007922	Homo sapiens chromosome 18 clone hRPK.178_F_10 map 18, *** SEQUENCING IN PROGRESS ***, 11 unordered pieces.	Homo sapiens	33,118	26-Jun-99
na02256 1125	GB_BA1:CGGAPPGK	3804	X59403	C.glutamicum gap, pgk and tpi genes for glyceraldehyde-3-phosphate, phosphoglycerate kinase and triosephosphate isomerase.	Corynebacterium glutamicum	99,289	05-OCT-1992
	GB_BA1:SCC54	30753	AL035591	Streptomyces coelicolor cosmid C54.	Streptomyces coelicolor	36,951	11-Jun-99
	GB_BA1:MTCY493	40790	Z95844	Mycobacterium tuberculosis H37Rv complete genome; segment 63/162.	Mycobacterium tuberculosis	64,196	19-Jun-98
na02257 1338	GB_BA1:CGGAPPGK	3804	X59403	C.glutamicum gap, pgk and tpi genes for glyceraldehyde-3-phosphate, phosphoglycerate kinase and triosephosphate isomerase.	Corynebacterium glutamicum	98,873	05-OCT-1992
	GB_BA1:MTCY493	40790	Z95844	Mycobacterium tuberculosis H37Rv complete genome; segment 63/162.	Mycobacterium tuberculosis	61,273	19-Jun-98
	GB_BA2:MAU82749	2530	U82749	Mycobacterium avium glyceraldehyde-3-phosphate dehydrogenase homolog (gapdh) gene, complete cds; and phosphoglycerate kinase gene, partial cds.	Mycobacterium avium	61,772	6-Jan-98
na02258 900	GB_BA1:CGGAPPGK	3804	X59403	C.glutamicum gap, pgk and tpi genes for glyceraldehyde-3-phosphate, phosphoglycerate kinase and triosephosphate isomerase.	Corynebacterium glutamicum	99,667	05-OCT-1992
	GB_BA1:CORPEPC	4885	M25819	C.glutamicum phosphoenolpyruvate carboxylase gene, complete cds.	Corynebacterium glutamicum	100,000	15-DEC-1995
	GB_PAT:A09073	4885	A09073	C.glutamicum ppg gene for phosphoenol pyruvate carboxylase.	Corynebacterium glutamicum	100,000	25-Aug-93
na02259 2895	GB_BA1:CORPEPC	4885	M25819	C.glutamicum phosphoenolpyruvate carboxylase gene, complete cds.	Corynebacterium glutamicum	100,000	15-DEC-1995
	GB_PAT:A09073	4885	A09073	C.glutamicum ppg gene for phosphoenol pyruvate carboxylase.	Corynebacterium glutamicum	100,000	25-Aug-93
	GB_BA1:CGPPC	3292	X14234	Corynebacterium glutamicum phosphoenolpyruvate carboxylase gene (EC 4.1.1.31).	Corynebacterium glutamicum	99,827	12-Sep-93

Table 4 (continued)

rx02288 969	GB_PR3:HSDJ94E24	243145	AL050317	Human DNA sequence from clone RP1-94E24 on chromosome 20q12, complete sequence.	Homo sapiens	36,039	03-DEC-1999
	GB_HTG3:AC010091	159526	AC010091	Homo sapiens clone NH0295A01, *** SEQUENCING IN PROGRESS ***	Homo sapiens	35,331	11-Sep-99
	GB_HTG3:AC010091	159526	AC010091	unordered pieces.	Homo sapiens	35,331	11-Sep-99
rx02292 798	GB_BA2:AF125164	26443	AF125164	Homo sapiens clone NH0295A01, *** SEQUENCING IN PROGRESS ***	Bacteroides fragilis	39,747	01-DEC-1999
	GB_GSS5:AQ744695	827	AQ744695	unordered pieces.	Homo sapiens	39,185	16-Jul-99
	GB_EST14:AA381925	309	AA381925	Bacteroides fragilis 638R polysaccharide B (PS B2) biosynthesis locus, complete sequence; and unknown genes.	Homo sapiens	35,922	21-Apr-97
rx02322 511	GB_BA1:MTCY22G8	22550	Z95585	genomic clone Plate=1081 Col=12 Row=E, genomic survey sequence.	Mycobacterium tuberculosis	57,677	17-Jun-98
	GB_BA1:MTCY22G8	22550	Z95585	EST95058 Activated T-cells 1 Homo sapiens cDNA 5' end, mRNA sequence.	Mycobacterium tuberculosis	37,143	17-Jun-98
rx02326 939	GB_BA1:CGPYC	3728	Y09548	Mycobacterium tuberculosis H37Rv complete genome; segment 49/162.	Corynebacterium glutamicum	100,000	08-MAY-1998
	GB_BA2:AF038548	3637	AF038548	Corynebacterium glutamicum pyc gene.	Corynebacterium glutamicum	100,000	24-DEC-1997
rx02327 1083	GB_BA1:MTCY349	43523	Z83018	Corynebacterium glutamicum pyruvate carboxylase (pyc) gene, complete cds.	Mycobacterium tuberculosis	37,363	17-Jun-98
	GB_BA1:CGPYC	3728	Y09548	Mycobacterium tuberculosis H37Rv complete genome; segment 131/162.	Corynebacterium glutamicum	99,259	08-MAY-1998
	GB_BA2:AF038548	3637	AF038548	Corynebacterium glutamicum pyc gene.	Corynebacterium glutamicum	99,259	24-DEC-1997
rx02328 1719	GB_BA1:MTCY349	43523	Z83018	Corynebacterium glutamicum pyruvate carboxylase (pyc) gene, complete cds.	Mycobacterium tuberculosis	41,317	17-Jun-98
	GB_BA1:CGPYC	3728	Y09548	Mycobacterium tuberculosis H37Rv complete genome; segment 131/162.	Corynebacterium glutamicum	100,000	08-MAY-1998
	GB_BA2:AF038548	3637	AF038548	Corynebacterium glutamicum pyc gene.	Corynebacterium glutamicum	100,000	24-DEC-1997
rx02332 1266	GB_PL2:AF097728	3916	AF097728	Corynebacterium glutamicum pyruvate carboxylase (pyc) gene, complete cds.	Aspergillus terreus	52,248	29-OCT-1998
	GB_BA1:MSGLTA	1776	X60513	M.smegmatis gltA gene for citrate synthase.	Mycobacterium smegmatis	58,460	20-Sep-91
rx02333 1038	GB_BA2:ABU85944	1334	U85944	Antarctic bacterium DS2-3R citrate synthase (cys) gene, complete cds.	Antarctic bacterium DS2-3R	57,154	23-Sep-97
	GB_BA2:AE000175	15067	AE000175	Escherichia coli K-12 MG1655 section 65 of 400 of the complete genome.	Escherichia coli	38,164	12-Nov-98
	GB_BA1:MSGLTA	1776	X60513	M.smegmatis gltA gene for citrate synthase.	Mycobacterium smegmatis	58,929	20-Sep-91
	GB_PR4:HUAC002299	171681	AC002299	Homo sapiens Chromosome 16 BAC clone CIT987-SKA-113A6 ~complete genomic sequence, complete sequence.	Homo sapiens	33,070	23-Nov-99

Table 4 (continued)

GB_HTG2:AC007889	127840	AC007889	Drosophila melanogaster chromosome 3 clone BACR48E12 (D695) RPCI-98 48.E.12 map 87A-87B strain y; cn bw sp, *** SEQUENCING IN PROGRESS***, 86 unordered pieces.	Drosophila melanogaster	34,897	2-Aug-99
GB_BA1:CGACEA	2427	X75504	C.glutamicum aceA gene and thiX genes (partial).	Corynebacterium glutamicum	100,000	9-Sep-94
GB_BA1:CORACEA	1905	L28760	Corynebacterium glutamicum isocitrate lyase (aceA) gene.	Corynebacterium glutamicum	100,000	10-Feb-95
GB_PAT:113693	2135	I13693	Sequence 3 from patent US 5439822.	Unknown.	99,795	26-Sep-95
GB_BA1:CGACEB	3024	X78491	C.glutamicum (ATCC 13032) aceB gene.	Corynebacterium glutamicum	99,914	13-Jan-95
GB_BA1:CORACEB	2725	L27123	Corynebacterium glutamicum malate synthase (aceB) gene, complete cds.	Corynebacterium glutamicum	99,786	8-Jun-95
GB_BA1:PFFC2	5588	Y11998	P.fluorescens FC2.1, FC2.2, FC2.3c, FC2.4 and FC2.5c open reading frames.	Pseudomonas fluorescens	63,539	11-Jul-97
GB_PR4:AC007102	176258	AC007102	Homo sapiens chromosome 4 clone C0162P16 map 4p16, complete sequence.	Homo sapiens	35,069	2-Jun-99
GB_HTG3:AC011214	183414	AC011214	Homo sapiens clone 5_C_3, LOW-PASS SEQUENCE SAMPLING.	Homo sapiens	36,885	03-OCT-1999
GB_HTG3:AC011214	183414	AC011214	Homo sapiens clone 5_C_3, LOW-PASS SEQUENCE SAMPLING.	Homo sapiens	36,885	03-OCT-1999
GB_BA2:AF101055	7457	AF101055	Clostridium acetobutylicum atp operon, complete sequence.	Clostridium acetobutylicum	39,605	03-MAR-1999
GB_OM:RABPKA	4441	J03247	Rabbit phosphorylase kinase (alpha subunit) mRNA, complete cds.	Oryctolagus cuniculus	36,051	27-Apr-93
GB_OM:RABPLASISM	4458	M64656	Oryctolagus cuniculus phosphorylase kinase alpha subunit mRNA, complete cds.	Oryctolagus cuniculus	36,000	22-Jun-98
GB_EST14:AA417723	374	AA417723	zV01b12.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:746207 3' similar to contains Alu repetitive element; contains element L1 repetitive element.; mRNA sequence.	Homo sapiens	38,770	18-OCT-1997
GB_EST11:AA215428	303	AA215428	zr95a07.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:683412 3' similar to contains Alu repetitive element.; mRNA sequence.	Homo sapiens	39,934	13-Aug-97
GB_BA1:MTCY77	22255	Z95389	Mycobacterium tuberculosis H37Rv complete genome; segment 146/162.	Mycobacterium tuberculosis	38,889	18-Jun-98
GB_EST14:AA426336	375	AA426336	zV53g02.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:757394 3' mRNA sequence.	Homo sapiens	38,043	16-OCT-1997
GB_BA1:STMAACC8	1353	M55426	S.fradiae aminoglycoside acetyltransferase (aacC8) gene, complete cds.	Streptomyces fradiae	37,097	05-MAY-1993
GB_PR3:AC004500	77538	AC004500	Homo sapiens chromosome 5, P1 clone 107689 (LBNL H14), complete sequence.	Homo sapiens	33,256	30-MAR-1998
GB_BA1:AB009078	2686	AB009078	Brevibacterium saccharolyticum gene for L-2,3-butanediol dehydrogenase, complete cds.	Brevibacterium saccharolyticum	96,990	13-Feb-99
GB_OM:BTUJ1200	877	U71200	Bos taurus acetoin reductase mRNA, complete cds.	Bos taurus	51,659	8-Oct-97
GB_EST2:F12685	287	F12685	HSC3DA031 normalized infant brain cDNA Homo sapiens cDNA clone c-3da03, mRNA sequence	Homo sapiens	41,509	14-Mar-95
GB_BA1:MTV012	70287	AL021287	Mycobacterium tuberculosis H37Rv complete genome; segment 132/162.	Mycobacterium tuberculosis	36,737	23-Jun-99

Table 4 (continued)

GB_BA1:SC6G10	36734	AL049497	Streptomyces coelicolor cosmid 6G10.	Streptomyces coelicolor	35,511	24-MAR-1999
GB_BA1:AP000060	347800	AP000060	Aeropyrum pernix genomic DNA, section 37.	Aeropyrum pernix	48,014	22-Jun-99
rx02492 840	921	M83661	Streptomyces coelicolor phosphoglycerate mutase (PGM) gene, complete cds.	Streptomyces coelicolor	65,672	26-Apr-93
	37218	Z77162	Mycobacterium tuberculosis H37Rv complete genome; segment 25/162.	Mycobacterium tuberculosis	61,436	17-Jun-98
	42991	U00018	Mycobacterium leprae cosmid B2168.	Mycobacterium leprae	37,893	01-MAR-1994
rx02528 1098	56075	AL008707	Human DNA sequence from PAC 161N10 on chromosome Xq25. Contains EST.	Homo sapiens	37,051	23-Nov-99
	136017	AC008235	Drosophila melanogaster chromosome 3 clone BACR15B19 (D995) RPCI-98	Drosophila melanogaster	36,822	2-Aug-99
	136017	AC008235	15.B.19 map 94F-95A strain y; cn bw sp. *** SEQUENCING IN PROGRESS ***. 125 unordered pieces.	Drosophila melanogaster	36,822	2-Aug-99
	17425	U17129	Rhodococcus erythropolis ThcA (thcA) gene, complete cds; and unknown genes.	Rhodococcus erythropolis	66,117	16-Jul-99
rx02539 1641	16094	AL021933	Mycobacterium tuberculosis H37Rv complete genome; segment 24/162.	Mycobacterium tuberculosis	65,174	17-Jun-98
	3152	AF068264	Pseudomonas aeruginosa quinoprotein ethanol dehydrogenase (exaA) gene, partial cds; cytochrome c550 precursor (exaB), NAD+ dependent acetaldehyde dehydrogenase (exaC), and pyrroloquinoline quinone synthesis A (pqqA) genes, complete cds; and pyrroloquinoline quinone synthesis B (pqqB) gene, partial cds.	Pseudomonas aeruginosa	65,448	18-MAR-1999
rx02551 483	17057	D29985	Bacillus subtilis wapA and orf genes for wall-associated protein and hypothetical proteins.	Bacillus subtilis	53,602	7-Feb-99
	335761	AC008128	Bacillus subtilis genome containing the hut and wapA loci.	Bacillus subtilis	53,602	7-Feb-99
	335761	AC008128	B. subtilis (Marburg 168) genes for beta-glucoside permease and beta-glucosidase.	Bacillus subtilis	53,602	3-Jul-95
rx02556 1281	99053	AC005292	Homo sapiens, *** SEQUENCING IN PROGRESS ***. 106 unordered pieces.	Homo sapiens	34,022	22-Aug-99
	99053	AC005292	Homo sapiens, *** SEQUENCING IN PROGRESS ***. 106 unordered pieces.	Homo sapiens	34,022	22-Aug-99
	35692	Z66511	Genomic sequence for Arabidopsis thaliana BAC F26F24, complete sequence.	Arabidopsis thaliana	33,858	16-Apr-99
rx02560 990	566	A1731605	Caenorhabditis elegans cosmid F07A11, complete sequence.	Caenorhabditis elegans	36,420	2-Sep-99
	35692	Z66511	BNLGH10201 Six-day Cotton fiber Gossypium hirsutum cDNA 5' similar to (AC004684) hypothetical protein [Arabidopsis thaliana], mRNA sequence.	Gossypium hirsutum	38,095	11-Jun-99
	35692	Z66511	Caenorhabditis elegans cosmid F07A11, complete sequence.	Caenorhabditis elegans	33,707	2-Sep-99

Table 4 (continued)

rx02572 668	GB_BA1:MTCY63	38900	Z96800	Mycobacterium tuberculosis H37Rv complete genome; segment 16/162.	Mycobacterium tuberculosis	61,677	17-Jun-98
	GB_BA1:MTCY63	38900	Z96800	Mycobacterium tuberculosis H37Rv complete genome; segment 16/162.	Mycobacterium tuberculosis	37,170	17-Jun-98
	GB_HTG1:HS24H01	46989	AL121632	Homo sapiens chromosome 21 clone LLNLc116H0124 map 21q21, *** SEQUENCING IN PROGRESS ***; in unsorted pieces.	Homo sapiens	19,820	29-Sep-99
rx02596 1326	GB_BA1:MTV026	23740	AL022076	Mycobacterium tuberculosis H37Rv complete genome; segment 157/162.	Mycobacterium tuberculosis	36,957	24-Jun-99
	GB_BA2:AF026540	1778	AF026540	Mycobacterium tuberculosis UDP-galactopyranose mutase (glf) gene, complete cds.	Mycobacterium tuberculosis	67,627	30-OCT-1998
	GB_BA2:MTU96128	1200	U96128	Mycobacterium tuberculosis UDP-galactopyranose mutase (glf) gene, complete cds.	Mycobacterium tuberculosis	70,417	25-MAR-1998
rx02611 1775	GB_BA1:MTCY130	32514	Z73902	Mycobacterium tuberculosis H37Rv complete genome; segment 59/162.	Mycobacterium tuberculosis	38,532	17-Jun-98
	GB_BA1:MSGY151	37036	AD000018	Mycobacterium tuberculosis sequence from clone y151.	Mycobacterium tuberculosis	60,575	10-DEC-1996
	GB_BA1:U00014	36470	U00014	Mycobacterium leprae cosmid B1549.	Mycobacterium leprae	57,486	29-Sep-94
rx02612 2316	GB_BA1:MTCY130	32514	Z73902	Mycobacterium tuberculosis H37Rv complete genome; segment 59/162.	Mycobacterium tuberculosis	38,018	17-Jun-98
	GB_BA1:MSGY151	37036	AD000018	Mycobacterium tuberculosis sequence from clone y151.	Mycobacterium tuberculosis	58,510	10-DEC-1996
	GB_BA1:STMGLGEN	2557	L11647	Streptomyces aureofaciens glycogen branching enzyme (glgB) gene, complete cds.	Streptomyces aureofaciens	57,193	25-MAY-1995
rx02621 942	GB_BA1:CGL133719	1839	AJ133719	Corynebacterium glutamicum yjcc gene, amtR gene and citE gene, partial.	Corynebacterium glutamicum	36,858	12-Aug-99
	GB_IN1:CEM106	39973	Z46935	Caenorhabditis elegans cosmid M106, complete sequence.	Caenorhabditis elegans	37,608	2-Sep-99
	GB_EST29:AI547662	377	AI547662	UI-R-C3-sz-h-03-0-UI.s1 UI-R-C3 Rattus norvegicus cDNA clone UI-R-C3-sz-h-03-0-UI 3', mRNA sequence.	Rattus norvegicus	50,667	3-Jul-99
rx02640 1650	GB_BA1:MTV025	121125	AL022121	Mycobacterium tuberculosis H37Rv complete genome; segment 155/162.	Mycobacterium tuberculosis	39,187	24-Jun-99
	GB_BA1:PAU49666	4495	U49666	Pseudomonas aeruginosa (orfX), glycerol diffusion facilitator (glpF), glycerol kinase (glpK), and Glp repressor (glpR) genes, complete cds, and (orfX) gene, partial cds.	Pseudomonas aeruginosa	59,273	18-MAY-1997
rx02654 1008	GB_BA1:AB015974	1641	AB015974	Pseudomonas tolaasii glpK gene for glycerol kinase, complete cds.	Pseudomonas tolaasii	58,339	28-Aug-99
	GB_EST6:N65787	512	N65787	20827 Lambda-PRL2 Arabidopsis thaliana cDNA clone 232B777, mRNA sequence.	Arabidopsis thaliana	39,637	5-Jan-98
	GB_PL2:T17H3	65839	AC005916	Arabidopsis thaliana chromosome 1 BAC T17H3 sequence, complete sequence.	Arabidopsis thaliana	33,735	5-Aug-99
	GB_RO:MMU58105	88871	U58105	Mus musculus Blk locus, alpha-D-galactosidase A (Ags), ribosomal protein (L44L), and Bruton's tyrosine kinase (Btk) genes, complete cds.	Mus musculus	35,431	13-Feb-97
rx02666 891	GB_PR3:AC004643	43411	AC004643	Homo sapiens chromosome 16, cosmid clone 363E3 (LANL), complete sequence.	Homo sapiens	38,851	01-MAY-1998

Table 4 (continued)

GB_PR3:AC004643	43411	AC004643	Homo sapiens chromosome 16, cosmid clone 363E3 (LANL), complete sequence.	Homo sapiens	41,599	01-MAY-1998
GB_BA2:AF049897	9196	AF049897	Corynebacterium glutamicum N-acetylglutarylphosphate reductase (argC), ornithine acetyltransferase (argJ), N-acetylglutamate kinase (argB), acetylornithine transaminase (argD), ornithine carbamoyltransferase (argF), arginine repressor (argR), argininosuccinate synthase (argG), and argininosuccinate lyase (argH) genes, complete cds.	Corynebacterium glutamicum	40,413	1-Jul-98
GB_BA1:PDENQOURF	10425	L02354	Paracoccus denitrificans NADH dehydrogenase (URF4), (NQO9), (URF5), (URF6), (NQO10), (NQO11), (NQO12), (NQO13), and (NQO14) genes, complete cds's; biotin [acetyl-CoA carboxyl] ligase (birA) gene, complete cds.	Paracoccus denitrificans	40,735	20-MAY-1993
GB_BA1:MTCY339	42861	Z77163	Mycobacterium tuberculosis H37Rv complete genome; segment 101/162.	Mycobacterium tuberculosis	36,471	17-Jun-98
GB_BA1:MXADEVRS	2452	L19029	Myxococcus xanthus devR and devS genes, complete cds's.	Myxococcus xanthus	38,477	27-Jan-94
GB_BA1:BACLDH	1147	M19394	B. caldolyticus lactate dehydrogenase (LDH) gene, complete cds.	Bacillus caldolyticus	57,371	26-Apr-93
GB_BA1:BACLDHL	1361	M14788	B. stearothermophilus lct gene encoding L-lactate dehydrogenase, complete cds.	Bacillus stearothermophilus	57,277	26-Apr-93
GB_PAT:A06664	1350	A06664	B. stearothermophilus lct gene.	Bacillus stearothermophilus	57,277	29-Jul-93
GB_EST15:AA494626	121	AA494626	fa09d04.r1 Zebrafish ICRFzfls Danio rerio cDNA clone 11A22 5' similar to TR:G1171163 G1171163 G/T-MISMATCH BINDING PROTEIN. ; mRNA sequence.	Danio rerio	50,746	27-Jun-97
GB_EST15:AA494626	121	AA494626	fa09d04.r1 Zebrafish ICRFzfls Danio rerio cDNA clone 11A22 5' similar to TR:G1171163 G1171163 G/T-MISMATCH BINDING PROTEIN. ; mRNA sequence.	Danio rerio	36,364	27-Jun-97
GB_EST19:AA758660	233	AA758660	ah67d06.s1 Soares_testis_NHT Homo sapiens cDNA clone 1320683 3', mRNA sequence.	Homo sapiens	37,059	29-DEC-1998
GB_EST15:AA494626	121	AA494626	fa09d04.r1 Zebrafish ICRFzfls Danio rerio cDNA clone 11A22 5' similar to TR:G1171163 G1171163 G/T-MISMATCH BINDING PROTEIN. ; mRNA sequence.	Danio rerio	42,149	27-Jun-97
GB_PR4:AC006285	150172	AC006285	Homo sapiens, complete sequence.	Homo sapiens	37,655	15-Nov-99
GB_PAT:E13655	2260	E13655	gDNA encoding glucose-6-phosphate dehydrogenase.	Corynebacterium glutamicum	99,580	24-Jun-98
GB_BA1:MTCY493	40790	Z95844	Mycobacterium tuberculosis H37Rv complete genome; segment 63/162.	Mycobacterium tuberculosis	38,363	19-Jun-98
GB_BA1:SC5A7	40337	AL031107	Streptomyces coelicolor cosmid 5A7.	Streptomyces coelicolor	39,444	27-Jul-98
GB_PAT:E13655	2260	E13655	gDNA encoding glucose-6-phosphate dehydrogenase.	Corynebacterium glutamicum	98,226	24-Jun-98
GB_BA1:SCC22	22115	AL096839	Streptomyces coelicolor cosmid C22.	Streptomyces coelicolor	60,399	12-Jul-99
GB_BA1:SC5A7	40337	AL031107	Streptomyces coelicolor cosmid 5A7.	Streptomyces coelicolor	36,426	27-Jul-98
GB_BA1:AB023377	2572	AB023377	Corynebacterium glutamicum tkt gene for transketolase, complete cds.	Corynebacterium glutamicum	99,640	20-Feb-99

Table 4 (continued)

ra02740 1053	GB_BA1:MLCL536	36224	Z99125	Mycobacterium leprae cosmid L536.	Mycobacterium leprae	61,573	04-DEC-1998 01-MAR-1994
	GB_BA1:U00013	35881	U00013	Mycobacterium leprae cosmid B1496.			
ra02740 1053	GB_HTG2:AC006247	174368	AC006247	Drosophila melanogaster chromosome 2 clone BACR48110 (D505) RPCI-98 48.1.10 map 49E6-49F8 strain y; cn bw sp, *** SEQUENCING IN PROGRESS ***, 17 unordered pieces.	Drosophila melanogaster	37,105	2-Aug-99
	GB_HTG2:AC006247	174368	AC006247	Drosophila melanogaster chromosome 2 clone BACR48110 (D505) RPCI-98 48.1.10 map 49E6-49F8 strain y; cn bw sp, *** SEQUENCING IN PROGRESS ***, 17 unordered pieces.			
	GB_HTG3:AC007150	121474	AC007150	Drosophila melanogaster chromosome 2 clone BACR16P13 (D597) RPCI-98 16.P.13 map 49E-49F strain y; cn bw sp, *** SEQUENCING IN PROGRESS***, 87 unordered pieces.			
	GB_HTG2:AC004951	129429	AC004951	Homo sapiens clone DJ1022114, *** SEQUENCING IN PROGRESS ***, 14 unordered pieces.			
ra02741 1089	GB_HTG2:AC004951	129429	AC004951	Homo sapiens clone DJ1022114, *** SEQUENCING IN PROGRESS ***, 14 unordered pieces.	Homo sapiens	33,116	12-Jun-98
	GB_HTG2:AC004951	129429	AC004951	Homo sapiens clone DJ1022114, *** SEQUENCING IN PROGRESS ***, 14 unordered pieces.			
	GB_IN1:AB006546	931	AB006546	Ephydatia fluviatilis mRNA for G protein a subunit 4, partial cds.			
	GB_BA1:MLCL536	36224	Z99125	Mycobacterium leprae cosmid L536.			
ra02743 1161	GB_BA1:U00013	35881	U00013	Mycobacterium leprae cosmid B1496.	Mycobacterium leprae	48,401	01-MAR-1994
	GB_HTG2:AC007401	83657	AC007401	Homo sapiens clone NH0501007, *** SEQUENCING IN PROGRESS ***, 3 unordered pieces.			
	GB_BA1:CGBETPGEN	2339	X93514	C. glutamicum batP gene.			
	GB_GSS9:AQ148714	405	AQ148714	HS_3136_A1_A03_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3136 Col=5 Row=A, genomic survey sequence.			
ra02797 1026	GB_BA1:BFU64514	3837	U64514	Bacillus firmus dppABC operon, dipeptide transporter protein dppA gene, partial cds, and dipeptide transporter proteins dppB and dppC genes, complete cds.	Bacillus firmus	38,072	1-Feb-97
	GB_BA1:CGBETPGEN	2339	X93514	C. glutamicum batP gene.			
	GB_GSS9:AQ148714	405	AQ148714	HS_3136_A1_A03_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3136 Col=5 Row=A, genomic survey sequence.			
	GB_HTG2:AC007401	83657	AC007401	Homo sapiens clone NH0501007, *** SEQUENCING IN PROGRESS ***, 3 unordered pieces.			
ra02803 680	GB_BA1:U00020	36947	U00020	Mycobacterium leprae cosmid B229.	Mycobacterium leprae	34,462	01-MAR-1994
	GB_BA2:PSU85643	4032	U85643	Pseudomonas syringae pv. syringae putative dihydropteroate synthase gene, partial cds, regulatory protein MraA (mraA), triose phosphate isomerase (tpiA), transport protein SecG (secG), tRNA-Leu, tRNA-Met, and 15 kDa protein genes, complete cds.			
	GB_BA1:SC6G4	41055	AL031317	Streptomyces coelicolor cosmid 6G4.			
	GB_HTG2:AC008105	91421	AC008105	Homo sapiens chromosome 17 clone 2020_K_17 map 17, *** SEQUENCING IN PROGRESS ***, 12 unordered pieces.			
ra02821 363	GB_HTG2:AC008105	91421	AC008105	Homo sapiens chromosome 17 clone 2020_K_17 map 17, *** SEQUENCING IN PROGRESS ***, 12 unordered pieces.	Homo sapiens	37,607	22-Jul-99
	GB_EST33:AV117143	222	AV117143	AV117143 Mus musculus C57BL/6J 10-day embryo Mus musculus cDNA clone Mus musculus 2610200J17, mRNA sequence.			
	GB_BA1:U00013	35881	U00013	Mycobacterium leprae cosmid B1496.			
	GB_HTG2:AC006247	174368	AC006247	Drosophila melanogaster chromosome 2 clone BACR48110 (D505) RPCI-98 48.1.10 map 49E6-49F8 strain y; cn bw sp, *** SEQUENCING IN PROGRESS ***, 17 unordered pieces.			

Table 4 (continued)

rx02829 373	GB_HTG1:HSU9G8	48735	AL008714	Homo sapiens chromosome X clone LLOXNC01-9G8, *** SEQUENCING IN PROGRESS ***; in unordered pieces.	Homo sapiens	41,595	23-Nov-99
	GB_HTG1:HSU9G8	48735	AL008714	Homo sapiens chromosome X clone LLOXNC01-9G8, *** SEQUENCING IN PROGRESS ***; in unordered pieces.	Homo sapiens	41,595	23-Nov-99
	GB_PR3:HSU85B5	39550	Z69724	Human DNA sequence from cosmid U85B5, between markers DXS366 and DXS87 on chromosome X.	Homo sapiens	41,595	23-Nov-99
rx03216 1141	GB_HTG3:AC008184	151720	AC008184	Drosophila melanogaster chromosome 2 clone BACR04D05 (D540) RPCI-98 04.D.5 map 36E5-36F2 strain Y; cn bw sp. *** SEQUENCING IN PROGRESS ***; 27 unordered pieces.	Drosophila melanogaster	39,600	2-Aug-99
	GB_EST15:AA477537	411	AA477537	zu36g12.r1 Soares ovary tumor NbHOT Homo sapiens cDNA clone IMAGE:740134 5' similar to contains Alu repetitive element; contains element HGR repetitive element.; mRNA sequence.	Homo sapiens	37,260	9-Nov-97
	GB_EST26:AI330662	412	AI330662	fa91d08.y1 zebrafish fin day1 regeneration Danio rerio cDNA 5' mRNA sequence.	Danio rerio	37,805	28-DEC-1998
rx03215 1038	GB_BA1:SC3F9	19830	AL023862	Streptomyces coelicolor cosmid 3F9.	Streptomyces coelicolor A3(2)	48,657	10-Feb-99
	GB_BA1:SLLNC	36270	X79146	S.lincolnensis (78-11) Lincomycin production genes.	Streptomyces lincolnensis	39,430	15-MAY-1996
	GB_HTG5:AC009660	204320	AC009660	Homo sapiens chromosome 15 clone RP11-424J10 map 15, *** SEQUENCING IN PROGRESS ***; 41 unordered pieces.	Homo sapiens	35,151	04-DEC-1999
rx03224 1288	GB_PR3:AC004076	41322	AC004076	Homo sapiens chromosome 19, cosmid R30217, complete sequence.	Homo sapiens	37,788	29-Jan-98
	GB_PL2:SPAC926	23193	AL110469	S.pombe chromosome I cosmid c926.	Schizosaccharomyces pombe	38,474	2-Sep-99
	GB_BA2:AE001081	11473	AE001081	Archaeoglobus fulgidus section 26 of 172 of the complete genome.	Archaeoglobus fulgidus	35,871	15-DEC-1997

Exemplification

Example 1: Preparation of total genomic DNA of *Corynebacterium glutamicum* ATCC 13032

5 A culture of *Corynebacterium glutamicum* (ATCC 13032) was grown overnight at 30°C with vigorous shaking in BHI medium (Difco). The cells were harvested by centrifugation, the supernatant was discarded and the cells were resuspended in 5 ml buffer-I (5% of the original volume of the culture — all indicated volumes have been calculated for 100 ml of culture volume). Composition of buffer-I: 140.34 g/l sucrose,
10 2.46 g/l $\text{MgSO}_4 \cdot 7\text{H}_2\text{O}$, 10 ml/l KH_2PO_4 solution (100 g/l, adjusted to pH 6.7 with KOH), 50 ml/l M12 concentrate (10 g/l $(\text{NH}_4)_2\text{SO}_4$, 1 g/l NaCl, 2 g/l $\text{MgSO}_4 \cdot 7\text{H}_2\text{O}$, 0.2 g/l CaCl_2 , 0.5 g/l yeast extract (Difco), 10 ml/l trace-elements-mix (200 mg/l $\text{FeSO}_4 \cdot \text{H}_2\text{O}$, 10 mg/l $\text{ZnSO}_4 \cdot 7\text{H}_2\text{O}$, 3 mg/l $\text{MnCl}_2 \cdot 4\text{H}_2\text{O}$, 30 mg/l H_3BO_3 , 20 mg/l $\text{CoCl}_2 \cdot 6\text{H}_2\text{O}$, 1 mg/l $\text{NiCl}_2 \cdot 6\text{H}_2\text{O}$, 3 mg/l $\text{Na}_2\text{MoO}_4 \cdot 2\text{H}_2\text{O}$, 500 mg/l complexing agent
15 (EDTA or critic acid), 100 ml/l vitamins-mix (0.2 mg/l biotin, 0.2 mg/l folic acid, 20 mg/l p-amino benzoic acid, 20 mg/l riboflavin, 40 mg/l ca-panthothenate, 140 mg/l nicotinic acid, 40 mg/l pyridoxole hydrochloride, 200 mg/l myo-inositol). Lysozyme was added to the suspension to a final concentration of 2.5 mg/ml. After an approximately 4 h incubation at 37°C, the cell wall was degraded and the resulting
20 protoplasts are harvested by centrifugation. The pellet was washed once with 5 ml buffer-I and once with 5 ml TE-buffer (10 mM Tris-HCl, 1 mM EDTA, pH 8). The pellet was resuspended in 4 ml TE-buffer and 0.5 ml SDS solution (10%) and 0.5 ml NaCl solution (5 M) are added. After adding of proteinase K to a final concentration of 200 µg/ml, the suspension is incubated for ca. 18 h at 37°C. The DNA was purified by
25 extraction with phenol, phenol-chloroform-isoamylalcohol and chloroform-isoamylalcohol using standard procedures. Then, the DNA was precipitated by adding 1/50 volume of 3 M sodium acetate and 2 volumes of ethanol, followed by a 30 min incubation at -20°C and a 30 min centrifugation at 12,000 rpm in a high speed centrifuge using a SS34 rotor (Sorvall). The DNA was dissolved in 1 ml TE-buffer containing 20
30 µg/ml RNaseA and dialysed at 4°C against 1000 ml TE-buffer for at least 3 hours. During this time, the buffer was exchanged 3 times. To aliquots of 0.4 ml of the dialysed DNA solution, 0.4 ml of 2 M LiCl and 0.8 ml of ethanol are added. After a 30

min incubation at -20°C, the DNA was collected by centrifugation (13,000 rpm, Biofuge Fresco, Heraeus, Hanau, Germany). The DNA pellet was dissolved in TE-buffer. DNA prepared by this procedure could be used for all purposes, including southern blotting or construction of genomic libraries.

5

Example 2: Construction of genomic libraries in *Escherichia coli* of *Corynebacterium glutamicum* ATCC13032.

Using DNA prepared as described in Example 1, cosmid and plasmid libraries were constructed according to known and well established methods (see e.g., Sambrook, J. *et al.* 10 (1989) "Molecular Cloning : A Laboratory Manual", Cold Spring Harbor Laboratory Press, or Ausubel, F.M. *et al.* (1994) "Current Protocols in Molecular Biology", John Wiley & Sons.)

Any plasmid or cosmid could be used. Of particular use were the plasmids pBR322 (Sutcliffe, J.G. (1979) *Proc. Natl. Acad. Sci. USA*, 75:3737-3741); pACYC177 (Change & 15 Cohen (1978) *J. Bacteriol* 134:1141-1156), plasmids of the pBS series (pBSSK+, pBSSK- and others; Stratagene, LaJolla, USA), or cosmids as SuperCos1 (Stratagene, LaJolla, USA) or Lorist6 (Gibson, T.J., Rosenthal A. and Waterson, R.H. (1987) *Gene* 53:283-286. Gene libraries specifically for use in *C. glutamicum* may be constructed using plasmid pSL109 (Lee, H.-S. and A. J. Sinskey (1994) *J. Microbiol. Biotechnol.* 4: 256-263).

20

Example 3: DNA Sequencing and Computational Functional Analysis

Genomic libraries as described in Example 2 were used for DNA sequencing according to standard methods, in particular by the chain termination method using ABI377 sequencing machines (see e.g., Fleischman, R.D. *et al.* (1995) "Whole-genome 25 Random Sequencing and Assembly of Haemophilus Influenzae Rd., *Science*, 269:496-512). Sequencing primers with the following nucleotide sequences were used: 5'-GGAAACAGTATGACCATG-3' or 5'-GTAAAACGACGGCCAGT-3'.

Example 4: *In vivo* Mutagenesis

30 *In vivo* mutagenesis of *Corynebacterium glutamicum* can be performed by passage of plasmid (or other vector) DNA through *E. coli* or other microorganisms (e.g. *Bacillus* spp. or yeasts such as *Saccharomyces cerevisiae*) which are impaired in their capabilities to maintain

the integrity of their genetic information. Typical mutator strains have mutations in the genes for the DNA repair system (*e.g.*, mutHLS, mutD, mutT, etc.; for reference, see Rupp, W.D. (1996) DNA repair mechanisms, in: *Escherichia coli* and *Salmonella*, p. 2277-2294, ASM: Washington.) Such strains are well known to those of ordinary skill in the art. The use of such
5 strains is illustrated, for example, in Greener, A. and Callahan, M. (1994) *Strategies* 7: 32-34.

Example 5: DNA Transfer Between *Escherichia coli* and *Corynebacterium glutamicum*

Several *Corynebacterium* and *Brevibacterium* species contain endogenous
10 plasmids (as *e.g.*, pHM1519 or pBL1) which replicate autonomously (for review see, *e.g.*, Martin, J.F. *et al.* (1987) *Biotechnology*, 5:137-146). Shuttle vectors for *Escherichia coli* and *Corynebacterium glutamicum* can be readily constructed by using standard vectors for *E. coli* (Sambrook, J. *et al.* (1989), "Molecular Cloning: A Laboratory Manual", Cold Spring Harbor Laboratory Press or Ausubel, F.M. *et al.* (1994) "Current Protocols in
15 Molecular Biology", John Wiley & Sons) to which a origin or replication for and a suitable marker from *Corynebacterium glutamicum* is added. Such origins of replication are preferably taken from endogenous plasmids isolated from *Corynebacterium* and *Brevibacterium* species. Of particular use as transformation markers for these species are genes for kanamycin resistance (such as those derived from the Tn5 or Tn903
20 transposons) or chloramphenicol (Winnacker, E.L. (1987) "From Genes to Clones — Introduction to Gene Technology, VCH, Weinheim). There are numerous examples in the literature of the construction of a wide variety of shuttle vectors which replicate in both *E. coli* and *C. glutamicum*, and which can be used for several purposes, including gene over-expression (for reference, see *e.g.*, Yoshihama, M. *et al.* (1985) *J. Bacteriol.* 162:591-597,
25 Martin J.F. *et al.* (1987) *Biotechnology*, 5:137-146 and Eikmanns, B.J. *et al.* (1991) *Gene*, 102:93-98).

Using standard methods, it is possible to clone a gene of interest into one of the shuttle vectors described above and to introduce such a hybrid vectors into strains of *Corynebacterium glutamicum*. Transformation of *C. glutamicum* can be achieved by
30 protoplast transformation (Kastsumata, R. *et al.* (1984) *J. Bacteriol.* 159:306-311), electroporation (Liebl, E. *et al.* (1989) *FEMS Microbiol. Letters*, 53:399-303) and in cases where special vectors are used, also by conjugation (as described *e.g.* in Schäfer, A *et al.*

(1990) *J. Bacteriol.* 172:1663-1666). It is also possible to transfer the shuttle vectors for *C. glutamicum* to *E. coli* by preparing plasmid DNA from *C. glutamicum* (using standard methods well-known in the art) and transforming it into *E. coli*. This transformation step can be performed using standard methods, but it is advantageous to use an Mcr-deficient
5 *E. coli* strain, such as NM522 (Gough & Murray (1983) *J. Mol. Biol.* 166:1-19).

Genes may be overexpressed in *C. glutamicum* strains using plasmids which comprise pCG1 (U.S. Patent No. 4,617,267) or fragments thereof, and optionally the gene for kanamycin resistance from TN903 (Grindley, N.D. and Joyce, C.M. (1980) *Proc. Natl. Acad. Sci. USA* 77(12): 7176-7180). In addition, genes may be
10 overexpressed in *C. glutamicum* strains using plasmid pSL109 (Lee, H.-S. and A. J. Sinskey (1994) *J. Microbiol. Biotechnol.* 4: 256-263).

Aside from the use of replicative plasmids, gene overexpression can also be achieved by integration into the genome. Genomic integration in *C. glutamicum* or other *Corynebacterium* or *Brevibacterium* species may be accomplished by well-known
15 methods, such as homologous recombination with genomic region(s), restriction endonuclease mediated integration (REMI) (see, *e.g.*, DE Patent 19823834), or through the use of transposons. It is also possible to modulate the activity of a gene of interest by modifying the regulatory regions (*e.g.*, a promoter, a repressor, and/or an enhancer) by sequence modification, insertion, or deletion using site-directed methods (such as
20 homologous recombination) or methods based on random events (such as transposon mutagenesis or REMI). Nucleic acid sequences which function as transcriptional terminators may also be inserted 3' to the coding region of one or more genes of the invention; such terminators are well-known in the art and are described, for example, in Winnacker, E.L. (1987) *From Genes to Clones – Introduction to Gene Technology*. VCH:
25 Weinheim.

Example 6: Assessment of the Expression of the Mutant Protein

Observations of the activity of a mutated protein in a transformed host cell rely on the fact that the mutant protein is expressed in a similar fashion and in a similar quantity
30 to that of the wild-type protein. A useful method to ascertain the level of transcription of the mutant gene (an indicator of the amount of mRNA available for translation to the gene product) is to perform a Northern blot (for reference see, for example, Ausubel *et al.*

(1988) Current Protocols in Molecular Biology, Wiley: New York), in which a primer designed to bind to the gene of interest is labeled with a detectable tag (usually radioactive or chemiluminescent), such that when the total RNA of a culture of the organism is extracted, run on gel, transferred to a stable matrix and incubated with this probe, the binding and quantity of binding of the probe indicates the presence and also the quantity of mRNA for this gene. This information is evidence of the degree of transcription of the mutant gene. Total cellular RNA can be prepared from *Corynebacterium glutamicum* by several methods, all well-known in the art, such as that described in Bormann, E.R. *et al.* (1992) *Mol. Microbiol.* 6: 317-326.

10 To assess the presence or relative quantity of protein translated from this mRNA, standard techniques, such as a Western blot, may be employed (see, for example, Ausubel *et al.* (1988) Current Protocols in Molecular Biology, Wiley: New York). In this process, total cellular proteins are extracted, separated by gel electrophoresis, transferred to a matrix such as nitrocellulose, and incubated with a probe, such as an antibody, which
15 specifically binds to the desired protein. This probe is generally tagged with a chemiluminescent or colorimetric label which may be readily detected. The presence and quantity of label observed indicates the presence and quantity of the desired mutant protein present in the cell.

20 **Example 7: Growth of Genetically Modified *Corynebacterium glutamicum* — Media and Culture Conditions**

Genetically modified *Corynebacteria* are cultured in synthetic or natural growth media. A number of different growth media for *Corynebacteria* are both well-known and readily available (Lieb *et al.* (1989) *Appl. Microbiol. Biotechnol.*, 32:205-210; von der
25 Osten *et al.* (1998) *Biotechnology Letters*, 11:11-16; Patent DE 4,120,867; Liebl (1992) "The Genus *Corynebacterium*, in: The Prokaryotes, Volume II, Balows, A. *et al.*, eds. Springer-Verlag). These media consist of one or more carbon sources, nitrogen sources, inorganic salts, vitamins and trace elements. Preferred carbon sources are sugars, such as mono-, di-, or polysaccharides. For example, glucose, fructose, mannose, galactose,
30 ribose, sorbose, ribulose, lactose, maltose, sucrose, raffinose, starch or cellulose serve as very good carbon sources. It is also possible to supply sugar to the media via complex compounds such as molasses or other by-products from sugar refinement. It can also be

advantageous to supply mixtures of different carbon sources. Other possible carbon sources are alcohols and organic acids, such as methanol, ethanol, acetic acid or lactic acid. Nitrogen sources are usually organic or inorganic nitrogen compounds, or materials which contain these compounds. Exemplary nitrogen sources include ammonia gas or
5 ammonia salts, such as NH_4Cl or $(\text{NH}_4)_2\text{SO}_4$, NH_4OH , nitrates, urea, amino acids or complex nitrogen sources like corn steep liquor, soy bean flour, soy bean protein, yeast extract, meat extract and others.

Inorganic salt compounds which may be included in the media include the chloride-, phosphorous- or sulfate- salts of calcium, magnesium, sodium, cobalt,
10 molybdenum, potassium, manganese, zinc, copper and iron. Chelating compounds can be added to the medium to keep the metal ions in solution. Particularly useful chelating compounds include dihydroxyphenols, like catechol or protocatechuate, or organic acids, such as citric acid. It is typical for the media to also contain other growth factors, such as vitamins or growth promoters, examples of which include biotin, riboflavin, thiamin, folic
15 acid, nicotinic acid, pantothenate and pyridoxin. Growth factors and salts frequently originate from complex media components such as yeast extract, molasses, corn steep liquor and others. The exact composition of the media compounds depends strongly on the immediate experiment and is individually decided for each specific case. Information about media optimization is available in the textbook "Applied Microbiol. Physiology, A
20 Practical Approach (*eds.* P.M. Rhodes, P.F. Stanbury, IRL Press (1997) pp. 53-73, ISBN 0 19 963577 3). It is also possible to select growth media from commercial suppliers, like standard 1 (Merck) or BHI (grain heart infusion, DIFCO) or others.

All medium components are sterilized, either by heat (20 minutes at 1.5 bar and 121°C) or by sterile filtration. The components can either be sterilized together or, if
25 necessary, separately. All media components can be present at the beginning of growth, or they can optionally be added continuously or batchwise.

Culture conditions are defined separately for each experiment. The temperature should be in a range between 15°C and 45°C. The temperature can be kept constant or can be altered during the experiment. The pH of the medium should be in the range of 5 to
30 8.5, preferably around 7.0, and can be maintained by the addition of buffers to the media. An exemplary buffer for this purpose is a potassium phosphate buffer. Synthetic buffers such as MOPS, HEPES, ACES and others can alternatively or simultaneously be used. It

is also possible to maintain a constant culture pH through the addition of NaOH or NH₄OH during growth. If complex medium components such as yeast extract are utilized, the necessity for additional buffers may be reduced, due to the fact that many complex compounds have high buffer capacities. If a fermentor is utilized for culturing the micro-organisms, the pH can also be controlled using gaseous ammonia.

The incubation time is usually in a range from several hours to several days. This time is selected in order to permit the maximal amount of product to accumulate in the broth. The disclosed growth experiments can be carried out in a variety of vessels, such as microtiter plates, glass tubes, glass flasks or glass or metal fermentors of different sizes.

For screening a large number of clones, the microorganisms should be cultured in microtiter plates, glass tubes or shake flasks, either with or without baffles. Preferably 100 ml shake flasks are used, filled with 10% (by volume) of the required growth medium. The flasks should be shaken on a rotary shaker (amplitude 25 mm) using a speed-range of 100 – 300 rpm. Evaporation losses can be diminished by the maintenance of a humid atmosphere; alternatively, a mathematical correction for evaporation losses should be performed.

If genetically modified clones are tested, an unmodified control clone or a control clone containing the basic plasmid without any insert should also be tested. The medium is inoculated to an OD₆₀₀ of 0.5 – 1.5 using cells grown on agar plates, such as CM plates (10 g/l glucose, 2.5 g/l NaCl, 2 g/l urea, 10 g/l polypeptone, 5 g/l yeast extract, 5 g/l meat extract, 22 g/l NaCl, 2 g/l urea, 10 g/l polypeptone, 5 g/l yeast extract, 5 g/l meat extract, 22 g/l agar, pH 6.8 with 2M NaOH) that had been incubated at 30°C. Inoculation of the media is accomplished by either introduction of a saline suspension of *C. glutamicum* cells from CM plates or addition of a liquid preculture of this bacterium.

25

Example 8 – *In vitro* Analysis of the Function of Mutant Proteins

The determination of activities and kinetic parameters of enzymes is well established in the art. Experiments to determine the activity of any given altered enzyme must be tailored to the specific activity of the wild-type enzyme, which is well within the ability of one of ordinary skill in the art. Overviews about enzymes in general, as well as specific details concerning structure, kinetics, principles, methods, applications and examples for the determination of many enzyme activities may be

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found, for example, in the following references: Dixon, M., and Webb, E.C., (1979) *Enzymes*. Longmans: London; Fersht, (1985) *Enzyme Structure and Mechanism*. Freeman: New York; Walsh, (1979) *Enzymatic Reaction Mechanisms*. Freeman: San Francisco; Price, N.C., Stevens, L. (1982) *Fundamentals of Enzymology*. Oxford Univ. Press: Oxford; Boyer, P.D., ed. (1983) *The Enzymes*, 3rd ed. Academic Press: New York; Bisswanger, H., (1994) *Enzymkinetik*, 2nd ed. VCH: Weinheim (ISBN 3527300325); Bergmeyer, H.U., Bergmeyer, J., Graßl, M., eds. (1983-1986) *Methods of Enzymatic Analysis*, 3rd ed., vol. I-XII, Verlag Chemie: Weinheim; and Ullmann's Encyclopedia of Industrial Chemistry (1987) vol. A9, "Enzymes". VCH: Weinheim, p. 352-363.

The activity of proteins which bind to DNA can be measured by several well-established methods, such as DNA band-shift assays (also called gel retardation assays). The effect of such proteins on the expression of other molecules can be measured using reporter gene assays (such as that described in Kolmar, H. *et al.* (1995) *EMBO J.* 14: 3895-3904 and references cited therein). Reporter gene test systems are well known and established for applications in both pro- and eukaryotic cells, using enzymes such as beta-galactosidase, green fluorescent protein, and several others.

The determination of activity of membrane-transport proteins can be performed according to techniques such as those described in Gennis, R.B. (1989) "Pores, Channels and Transporters", in *Biomembranes, Molecular Structure and Function*, Springer: Heidelberg, p. 85-137; 199-234; and 270-322.

Example 9: Analysis of Impact of Mutant Protein on the Production of the Desired Product

The effect of the genetic modification in *C. glutamicum* on production of a desired compound (such as an amino acid) can be assessed by growing the modified microorganism under suitable conditions (such as those described above) and analyzing the medium and/or the cellular component for increased production of the desired product (*i.e.*, an amino acid). Such analysis techniques are well known to one of ordinary skill in the art, and include spectroscopy, thin layer chromatography, staining methods of various kinds, enzymatic and microbiological methods, and analytical chromatography such as high performance liquid chromatography (see, for example,

- Ullman, Encyclopedia of Industrial Chemistry, vol. A2, p. 89-90 and p. 443-613, VCH: Weinheim (1985); Fallon, A. *et al.*, (1987) "Applications of HPLC in Biochemistry" in: Laboratory Techniques in Biochemistry and Molecular Biology, vol. 17; Rehm *et al.* (1993) Biotechnology, vol. 3, Chapter III: "Product recovery and purification", page 469-714, VCH: Weinheim; Belter, P.A. *et al.* (1988) Bioseparations: downstream processing for biotechnology, John Wiley and Sons; Kennedy, J.F. and Cabral, J.M.S. (1992) Recovery processes for biological materials, John Wiley and Sons; Shaeiwitz, J.A. and Henry, J.D. (1988) Biochemical separations, in: Ulmann's Encyclopedia of Industrial Chemistry, vol. B3, Chapter 11, page 1-27, VCH: Weinheim; and Dechow, F.J. (1989) Separation and purification techniques in biotechnology, Noyes Publications.)

- In addition to the measurement of the final product of fermentation, it is also possible to analyze other components of the metabolic pathways utilized for the production of the desired compound, such as intermediates and side-products, to determine the overall efficiency of production of the compound. Analysis methods include measurements of nutrient levels in the medium (*e.g.*, sugars, hydrocarbons, nitrogen sources, phosphate, and other ions), measurements of biomass composition and growth, analysis of the production of common metabolites of biosynthetic pathways, and measurement of gasses produced during fermentation. Standard methods for these measurements are outlined in Applied Microbial Physiology, A Practical Approach, P.M. Rhodes and P.F. Stanbury, eds., IRL Press, p. 103-129; 131-163; and 165-192 (ISBN: 0199635773) and references cited therein.

Example 10: Purification of the Desired Product from *C. glutamicum* Culture

- Recovery of the desired product from the *C. glutamicum* cells or supernatant of the above-described culture can be performed by various methods well known in the art. If the desired product is not secreted from the cells, the cells can be harvested from the culture by low-speed centrifugation, the cells can be lysed by standard techniques, such as mechanical force or sonication. The cellular debris is removed by centrifugation, and the supernatant fraction containing the soluble proteins is retained for further purification of the desired compound. If the product is secreted from the *C. glutamicum*

cells, then the cells are removed from the culture by low-speed centrifugation, and the supernate fraction is retained for further purification.

The supernatant fraction from either purification method is subjected to chromatography with a suitable resin, in which the desired molecule is either retained on
5 a chromatography resin while many of the impurities in the sample are not, or where the impurities are retained by the resin while the sample is not. Such chromatography steps may be repeated as necessary, using the same or different chromatography resins. One of ordinary skill in the art would be well-versed in the selection of appropriate chromatography resins and in their most efficacious application for a particular molecule
10 to be purified. The purified product may be concentrated by filtration or ultrafiltration, and stored at a temperature at which the stability of the product is maximized.

There are a wide array of purification methods known to the art and the preceding method of purification is not meant to be limiting. Such purification techniques are described, for example, in Bailey, J.E. & Ollis, D.F. *Biochemical*
15 *Engineering Fundamentals*, McGraw-Hill: New York (1986).

The identity and purity of the isolated compounds may be assessed by techniques standard in the art. These include high-performance liquid chromatography (HPLC), spectroscopic methods, staining methods, thin layer chromatography, NIRS, enzymatic assay, or microbiologically. Such analysis methods are reviewed in: Patek *et al.* (1994)
20 *Appl. Environ. Microbiol.* 60: 133-140; Malakhova *et al.* (1996) *Biotekhnologiya* 11: 27-32; and Schmidt *et al.* (1998) *Bioprocess Engineer.* 19: 67-70. *Ulmann's Encyclopedia of Industrial Chemistry*, (1996) vol. A27, VCH: Weinheim, p. 89-90, p. 521-540, p. 540-547, p. 559-566, 575-581 and p. 581-587; Michal, G. (1999) *Biochemical Pathways: An Atlas of Biochemistry and Molecular Biology*, John Wiley and Sons; Fallon, A. *et al.*
25 (1987) *Applications of HPLC in Biochemistry in: Laboratory Techniques in Biochemistry and Molecular Biology*, vol. 17.

Example 11: Analysis of the Gene Sequences of the Invention

The comparison of sequences and determination of percent homology between
30 two sequences are art-known techniques, and can be accomplished using a mathematical algorithm, such as the algorithm of Karlin and Altschul (1990) *Proc. Natl. Acad. Sci. USA* 87:2264-68, modified as in Karlin and Altschul (1993) *Proc. Natl. Acad. Sci. USA*

90:5873-77. Such an algorithm is incorporated into the NBLAST and XBLAST programs (version 2.0) of Altschul, *et al.* (1990) *J. Mol. Biol.* 215:403-10. BLAST nucleotide searches can be performed with the NBLAST program, score = 100, wordlength = 12 to obtain nucleotide sequences homologous to SMP nucleic acid
5 molecules of the invention. BLAST protein searches can be performed with the XBLAST program, score = 50, wordlength = 3 to obtain amino acid sequences homologous to SMP protein molecules of the invention. To obtain gapped alignments for comparison purposes, Gapped BLAST can be utilized as described in Altschul *et al.*, (1997) *Nucleic Acids Res.* 25(17):3389-3402. When utilizing BLAST and Gapped
10 BLAST programs, one of ordinary skill in the art will know how to optimize the parameters of the program (*e.g.*, XBLAST and NBLAST) for the specific sequence being analyzed.

Another example of a mathematical algorithm utilized for the comparison of sequences is the algorithm of Meyers and Miller ((1988) *Comput. Appl. Biosci.* 4: 11-
15 17). Such an algorithm is incorporated into the ALIGN program (version 2.0) which is part of the GCG sequence alignment software package. When utilizing the ALIGN program for comparing amino acid sequences, a PAM120 weight residue table, a gap length penalty of 12, and a gap penalty of 4 can be used. Additional algorithms for sequence analysis are known in the art, and include ADVANCE and ADAM, described
20 in Torelli and Robotti (1994) *Comput. Appl. Biosci.* 10:3-5; and FASTA, described in Pearson and Lipman (1988) *P.N.A.S.* 85:2444-8.

The percent homology between two amino acid sequences can also be accomplished using the GAP program in the GCG software package (available at <http://www.gcg.com>), using either a Blosum 62 matrix or a PAM250 matrix, and a gap
25 weight of 12, 10, 8, 6, or 4 and a length weight of 2, 3, or 4. The percent homology between two nucleic acid sequences can be accomplished using the GAP program in the GCG software package, using standard parameters, such as a gap weight of 50 and a length weight of 3.

A comparative analysis of the gene sequences of the invention with those present
30 in Genbank has been performed using techniques known in the art (see, *e.g.*, Bexevanis and Ouellette, eds. (1998) *Bioinformatics: A Practical Guide to the Analysis of Genes and Proteins*. John Wiley and Sons: New York). The gene sequences of the invention

were compared to genes present in Genbank in a three-step process. In a first step, a BLASTN analysis (*e.g.*, a local alignment analysis) was performed for each of the sequences of the invention against the nucleotide sequences present in Genbank, and the top 500 hits were retained for further analysis. A subsequent FASTA search (*e.g.*, a
5 combined local and global alignment analysis, in which limited regions of the sequences are aligned) was performed on these 500 hits. Each gene sequence of the invention was subsequently globally aligned to each of the top three FASTA hits, using the GAP program in the GCG software package (using standard parameters). In order to obtain correct results, the length of the sequences extracted from Genbank were adjusted to the
10 length of the query sequences by methods well-known in the art. The results of this analysis are set forth in Table 4. The resulting data is identical to that which would have been obtained had a GAP (global) analysis alone been performed on each of the genes of the invention in comparison with each of the references in Genbank, but required significantly reduced computational time as compared to such a database-wide GAP
15 (global) analysis. Sequences of the invention for which no alignments above the cutoff values were obtained are indicated on Table 4 by the absence of alignment information. It will further be understood by one of ordinary skill in the art that the GAP alignment homology percentages set forth in Table 4 under the heading "% homology (GAP)" are listed in the European numerical format, wherein a ',' represents a decimal point. For
20 example, a value of "40,345" in this column represents "40.345%".

Example 12: Construction and Operation of DNA Microarrays

The sequences of the invention may additionally be used in the construction and application of DNA microarrays (the design, methodology, and uses of DNA arrays are
25 well known in the art, and are described, for example, in Schena, M. *et al.* (1995) *Science* 270: 467-470; Wodicka, L. *et al.* (1997) *Nature Biotechnology* 15: 1359-1367; DeSaizieu, A. *et al.* (1998) *Nature Biotechnology* 16: 45-48; and DeRisi, J.L. *et al.* (1997) *Science* 278: 680-686).

DNA microarrays are solid or flexible supports consisting of nitrocellulose,
30 nylon, glass, silicone, or other materials. Nucleic acid molecules may be attached to the surface in an ordered manner. After appropriate labeling, other nucleic acids or nucleic acid mixtures can be hybridized to the immobilized nucleic acid molecules, and the label

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may be used to monitor and measure the individual signal intensities of the hybridized molecules at defined regions. This methodology allows the simultaneous quantification of the relative or absolute amount of all or selected nucleic acids in the applied nucleic acid sample or mixture. DNA microarrays, therefore, permit an analysis of the
5 expression of multiple (as many as 6800 or more) nucleic acids in parallel (see, *e.g.*, Schena, M. (1996) *BioEssays* 18(5): 427-431).

The sequences of the invention may be used to design oligonucleotide primers which are able to amplify defined regions of one or more *C. glutamicum* genes by a nucleic acid amplification reaction such as the polymerase chain reaction. The choice
10 and design of the 5' or 3' oligonucleotide primers or of appropriate linkers allows the covalent attachment of the resulting PCR products to the surface of a support medium described above (and also described, for example, Schena, M. *et al.* (1995) *Science* 270: 467-470).

Nucleic acid microarrays may also be constructed by *in situ* oligonucleotide
15 synthesis as described by Wodicka, L. *et al.* (1997) *Nature Biotechnology* 15: 1359-1367. By photolithographic methods, precisely defined regions of the matrix are exposed to light. Protective groups which are photolabile are thereby activated and undergo nucleotide addition, whereas regions that are masked from light do not undergo any modification. Subsequent cycles of protection and light activation permit the
20 synthesis of different oligonucleotides at defined positions. Small, defined regions of the genes of the invention may be synthesized on microarrays by solid phase oligonucleotide synthesis.

The nucleic acid molecules of the invention present in a sample or mixture of nucleotides may be hybridized to the microarrays. These nucleic acid molecules can be
25 labeled according to standard methods. In brief, nucleic acid molecules (*e.g.*, mRNA molecules or DNA molecules) are labeled by the incorporation of isotopically or fluorescently labeled nucleotides, *e.g.*, during reverse transcription or DNA synthesis. Hybridization of labeled nucleic acids to microarrays is described (*e.g.*, in Schena, M. *et al.* (1995) *supra*; Wodicka, L. *et al.* (1997), *supra*; and DeSaizieu A. *et al.* (1998),
30 *supra*). The detection and quantification of the hybridized molecule are tailored to the specific incorporated label. Radioactive labels can be detected, for example, as

described in Schena, M. *et al.* (1995) *supra*) and fluorescent labels may be detected, for example, by the method of Shalon *et al.* (1996) *Genome Research* 6: 639-645).

The application of the sequences of the invention to DNA microarray technology, as described above, permits comparative analyses of different strains of *C. glutamicum* or other Corynebacteria. For example, studies of inter-strain variations based on individual transcript profiles and the identification of genes that are important for specific and/or desired strain properties such as pathogenicity, productivity and stress tolerance are facilitated by nucleic acid array methodologies. Also, comparisons of the profile of expression of genes of the invention during the course of a fermentation reaction are possible using nucleic acid array technology.

Example 13: Analysis of the Dynamics of Cellular Protein Populations (Proteomics)

The genes, compositions, and methods of the invention may be applied to study the interactions and dynamics of populations of proteins, termed 'proteomics'. Protein populations of interest include, but are not limited to, the total protein population of *C. glutamicum* (*e.g.*, in comparison with the protein populations of other organisms), those proteins which are active under specific environmental or metabolic conditions (*e.g.*, during fermentation, at high or low temperature, or at high or low pH), or those proteins which are active during specific phases of growth and development.

Protein populations can be analyzed by various well-known techniques, such as gel electrophoresis. Cellular proteins may be obtained, for example, by lysis or extraction, and may be separated from one another using a variety of electrophoretic techniques. Sodium dodecyl sulfate polyacrylamide gel electrophoresis (SDS-PAGE) separates proteins largely on the basis of their molecular weight. Isoelectric focusing polyacrylamide gel electrophoresis (IEF-PAGE) separates proteins by their isoelectric point (which reflects not only the amino acid sequence but also posttranslational modifications of the protein). Another, more preferred method of protein analysis is the consecutive combination of both IEF-PAGE and SDS-PAGE, known as 2-D-gel electrophoresis (described, for example, in Hermann *et al.* (1998) *Electrophoresis* 19: 3217-3221; Fountoulakis *et al.* (1998) *Electrophoresis* 19: 1193-1202; Langen *et al.* (1997) *Electrophoresis* 18: 1184-1192; Antelmann *et al.* (1997) *Electrophoresis* 18:

1451-1463). Other separation techniques may also be utilized for protein separation, such as capillary gel electrophoresis; such techniques are well known in the art.

Proteins separated by these methodologies can be visualized by standard techniques, such as by staining or labeling. Suitable stains are known in the art, and
5 include Coomassie Brilliant Blue, silver stain, or fluorescent dyes such as Sypro Ruby (Molecular Probes). The inclusion of radioactively labeled amino acids or other protein precursors (*e.g.*, ^{35}S -methionine, ^{35}S -cysteine, ^{14}C -labelled amino acids, ^{15}N -amino acids, $^{15}\text{NO}_3$ or $^{15}\text{NH}_4^+$ or ^{13}C -labelled amino acids) in the medium of *C. glutamicum* permits the labeling of proteins from these cells prior to their separation. Similarly,
10 fluorescent labels may be employed. These labeled proteins can be extracted, isolated and separated according to the previously described techniques.

Proteins visualized by these techniques can be further analyzed by measuring the amount of dye or label used. The amount of a given protein can be determined quantitatively using, for example, optical methods and can be compared to the amount
15 of other proteins in the same gel or in other gels. Comparisons of proteins on gels can be made, for example, by optical comparison, by spectroscopy, by image scanning and analysis of gels, or through the use of photographic films and screens. Such techniques are well-known in the art.

To determine the identity of any given protein, direct sequencing or other
20 standard techniques may be employed. For example, N- and/or C-terminal amino acid sequencing (such as Edman degradation) may be used, as may mass spectrometry (in particular MALDI or ESI techniques (see, *e.g.*, Langen *et al.* (1997) *Electrophoresis* 18: 1184-1192)). The protein sequences provided herein can be used for the identification of *C. glutamicum* proteins by these techniques.

25 The information obtained by these methods can be used to compare patterns of protein presence, activity, or modification between different samples from various biological conditions (*e.g.*, different organisms, time points of fermentation, media conditions, or different biotopes, among others). Data obtained from such experiments alone, or in combination with other techniques, can be used for various applications,
30 such as to compare the behavior of various organisms in a given (*e.g.*, metabolic) situation, to increase the productivity of strains which produce fine chemicals or to increase the efficiency of the production of fine chemicals.

Equivalents

Those of ordinary skill in the art will recognize, or will be able to ascertain using no more than routine experimentation, many equivalents to the specific embodiments of
5 the invention described herein. Such equivalents are intended to be encompassed by the following claims.

What is claimed:

1. An isolated nucleic acid molecule from *Corynebacterium glutamicum* encoding an SMP protein, or a portion thereof, provided that the nucleic acid molecule does not consist of any of the F-designated genes set forth in Table 1.
2. The isolated nucleic acid molecule of claim 1, wherein said nucleic acid molecule encodes an SMP protein involved in the production of a fine chemical.
3. An isolated *Corynebacterium glutamicum* nucleic acid molecule selected from the group consisting of those sequences set forth as odd-numbered SEQ ID NOs of the Sequence Listing, or a portion thereof, provided that the nucleic acid molecule does not consist of any of the F-designated genes set forth in Table 1.
4. An isolated nucleic acid molecule which encodes a polypeptide sequence selected from the group consisting of those sequences set forth as even-numbered SEQ ID NOs of the Sequence Listing,, provided that the nucleic acid molecule does not consist of any of the F-designated genes set forth in Table 1.
5. An isolated nucleic acid molecule which encodes a naturally occurring allelic variant of a polypeptide selected from the group of amino acid sequences consisting of those sequences set forth in as even-numbered SEQ ID NOs of the Sequence Listing, provided that the nucleic acid molecule does not consist of any of the F-designated genes set forth in Table 1.
6. An isolated nucleic acid molecule comprising a nucleotide sequence which is at least 50% homologous to a nucleotide sequence selected from the group consisting of those sequences set forth as odd-numbered SEQ ID NOs of the Sequence Listing, or a portion thereof, provided that the nucleic acid molecule does not consist of any of the F-designated genes set forth in Table 1.

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7. An isolated nucleic acid molecule comprising a fragment of at least 15 nucleotides of a nucleic acid comprising a nucleotide sequence selected from the group consisting of those sequences set forth as odd-numbered SEQ ID NOs of the Sequence Listing, provided that the nucleic acid molecule does not consist of any of the F-designated genes set forth in Table 1.
8. An isolated nucleic acid molecule which hybridizes to the nucleic acid molecule of any one of claims 1-7 under stringent conditions.
9. An isolated nucleic acid molecule comprising the nucleic acid molecule of any one of claims 1-8 or a portion thereof and a nucleotide sequence encoding a heterologous polypeptide.
10. A vector comprising the nucleic acid molecule of any one of claims 1-9.
11. The vector of claim 10, which is an expression vector.
12. A host cell transfected with the expression vector of claim 11.
13. The host cell of claim 12, wherein said cell is a microorganism.
14. The host cell of claim 13, wherein said cell belongs to the genus *Corynebacterium* or *Brevibacterium*.
15. The host cell of claim 12, wherein the expression of said nucleic acid molecule results in the modulation in production of a fine chemical from said cell.
16. The host cell of claim 15, wherein said fine chemical is selected from the group consisting of: organic acids, proteinogenic and nonproteinogenic amino acids, purine and pyrimidine bases, nucleosides, nucleotides, lipids, saturated and unsaturated fatty acids, diols, carbohydrates, aromatic compounds, vitamins, cofactors, polyketides, and enzymes.

17. A method of producing a polypeptide comprising culturing the host cell of claim 12 in an appropriate culture medium to, thereby, produce the polypeptide.
- 5 18. An isolated SMP polypeptide from *Corynebacterium glutamicum*, or a portion thereof.
19. The polypeptide of claim 18, wherein said polypeptide is involved in the production of a fine chemical.
- 10 20. An isolated polypeptide comprising an amino acid sequence selected from the group consisting of those sequences set forth as even-numbered SEQ ID NOs of the Sequence Listing, provided that the amino acid sequence is not encoded by any of the F-designated genes set forth in Table 1,
- 15 21. An isolated polypeptide comprising a naturally occurring allelic variant of a polypeptide comprising an amino acid sequence selected from the group consisting of those sequences set forth as even-numbered SEQ ID NOs of the Sequence Listing, or a portion thereof, provided that the amino acid sequence is not encoded
- 20 by any of the F-designated genes set forth in Table 1.
22. The isolated polypeptide of any of claims 18-21, further comprising heterologous amino acid sequences.
- 25 23. An isolated polypeptide which is encoded by a nucleic acid molecule comprising a nucleotide sequence which is at least 50% homologous to a nucleic acid selected from the group consisting of those sequences set forth as odd-numbered SEQ ID NOs of the Sequence Listing, provided that the nucleic acid molecule does not consist of any of the F-designated nucleic acid molecules set forth in Table 1.
- 30 24. An isolated polypeptide comprising an amino acid sequence which is at least 50% homologous to an amino acid sequence selected from the group consisting of those

sequences as even-numbered SEQ ID NOs of the Sequence Listing, provided that the amino acid sequence is not encoded by any of the F-designated genes set forth in Table 1.

- 5 25. A method for producing a fine chemical, comprising culturing a cell containing a vector of claim 12 such that the fine chemical is produced.
26. The method of claim 25, wherein said method further comprises the step of recovering the fine chemical from said culture.
- 10 27. The method of claim 25, wherein said method further comprises the step of transfecting said cell with the vector of claim 11 to result in a cell containing said vector.
- 15 28. The method of claim 25, wherein said cell belongs to the genus *Corynebacterium* or *Brevibacterium*.
29. The method of claim 25, wherein said cell is selected from the group consisting of: *Corynebacterium glutamicum*, *Corynebacterium herculis*, *Corynebacterium lilium*,
20 *Corynebacterium acetoacidophilum*, *Corynebacterium acetoglutamicum*,
Corynebacterium acetophilum, *Corynebacterium ammoniagenes*, *Corynebacterium fujiokense*, *Corynebacterium nitrilophilus*, *Brevibacterium ammoniagenes*,
Brevibacterium butanicum, *Brevibacterium divaricatum*, *Brevibacterium flavum*,
Brevibacterium healii, *Brevibacterium ketoglutamicum*, *Brevibacterium*
25 *ketosoreductum*, *Brevibacterium lactofermentum*, *Brevibacterium linens*,
Brevibacterium paraffinolyticum, and those strains set forth in Table 3.
30. The method of claim 25, wherein expression of the nucleic acid molecule from said vector results in modulation of production of said fine chemical.
- 30 31. The method of claim 25, wherein said fine chemical is selected from the group consisting of: organic acids, proteinogenic and nonproteinogenic amino acids, purine

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and pyrimidine bases, nucleosides, nucleotides, lipids, saturated and unsaturated fatty acids, diols, carbohydrates, aromatic compounds, vitamins, cofactors, polyketides, and enzymes.

- 5 32. The method of claim 25, wherein said fine chemical is an amino acid.
33. The method of claim 32, wherein said amino acid is drawn from the group consisting of: lysine, glutamate, glutamine, alanine, aspartate, glycine, serine, threonine, methionine, cysteine, valine, leucine, isoleucine, arginine, proline, histidine,
10 tyrosine, phenylalanine, and tryptophan.
34. A method for producing a fine chemical, comprising culturing a cell whose genomic DNA has been altered by the inclusion of a nucleic acid molecule of any one of claims 1-9.
- 15 35. A method for diagnosing the presence or activity of *Corynebacterium diphtheriae* in a subject, comprising detecting the presence of one or more of SEQ ID NOs 1 through 782 of the Sequence Listing in the subject, provided that the sequences are not or are not encoded by any of the F-designated sequences set forth in Table 1,
20 thereby diagnosing the presence or activity of *Corynebacterium diphtheriae* in the subject.
36. A host cell comprising a nucleic acid molecule selected from the group consisting of the nucleic acid molecules set forth as odd-numbered SEQ ID NOs of the
25 Sequence Listing, wherein the nucleic acid molecule is disrupted.
35. 37. A host cell comprising a nucleic acid molecule selected from the group consisting of the nucleic acid molecules set forth as odd-numbered SEQ ID NOs in the Sequence Listing, wherein the nucleic acid molecule comprises one or more
30 nucleic acid modifications from the sequence set forth as odd-numbered SEQ ID NOs of the Sequence Listing s.

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38. A host cell comprising a nucleic acid molecule selected from the group consisting of the nucleic acid molecules set forth as odd-numbered SEQ ID NOs of the Sequence Listing, wherein the regulatory region of the nucleic acid molecule is modified
- 5 relative to the wild-type regulatory region of the molecule.

SEQUENCE LISTING

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 Met Val Asp Val Val
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 Val Leu Thr Gly Gly Gly Ala Gly Ile Lys Leu Leu Glu Lys Leu Ser
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 90 95 100

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 His Gly Tyr Gly Leu Gly Asp Val Asp Leu Ala Glu Ala Ala Arg Ala
 105 110 115

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 Tyr Glu Ala Val Leu Asp Glu Phe Ala Pro Asn Gly Phe Asp Leu His
 120 125 130

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 Pro Glu Ala Asn Ile His Gly Tyr Gly Leu Gly Asp Val Asp Leu Ala
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 Glu Ala Ala Arg Ala Tyr Glu Ala Val Leu Asp Glu Phe Ala Pro Asn
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Ser Leu Phe Pro His Thr Asp Ala Val Lys Glu Ser Ser Ala Lys Val
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 Met Ser Lys Thr Ile
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 10 15 20

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 25 30 35

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 Gln Met Cys Lys Met Gln Arg Ile Ile Glu Leu Ala Gly Thr Ala Glu
 40 45 50

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 Gly Ser Asn Phe Gln Leu Asn Asn Glu Pro Asn Glu Val Val Pro His
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 Met Ala Gln Arg Thr
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 Pro Leu Ile Ala Pro Ser Ile Leu Ala Ala Asp Phe Ser Arg Leu Gly
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 Glu Gln Val Leu Ala Val Pro Asp Ala Asp Trp Ile His Val Asp Ile
 25 30 35

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 Met Asp Gly His Phe Val Pro Asn Leu Ser Phe Gly Ala Asp Ile Thr
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 Ala Ala Val Asn Arg Val Thr Asp Lys Glu Leu Asp Val His Leu Met
 55 60 65
 atc gaa aac cca gag aag tgg gtg gac aac tac atc gac gct ggc gcg 355
 Ile Glu Asn Pro Glu Lys Trp Val Asp Asn Tyr Ile Asp Ala Gly Ala
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 Asp Cys Ile Val Phe His Val Glu Ala Thr Glu Gly His Val Glu Leu
 90 95 100
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 Ala Lys Tyr Ile Arg Ser Lys Gly Val Arg Ala Gly Phe Ser Leu Arg
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 Pro Gly Thr Pro Ile Glu Asp Tyr Leu Asp Asp Leu Glu His Phe Asp
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 Glu Val Ile Val Met Ser Val Glu Pro Gly Phe Gly Gly Gln Ser Phe
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 Met Pro Glu Gln Leu Glu Lys Val Arg Thr Leu Arg Lys Val Ile Asp
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 aag acc atc aag cag gct gcc gac gct ggc gtg gat gcc ttc gtt gca 691
 Lys Thr Ile Lys Gln Ala Ala Asp Ala Gly Val Asp Ala Phe Val Ala
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 Gly Ser Ala Val Tyr Gly Ala Glu Asp Pro Asn Lys Ala Ile Gln Glu
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 Gly Ala Asp Ile Thr Ala Ala Val Asn Arg Val Thr Asp Lys Glu Leu
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 Asp Val His Leu Met Ile Glu Asn Pro Glu Lys Trp Val Asp Asn Tyr
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 Ile Asp Ala Gly Ala Asp Cys Ile Val Phe His Val Glu Ala Thr Glu
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 Gly His Val Glu Leu Ala Lys Tyr Ile Arg Ser Lys Gly Val Arg Ala
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 Gly Phe Ser Leu Arg Pro Gly Thr Pro Ile Glu Asp Tyr Leu Asp Asp
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 Leu Glu His Phe Asp Glu Val Ile Val Met Ser Val Glu Pro Gly Phe
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 Gly Gly Gln Ser Phe Met Pro Glu Gln Leu Glu Lys Val Arg Thr Leu
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 Arg Lys Val Ile Asp Glu Arg Gly Leu Asn Thr Val Ile Glu Ile Asp
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 Met Arg Val Tyr Leu
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 Gly Ala Asp His Ala Gly Phe Glu Thr Lys Asn Ala Ile Ala Glu His
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 Leu Lys Ala His Gly His Glu Val Ile Asp Cys Gly Ala His Thr Tyr

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Asp	Ala	Glu	Asp	Asp	Tyr	Pro	Ala	Phe	Cys	Ile	Glu	Ala	Ala	Ser	Arg					
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Thr	Val	Asn	Asp	Pro	Gly	Ser	Leu	Gly	Ile	Val	Leu	Gly	Gly	Ser	Gly					
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Asn	Gly	Glu	Gln	Ile	Ala	Ala	Asn	Lys	Val	Lys	Gly	Ala	Arg	Cys	Ala					
70						75						80			85					
ctt	gct	tgg	tct	gtt	gaa	act	gca	cgc	ctc	gcc	cgc	gag	cac	aac	aat	403				
Leu	Ala	Trp	Ser	Val	Glu	Thr	Ala	Arg	Leu	Ala	Arg	Glu	His	Asn	Asn					
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gcg	aac	ctc	atc	ggc	atc	ggc	ggc	cgc	atg	cac	tca	gag				442				
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 Glu Ala Ala Ser Arg Thr Val Asn Asp Pro Gly Ser Leu Gly Ile Val
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 Leu Gly Gly Ser Gly Asn Gly Glu Gln Ile Ala Ala Asn Lys Val Lys
 65 70 75 80
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 Ser Glu

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Glu Thr Thr Arg Pro Glu Phe Ile His Pro Val Ser Val Leu Pro Glu
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Val Ser Ala Gly Thr Val Leu Asp Ala Ala Glu Pro Ala Gly Val Pro
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Pro Leu Asn Arg Arg Lys Phe Arg Val Leu Val Val Gly Thr Gly Leu
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Ser Gly Gly Ala Ala Ala Ala Ala Leu Gly Glu Leu Gly Tyr Asp Val
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Lys Ala Phe Thr Tyr His Asp Ala Pro Arg Arg Ala His Ser Ile Ala
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Gly Arg Glu Ser Asp Cys Trp Arg Leu Ala Val Glu Ser Val Arg Val
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Ile Asp His Met Asn Ala Ile Gly Ala Pro Phe Ala Arg Glu Tyr Gly
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ggc gcc ttg gca acc cgt tcc ttc ggt ggt gtg cag gtc tcc cgt acc 643
Gly Ala Leu Ala Thr Arg Ser Phe Gly Gly Val Gln Val Ser Arg Thr
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tac tac acc cgt gga caa acc gga cag cag ctg cag ttc tcc acc gca 691
Tyr Tyr Thr Arg Gly Gln Thr Gly Gln Gln Leu Gln Phe Ser Thr Ala
185 190 195

tcc gca cta cag cgc cag atc cac ctc ggc tcc gta gaa atc ttc acc 739
Ser Ala Leu Gln Arg Gln Ile His Leu Gly Ser Val Glu Ile Phe Thr
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His Asn Glu Met Val Asp Val Ile Val Thr Glu Arg Asn Gly Glu Lys	
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Arg Cys Glu Gly Leu Ile Met Arg Asn Leu Ile Thr Gly Glu Leu Thr	
230 235 240 245	
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Ala His Thr Gly His Ala Val Ile Leu Ala Thr Gly Gly Tyr Gly Asn	
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gtg tac cac atg tcc acc ctg gcc aag aac tcc aac gcc tcg gcc atc	931
Val Tyr His Met Ser Thr Leu Ala Lys Asn Ser Asn Ala Ser Ala Ile	
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Met Arg Ala Tyr Glu Ala Gly Ala Tyr Phe Ala Ser Pro Ser Phe Ile	
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Gln Phe His Pro Thr Gly Leu Pro Val Asn Ser Thr Trp Gln Ser Lys	
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Thr Ile Leu Met Ser Glu Ser Leu Arg Asn Asp Gly Arg Ile Trp Ser	
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Pro Lys Glu Pro Asn Asp Asn Arg Asp Pro Asn Thr Ile Pro Glu Asp	
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Glu Arg Asp Tyr Phe Leu Glu Arg Arg Tyr Pro Ala Phe Gly Asn Leu	
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Asp Ala Thr Glu Arg Leu Gly Gln Asp Thr Ile Arg Glu Arg Tyr Ser	
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Asn Leu Phe Thr Met Tyr Glu Glu Ala Ile Gly Glu Asp Pro Tyr Ser	
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Ser Pro Met Arg Ile Ala Pro Thr Cys His Phe Thr Met Gly Gly Leu	
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Trp Thr Asp Phe Asn Glu Met Thr Ser Leu Pro Gly Leu Phe Cys Ala	
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 Ile Pro Asn Tyr Leu Gly Pro Leu Leu Gly Ser Glu Arg Leu Ser Glu
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 Asp Ala Pro Glu Ala Gln Ala Ala Ile Ala Arg Ala Gln Ala Arg Ile
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 Asp Arg Leu Met Gly Asn Arg Pro Glu Trp Val Gly Asp Asn Val His
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 Gly Pro Glu Tyr Tyr His Arg Gln Leu Gly Asp Ile Leu Tyr Phe Ser
 535 540 545

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 Cys Gly Val Ser Arg Asn Val Glu Asp Leu Gln Asp Gly Ile Asn Lys
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 Ser Thr Asp Glu Met Asn Gln Val Leu Glu Tyr Ala Ala Arg Val Ala
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 Asp Tyr Ile Asp Leu Gly Glu Leu Met Cys Val Asp Ala Leu Asp Arg
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gaa cca ggc gag aat gga acc ttc gtc tgc cac gca gaa cca ctg ttc 2083
 Glu Pro Gly Glu Asn Gly Thr Phe Val Cys His Ala Glu Pro Leu Phe
 650 655 660

ttc gaa tct gtc cca ctg cag aca agg aac tac aag taatgaaact 2129
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<212> PRT

<213> Corynebacterium glutamicum

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Pro Ala Gly Val Pro Thr Lys Asp Met Trp Glu Tyr Gln Lys Asp His
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Met Asn Leu Val Ser Pro Leu Asn Arg Arg Lys Phe Arg Val Leu Val
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Val Gly Thr Gly Leu Ser Gly Gly Ala Ala Ala Ala Leu Gly Glu
 65           70           75           80

Leu Gly Tyr Asp Val Lys Ala Phe Thr Tyr His Asp Ala Pro Arg Arg
          85           90           95

Ala His Ser Ile Ala Ala Gln Gly Gly Val Asn Ser Ala Arg Gly Lys
          100          105          110

Lys Val Asp Asn Asp Gly Ala Tyr Arg His Val Lys Asp Thr Val Lys
          115          120          125

Gly Gly Asp Tyr Arg Gly Arg Glu Ser Asp Cys Trp Arg Leu Ala Val
 130           135           140

Glu Ser Val Arg Val Ile Asp His Met Asn Ala Ile Gly Ala Pro Phe
 145           150          155          160

Ala Arg Glu Tyr Gly Gly Ala Leu Ala Thr Arg Ser Phe Gly Gly Val
          165          170          175

Gln Val Ser Arg Thr Tyr Tyr Thr Arg Gly Gln Thr Gly Gln Gln Leu
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Gln Phe Ser Thr Ala Ser Ala Leu Gln Arg Gln Ile His Leu Gly Ser
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Val Glu Ile Phe Thr His Asn Glu Met Val Asp Val Ile Val Thr Glu
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Arg Asn Gly Glu Lys Arg Cys Glu Gly Leu Ile Met Arg Asn Leu Ile
 225           230          235          240

Thr Gly Glu Leu Thr Ala His Thr Gly His Ala Val Ile Leu Ala Thr
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Gly Gly Tyr Gly Asn Val Tyr His Met Ser Thr Leu Ala Lys Asn Ser
          260          265          270

Asn Ala Ser Ala Ile Met Arg Ala Tyr Glu Ala Gly Ala Tyr Phe Ala
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Ser Pro Ser Phe Ile Gln Phe His Pro Thr Gly Leu Pro Val Asn Ser
 290           295          300

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 Gly Arg Ile Trp Ser Pro Lys Glu Pro Asn Asp Asn Arg Asp Pro Asn
 325 330 335
 Thr Ile Pro Glu Asp Glu Arg Asp Tyr Phe Leu Glu Arg Arg Tyr Pro
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 Ala Phe Gly Asn Leu Val Pro Arg Asp Val Ala Ser Arg Ala Ile Ser
 355 360 365
 Gln Gln Ile Asn Ala Gly Leu Gly Val Gly Pro Leu Asn Asn Ala Ala
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 Tyr Leu Asp Phe Arg Asp Ala Thr Glu Arg Leu Gly Gln Asp Thr Ile
 385 390 395 400
 Arg Glu Arg Tyr Ser Asn Leu Phe Thr Met Tyr Glu Glu Ala Ile Gly
 405 410 415
 Glu Asp Pro Tyr Ser Ser Pro Met Arg Ile Ala Pro Thr Cys His Phe
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 Thr Met Gly Gly Leu Trp Thr Asp Phe Asn Glu Met Thr Ser Leu Pro
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 Gly Leu Phe Cys Ala Gly Glu Ala Ser Trp Thr Tyr His Gly Ala Asn
 450 455 460
 Arg Leu Gly Ala Asn Ser Leu Leu Ser Ala Ser Val Asp Gly Trp Phe
 465 470 475 480
 Thr Leu Pro Phe Thr Ile Pro Asn Tyr Leu Gly Pro Leu Leu Gly Ser
 485 490 495
 Glu Arg Leu Ser Glu Asp Ala Pro Glu Ala Gln Ala Ala Ile Ala Arg
 500 505 510
 Ala Gln Ala Arg Ile Asp Arg Leu Met Gly Asn Arg Pro Glu Trp Val
 515 520 525
 Gly Asp Asn Val His Gly Pro Glu Tyr Tyr His Arg Gln Leu Gly Asp
 530 535 540
 Ile Leu Tyr Phe Ser Cys Gly Val Ser Arg Asn Val Glu Asp Leu Gln
 545 550 555 560
 Asp Gly Ile Asn Lys Ile Arg Ala Leu Arg Asp Asp Phe Trp Lys Asn
 565 570 575
 Met Arg Ile Thr Gly Ser Thr Asp Glu Met Asn Gln Val Leu Glu Tyr
 580 585 590
 Ala Ala Arg Val Ala Asp Tyr Ile Asp Leu Gly Glu Leu Met Cys Val
 595 600 605
 Asp Ala Leu Asp Arg Asp Glu Ser Cys Gly Ala His Phe Arg Asp Asp
 610 615 620
 His Leu Ser Glu Asp Gly Glu Ala Gln Arg Asp Asp Gln Asn Trp Cys

625		630		635		640
Phe Val Ser Ala Trp	Glu Pro Gly Glu Asn Gly Thr Phe Val Cys His					
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Lys

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 <223> FRXA01312

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Asp Asn Arg Asp Pro Asn Thr Ile Pro Glu Asp Glu Arg Asp Tyr Phe	
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ctg gag cgc cgc tac cca gca ttc ggt aac ctc gtc cca cgt gac gtt	144
Leu Glu Arg Arg Tyr Pro Ala Phe Gly Asn Leu Val Pro Arg Asp Val	
35 40 45	
gct tcc cgt gcg atc tcc cag cag atc aat gct ggt ctc ggt gtt gga	192
Ala Ser Arg Ala Ile Ser Gln Gln Ile Asn Ala Gly Leu Gly Val Gly	
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cct ctg aac aac gct gca tac ctg gac ttc cgc gac gcc acc gag cgc	240
Pro Leu Asn Asn Ala Ala Tyr Leu Asp Phe Arg Asp Ala Thr Glu Arg	
65 70 75 80	
ctc gga cag gac acc atc cgc gag cgt tac tcc aac ctc ttc acc atg	288
Leu Gly Gln Asp Thr Ile Arg Glu Arg Tyr Ser Asn Leu Phe Thr Met	
85 90 95	
tac gaa gag gca att ggc gag gac cca tac tcc agc cca atg cgt att	336
Tyr Glu Glu Ala Ile Gly Glu Asp Pro Tyr Ser Ser Pro Met Arg Ile	
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gca ccg acc tgc cac ttc acc atg ggt ggc ctc tgg act gac ttc aac	384
Ala Pro Thr Cys His Phe Thr Met Gly Gly Leu Trp Thr Asp Phe Asn	
115 120 125	
gaa atg acg tca ctc cca ggt ctg ttc tgc gca ggc gaa gca tcc tgg	432
Glu Met Thr Ser Leu Pro Gly Leu Phe Cys Ala Gly Glu Ala Ser Trp	
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acc tac cac ggt gca aac cgt ctg ggc gca aac tcc ctg ctc tcc gct	480
Thr Tyr His Gly Ala Asn Arg Leu Gly Ala Asn Ser Leu Leu Ser Ala	

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Ser Val Asp Gly Trp Phe Thr Leu Pro Phe Thr Ile Pro Asn Tyr Leu	165	170	175	
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Gly Pro Leu Leu Gly Ser Glu Arg Leu Ser Glu Asp Ala Pro Glu Ala	180	185	190	
cag gca gcg att gcg cgt gca cag gct cgc att gac cgc ctc atg ggc				624
Gln Ala Ala Ile Ala Arg Ala Gln Ala Arg Ile Asp Arg Leu Met Gly	195	200	205	
aac cgc cca gag tgg gtc ggt gac aac gtt cac gga cct gag tac tac				672
Asn Arg Pro Glu Trp Val Gly Asp Asn Val His Gly Pro Glu Tyr Tyr	210	215	220	
cac cgc cag ctt ggc gat atc ctg tac ttc tcc tgt ggc gtt tcc cga				720
His Arg Gln Leu Gly Asp Ile Leu Tyr Phe Ser Cys Gly Val Ser Arg	225	230	235	240
aac gta gaa gac ctc cag gat ggc atc aac aag atc cgt gcc ctc cgc				768
Asn Val Glu Asp Leu Gln Asp Gly Ile Asn Lys Ile Arg Ala Leu Arg	245	250	255	
gat gac ttc tgg aag aac atg cgc atc acc ggc agc acc gat gag atg				816
Asp Asp Phe Trp Lys Asn Met Arg Ile Thr Gly Ser Thr Asp Glu Met	260	265	270	
aac cag gtt ctc gaa tac gca gca cgc gta gcc gac tac atc gac ctc				864
Asn Gln Val Leu Glu Tyr Ala Ala Arg Val Ala Asp Tyr Ile Asp Leu	275	280	285	
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Gly Glu Leu Met Cys Val Asp Ala Leu Asp Arg Asp Glu Ser Cys Gly	290	295	300	
gct cac ttc cgc gac gac cac ctc tcc gaa gat ggc gaa gca caa cgt				960
Ala His Phe Arg Asp Asp His Leu Ser Glu Asp Gly Glu Ala Gln Arg	305	310	315	320
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Asp Asp Gln Asn Trp Cys Phe Val Ser Ala Trp Glu Pro Gly Glu Asn	325	330	335	
gga acc ttc gtc tgc cac gca gaa cca ctg ttc ttc gaa tct gtc cca				1056
Gly Thr Phe Val Cys His Ala Glu Pro Leu Phe Phe Glu Ser Val Pro	340	345	350	
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Leu Gln Thr Arg Asn Tyr Lys	355			

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<211> 359

<212> PRT

<213> Corynebacterium glutamicum

<400> 12

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 35 40 45
 Ala Ser Arg Ala Ile Ser Gln Gln Ile Asn Ala Gly Leu Gly Val Gly
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 Pro Leu Asn Asn Ala Ala Tyr Leu Asp Phe Arg Asp Ala Thr Glu Arg
 65 70 75 80
 Leu Gly Gln Asp Thr Ile Arg Glu Arg Tyr Ser Asn Leu Phe Thr Met
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 Tyr Glu Glu Ala Ile Gly Glu Asp Pro Tyr Ser Ser Pro Met Arg Ile
 100 105 110
 Ala Pro Thr Cys His Phe Thr Met Gly Gly Leu Trp Thr Asp Phe Asn
 115 120 125
 Glu Met Thr Ser Leu Pro Gly Leu Phe Cys Ala Gly Glu Ala Ser Trp
 130 135 140
 Thr Tyr His Gly Ala Asn Arg Leu Gly Ala Asn Ser Leu Leu Ser Ala
 145 150 155 160
 Ser Val Asp Gly Trp Phe Thr Leu Pro Phe Thr Ile Pro Asn Tyr Leu
 165 170 175
 Gly Pro Leu Leu Gly Ser Glu Arg Leu Ser Glu Asp Ala Pro Glu Ala
 180 185 190
 Gln Ala Ala Ile Ala Arg Ala Gln Ala Arg Ile Asp Arg Leu Met Gly
 195 200 205
 Asn Arg Pro Glu Trp Val Gly Asp Asn Val His Gly Pro Glu Tyr Tyr
 210 215 220
 His Arg Gln Leu Gly Asp Ile Leu Tyr Phe Ser Cys Gly Val Ser Arg
 225 230 235 240
 Asn Val Glu Asp Leu Gln Asp Gly Ile Asn Lys Ile Arg Ala Leu Arg
 245 250 255
 Asp Asp Phe Trp Lys Asn Met Arg Ile Thr Gly Ser Thr Asp Glu Met
 260 265 270
 Asn Gln Val Leu Glu Tyr Ala Ala Arg Val Ala Asp Tyr Ile Asp Leu
 275 280 285
 Gly Glu Leu Met Cys Val Asp Ala Leu Asp Arg Asp Glu Ser Cys Gly
 290 295 300
 Ala His Phe Arg Asp Asp His Leu Ser Glu Asp Gly Glu Ala Gln Arg
 305 310 315 320
 Asp Asp Gln Asn Trp Cys Phe Val Ser Ala Trp Glu Pro Gly Glu Asn

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Gly Thr Phe Val Cys His Ala Glu Pro Leu Phe Phe Glu Ser Val Pro				
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Leu Gln Thr Arg Asn Tyr Lys				
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		Met Thr Ile Asn Val		
		1 5		
ttc gaa cta ctt gtc aaa agt ccc acg ggt cta ctg att ggt gat tcc	163			
Phe Glu Leu Leu Val Lys Ser Pro Thr Gly Leu Leu Ile Gly Asp Ser				
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tgg gtg gaa gca tcc gac ggc ggt act ttc gat gtg gaa aac cca gcg	211			
Trp Val Glu Ala Ser Asp Gly Gly Thr Phe Asp Val Glu Asn Pro Ala				
	25	30	35	
acg ggt gaa aca atc gca acg ctc gcg tct gct act tcc gag gat gca	259			
Thr Gly Glu Thr Ile Ala Thr Leu Ala Ser Ala Thr Ser Glu Asp Ala				
	40	45	50	
ctg gct gct ctt gat gct gca tgc gct gtt cag gcc gag tgg gct agg	307			
Leu Ala Ala Leu Asp Ala Cys Ala Val Gln Ala Glu Trp Ala Arg				
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atg cca gcg cgc gag cgt tct aat att tta cgc cgc ggt ttt gag ctc	355			
Met Pro Ala Arg Glu Arg Ser Asn Ile Leu Arg Arg Gly Phe Glu Leu				
	70	75	80	85
gta gca gaa cgt gca gaa gag ttc gcc acc ctc atg acc ttg gaa atg	403			
Val Ala Glu Arg Ala Glu Glu Phe Ala Thr Leu Met Thr Leu Glu Met				
	90	95	100	
ggc aag cct ttg gct gaa gct cgc ggc gaa gtc acc tac ggc aac gaa	451			
Gly Lys Pro Leu Ala Glu Ala Arg Gly Glu Val Thr Tyr Gly Asn Glu				
	105	110	115	
ttc ctg cgc tgg ttc tct gag gaa gca gtt cgt ctg tat ggc cgt tac	499			
Phe Leu Arg Trp Phe Ser Glu Glu Ala Val Arg Leu Tyr Gly Arg Tyr				
	120	125	130	
gga acc aca cca gaa ggc aac ttg cgg atg ctg acc gcc ctc aag cca	547			
Gly Thr Thr Pro Glu Gly Asn Leu Arg Met Leu Thr Ala Leu Lys Pro				
	135	140	145	

gtt ggc ccg tgc ctc ctg atc acc cca tgg aac ttc cca cta gca atg	595
Val Gly Pro Cys Leu Leu Ile Thr Pro Trp Asn Phe Pro Leu Ala Met	
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gct acc cgc aag gtc gca cct gcg atc gct gca ggt tgt gtc atg gtg	643
Ala Thr Arg Lys Val Ala Pro Ala Ile Ala Ala Gly Cys Val Met Val	
170 175 180	
ctc aag cca gct cga ctt acc ccg ctg acc tcc cag tat ttt gct cag	691
Leu Lys Pro Ala Arg Leu Thr Pro Leu Thr Ser Gln Tyr Phe Ala Gln	
185 190 195	
acc atg ctt gat gcc ggt ctt cca gca ggt gtc ctc aat gtg gtc tcc	739
Thr Met Leu Asp Ala Gly Leu Pro Ala Gly Val Leu Asn Val Val Ser	
200 205 210	
ggt gct tcc gcc tct gcg att tcc aac ccg att atg gaa gac gat cgc	787
Gly Ala Ser Ala Ser Ala Ile Ser Asn Pro Ile Met Glu Asp Asp Arg	
215 220 225	
ctt cgt aaa gtc tcc ttc acc gcc tcc acc cca gtt ggc cag cag ctg	835
Leu Arg Lys Val Ser Phe Thr Gly Ser Thr Pro Val Gly Gln Gln Leu	
230 235 240 245	
ctc aaa aag gct gcc gat aaa gtt ctg cgc acc tcc atg gaa ctt ggt	883
Leu Lys Lys Ala Ala Asp Lys Val Leu Arg Thr Ser Met Glu Leu Gly	
250 255 260	
ggc aac gca cct ttc att gtc ttc gag gac gcc gac cta gat ctc gcg	931
Gly Asn Ala Pro Phe Ile Val Phe Glu Asp Ala Asp Leu Asp Leu Ala	
265 270 275	
atc gaa ggt gcc atg ggt gcc aaa atg cgc aac atc ggc gaa gct tgc	979
Ile Glu Gly Ala Met Gly Ala Lys Met Arg Asn Ile Gly Glu Ala Cys	
280 285 290	
acc gca gcc aac cgt ttc tta gtc cac gaa tcc gtc gcc gat gaa ttc	1027
Thr Ala Ala Asn Arg Phe Leu Val His Glu Ser Val Ala Asp Glu Phe	
295 300 305	
ggc cgt cgc ttc gct gcc cgc ctt gaa gag caa gtc cta ggc aac ggc	1075
Gly Arg Arg Phe Ala Ala Arg Leu Glu Glu Gln Val Leu Gly Asn Gly	
310 315 320 325	
ctc gac gaa ggc gtc acc gtg ggc ccc ctg gtt gag gaa aaa gca cga	1123
Leu Asp Glu Gly Val Thr Val Gly Pro Leu Val Glu Glu Lys Ala Arg	
330 335 340	
gac agc gtt gca tcg ctt gtc gac gcc gcc gtc gcc gaa ggt gcc acc	1171
Asp Ser Val Ala Ser Leu Val Asp Ala Ala Val Ala Glu Gly Ala Thr	
345 350 355	
gtc ctc acc ggc ggc aag gcc ggc aca ggt gca ggc tac ttc tac gaa	1219
Val Leu Thr Gly Gly Lys Ala Gly Thr Gly Ala Gly Tyr Phe Tyr Glu	
360 365 370	
cca acg gtg ctc acg gga gtt tca aca gat gcg gct atc ctg aac gaa	1267
Pro Thr Val Leu Thr Gly Val Ser Thr Asp Ala Ala Ile Leu Asn Glu	
375 380 385	

gag atc ttc ggt ccc gtc gca ccg atc gtc acc ttc caa acc gag gaa 1315
 Glu Ile Phe Gly Pro Val Ala Pro Ile Val Thr Phe Gln Thr Glu Glu
 390 395 400 405

 gaa gcc ctg cgt cta gcc aac tcc acc gaa tac gga ctg gcc tcc tat 1363
 Glu Ala Leu Arg Leu Ala Asn Ser Thr Glu Tyr Gly Leu Ala Ser Tyr
 410 415 420

 gtg ttc acc cag gac acc tca cgt att ttc cgc gtc tcc gat ggt ctc 1411
 Val Phe Thr Gln Asp Thr Ser Arg Ile Phe Arg Val Ser Asp Gly Leu
 425 430 435

 gag ttc ggc cta gtg ggc gtc aat tcc ggt gtc atc tct aac gct gct 1459
 Glu Phe Gly Leu Val Gly Val Asn Ser Gly Val Ile Ser Asn Ala Ala
 440 445 450

 gca cct ttt ggt ggc gta aaa caa tcc gga atg ggc cgc gaa ggt ggt 1507
 Ala Pro Phe Gly Gly Val Lys Gln Ser Gly Met Gly Arg Glu Gly Gly
 455 460 465

 ctc gaa gga atc gag gag tac acc tcc gtg cag tac atc ggt atc cgg 1555
 Leu Glu Gly Ile Glu Glu Tyr Thr Ser Val Gln Tyr Ile Gly Ile Arg
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 Asp Pro Tyr Ala Gly
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 <213> Corynebacterium glutamicum

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 Val Glu Asn Pro Ala Thr Gly Glu Thr Ile Ala Thr Leu Ala Ser Ala
 35 40 45

 Thr Ser Glu Asp Ala Leu Ala Ala Leu Asp Ala Ala Cys Ala Val Gln
 50 55 60

 Ala Glu Trp Ala Arg Met Pro Ala Arg Glu Arg Ser Asn Ile Leu Arg
 65 70 75 80

 Arg Gly Phe Glu Leu Val Ala Glu Arg Ala Glu Glu Phe Ala Thr Leu
 85 90 95

 Met Thr Leu Glu Met Gly Lys Pro Leu Ala Glu Ala Arg Gly Glu Val
 100 105 110

 Thr Tyr Gly Asn Glu Phe Leu Arg Trp Phe Ser Glu Glu Ala Val Arg
 115 120 125

 Leu Tyr Gly Arg Tyr Gly Thr Thr Pro Glu Gly Asn Leu Arg Met Leu
 130 135 140

Thr Ala Leu Lys Pro Val Gly Pro Cys Leu Leu Ile Thr Pro Trp Asn
 145 150 155 160
 Phe Pro Leu Ala Met Ala Thr Arg Lys Val Ala Pro Ala Ile Ala Ala
 165 170 175
 Gly Cys Val Met Val Leu Lys Pro Ala Arg Leu Thr Pro Leu Thr Ser
 180 185 190
 Gln Tyr Phe Ala Gln Thr Met Leu Asp Ala Gly Leu Pro Ala Gly Val
 195 200 205
 Leu Asn Val Val Ser Gly Ala Ser Ala Ser Ala Ile Ser Asn Pro Ile
 210 215 220
 Met Glu Asp Asp Arg Leu Arg Lys Val Ser Phe Thr Gly Ser Thr Pro
 225 230 235 240
 Val Gly Gln Gln Leu Leu Lys Lys Ala Ala Asp Lys Val Leu Arg Thr
 245 250 255
 Ser Met Glu Leu Gly Gly Asn Ala Pro Phe Ile Val Phe Glu Asp Ala
 260 265 270
 Asp Leu Asp Leu Ala Ile Glu Gly Ala Met Gly Ala Lys Met Arg Asn
 275 280 285
 Ile Gly Glu Ala Cys Thr Ala Ala Asn Arg Phe Leu Val His Glu Ser
 290 295 300
 Val Ala Asp Glu Phe Gly Arg Arg Phe Ala Ala Arg Leu Glu Glu Gln
 305 310 315 320
 Val Leu Gly Asn Gly Leu Asp Glu Gly Val Thr Val Gly Pro Leu Val
 325 330 335
 Glu Glu Lys Ala Arg Asp Ser Val Ala Ser Leu Val Asp Ala Ala Val
 340 345 350
 Ala Glu Gly Ala Thr Val Leu Thr Gly Gly Lys Ala Gly Thr Gly Ala
 355 360 365
 Gly Tyr Phe Tyr Glu Pro Thr Val Leu Thr Gly Val Ser Thr Asp Ala
 370 375 380
 Ala Ile Leu Asn Glu Glu Ile Phe Gly Pro Val Ala Pro Ile Val Thr
 385 390 395 400
 Phe Gln Thr Glu Glu Glu Ala Leu Arg Leu Ala Asn Ser Thr Glu Tyr
 405 410 415
 Gly Leu Ala Ser Tyr Val Phe Thr Gln Asp Thr Ser Arg Ile Phe Arg
 420 425 430
 Val Ser Asp Gly Leu Glu Phe Gly Leu Val Gly Val Asn Ser Gly Val
 435 440 445
 Ile Ser Asn Ala Ala Ala Pro Phe Gly Gly Val Lys Gln Ser Gly Met
 450 455 460

Gly Arg Glu Gly Gly Leu Glu Gly Ile Glu Glu Tyr Thr Ser Val Gln
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Tyr Ile Gly Ile Arg Asp Pro Tyr Ala Gly
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 <213> Corynebacterium glutamicum

<220>
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 <223> RXA01311

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 Met Lys Leu Thr Leu
 1 5
 gag atc tgg cgt caa gca ggc cca act gcg gaa ggc aag ttc gaa acc 163
 Glu Ile Trp Arg Gln Ala Gly Pro Thr Ala Glu Gly Lys Phe Glu Thr
 10 15 20
 gtc cag gtt gac gac gcc gtc gcg cag atg tcc atc ctg gag ctg ctt 211
 Val Gln Val Asp Asp Ala Val Ala Gln Met Ser Ile Leu Glu Leu Leu
 25 30 35
 gac cac gta aac aac aag ttc atc gaa gaa ggc aaa gaa cca ttc gcg 259
 Asp His Val Asn Asn Lys Phe Ile Glu Glu Gly Lys Glu Pro Phe Ala
 40 45 50
 ttc gcc tct gac tgc cgc gaa ggc att tgt ggt acc tgt ggt ctc ctc 307
 Phe Ala Ser Asp Cys Arg Glu Gly Ile Cys Gly Thr Cys Gly Leu Leu
 55 60 65
 gtg aac ggt cgc cct cac ggc gcc gac cag aac aag cct gcc tgt gcg 355
 Val Asn Gly Arg Pro His Gly Ala Asp Gln Asn Lys Pro Ala Cys Ala
 70 75 80 85
 cag cgc ctg gtc agc tac aag gaa ggc gac acc ctc aag atc gaa cca 403
 Gln Arg Leu Val Ser Tyr Lys Glu Gly Asp Thr Leu Lys Ile Glu Pro
 90 95 100
 ctg cgt tcc gcc gca tac cca gtg atc aag gac atg gtc gtc gac cgc 451
 Leu Arg Ser Ala Ala Tyr Pro Val Ile Lys Asp Met Val Val Asp Arg
 105 110 115
 tcc gca ctg gac cgt gtc atg gaa cag ggt ggc tac gtg acc atc aac 499
 Ser Ala Leu Asp Arg Val Met Glu Gln Gly Gly Tyr Val Thr Ile Asn
 120 125 130
 gca ggt acc gca cct gac gct gat acc ctc cac gtc aac cac gaa acc 547
 Ala Gly Thr Ala Pro Asp Ala Asp Thr Leu His Val Asn His Glu Thr
 135 140 145
 gca gaa ctc gca ctt gac cac gca gcc tgc atc ggc tgt ggc gca tgt 595

Ala Glu Leu Ala Leu Asp His Ala Ala Cys Ile Gly Cys Gly Ala Cys
 150 155 160 165

ggt gct gcc tgc cct aac ggc gca gca cac ctg ttc acc ggc gca aag 643
 Val Ala Ala Cys Pro Asn Gly Ala Ala His Leu Phe Thr Gly Ala Lys
 170 175 180

ctt gtt cac ctg tcc ctg ctg cca ctg ggt aag gaa gag cgc gga ctg 691
 Leu Val His Leu Ser Leu Leu Pro Leu Gly Lys Glu Glu Arg Gly Leu
 185 190 195

cgt gca cgt aag atg gtt gat gaa atg gaa acc aac ttc gga cac tgc 739
 Arg Ala Arg Lys Met Val Asp Glu Met Glu Thr Asn Phe Gly His Cys
 200 205 210

tcc ctg tac ggc gag tgc gca gat gtc tgc ccc gca ggc atc cca ctg 787
 Ser Leu Tyr Gly Glu Cys Ala Asp Val Cys Pro Ala Gly Ile Pro Leu
 215 220 225

acc gct gtg gca gct gtc acc aag gaa cgt gcg cgt gca gct ttc cga 835
 Thr Ala Val Ala Ala Val Thr Lys Glu Arg Ala Arg Ala Ala Phe Arg
 230 235 240 245

ggc aaa gac gac tagtctttaa tccaagtaag tac 870
 Gly Lys Asp Asp

<210> 16

<211> 249

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 16

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Gly Lys Phe Glu Thr Val Gln Val Asp Asp Ala Val Ala Gln Met Ser
 20 25 30

Ile Leu Glu Leu Leu Asp His Val Asn Asn Lys Phe Ile Glu Glu Gly
 35 40 45

Lys Glu Pro Phe Ala Phe Ala Ser Asp Cys Arg Glu Gly Ile Cys Gly
 50 55 60

Thr Cys Gly Leu Leu Val Asn Gly Arg Pro His Gly Ala Asp Gln Asn
 65 70 75 80

Lys Pro Ala Cys Ala Gln Arg Leu Val Ser Tyr Lys Glu Gly Asp Thr
 85 90 95

Leu Lys Ile Glu Pro Leu Arg Ser Ala Ala Tyr Pro Val Ile Lys Asp
 100 105 110

Met Val Val Asp Arg Ser Ala Leu Asp Arg Val Met Glu Gln Gly Gly
 115 120 125

Tyr Val Thr Ile Asn Ala Gly Thr Ala Pro Asp Ala Asp Thr Leu His
 130 135 140

Val Asn His Glu Thr Ala Glu Leu Ala Leu Asp His Ala Ala Cys Ile
 145 150 155 160

Gly Cys Gly Ala Cys Val Ala Ala Cys Pro Asn Gly Ala Ala His Leu
 165 170 175

Phe Thr Gly Ala Lys Leu Val His Leu Ser Leu Leu Pro Leu Gly Lys
 180 185 190

Glu Glu Arg Gly Leu Arg Ala Arg Lys Met Val Asp Glu Met Glu Thr
 195 200 205

Asn Phe Gly His Cys Ser Leu Tyr Gly Glu Cys Ala Asp Val Cys Pro
 210 215 220

Ala Gly Ile Pro Leu Thr Ala Val Ala Ala Val Thr Lys Glu Arg Ala
 225 230 235 240

Arg Ala Ala Phe Arg Gly Lys Asp Asp
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<210> 17
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 <212> DNA
 <213> Corynebacterium glutamicum

<220>
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 <222> (101)..(1507)
 <223> RXA01535

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 Met Thr Glu Gln Glu 5
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ttc cgt att gag cac gac acc atg ggt gaa gtg aag gtt cca gca aag 163
 Phe Arg Ile Glu His Asp Thr Met Gly Glu Val Lys Val Pro Ala Lys 20
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gct ctg tgg cag gca cag acc cag cgc gct gtt gag aac ttc cct atc 211
 Ala Leu Trp Gln Ala Gln Thr Gln Arg Ala Val Glu Asn Phe Pro Ile 35
 25 30

tct ggt cgt ggt ctg gaa tcc gca cag atc cgc gca atg ggt ctg ctg 259
 Ser Gly Arg Gly Leu Glu Ser Ala Gln Ile Arg Ala Met Gly Leu Leu 50
 40 45

aag gca gct tgt gcg cag gta aac aag gac tcc ggt gcg ctg gat gca 307
 Lys Ala Ala Cys Ala Gln Val Asn Lys Asp Ser Gly Ala Leu Asp Ala 65
 55 60

gag aag gca gat gcc atc att gca gct ggt aag gag atc gcg tcc ggt 355
 Glu Lys Ala Asp Ala Ile Ile Ala Ala Gly Lys Glu Ile Ala Ser Gly 85
 70 75 80

aag cat gac gct gag ttc cca att gat gtg ttc cag act ggt tcc ggt 403
 Lys His Asp Ala Glu Phe Pro Ile Asp Val Phe Gln Thr Gly Ser Gly

90								95								100	
act	tcc	tcc	aac	atg	aac	acc	aat	gag	gtt	atc	gct	tcc	atc	gcg	aag	451	
Thr	Ser	Ser	Asn	Met	Asn	Thr	Asn	Glu	Val	Ile	Ala	Ser	Ile	Ala	Lys		
105								110								115	
gct	aac	ggc	gtt	gag	gtt	cac	cca	aat	gac	cac	gtc	aac	atg	ggt	cag	499	
Ala	Asn	Gly	Val	Glu	Val	His	Pro	Asn	Asp	His	Val	Asn	Met	Gly	Gln		
120								125								130	
tcc	tcc	aat	gac	acc	ttc	cct	act	gca	act	cac	gtt	gct	gca	acc	gaa	547	
Ser	Ser	Asn	Asp	Thr	Phe	Pro	Thr	Ala	Thr	His	Val	Ala	Ala	Thr	Glu		
135								140								145	
gct	gct	gtc	aat	gac	ctc	atc	cca	ggc	ctg	aag	gtt	ctg	cac	gag	tct	595	
Ala	Ala	Val	Asn	Asp	Leu	Ile	Pro	Gly	Leu	Lys	Val	Leu	His	Glu	Ser		
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ttg	gcg	aag	aag	gct	aac	gag	tgg	tct	gag	gtt	gtt	aag	tcc	ggc	cgc	643	
Leu	Ala	Lys	Lys	Ala	Asn	Glu	Trp	Ser	Glu	Val	Val	Lys	Ser	Gly	Arg		
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acc	cac	ctg	atg	gac	gct	gtt	cca	gta	acc	ctg	ggc	cag	gag	ttc	ggt	691	
Thr	His	Leu	Met	Asp	Ala	Val	Pro	Val	Thr	Leu	Gly	Gln	Glu	Phe	Gly		
185								190								195	
ggc	tac	gct	cgc	cag	atc	cag	ctc	ggc	atc	gag	cgc	gtt	gag	gct	act	739	
Gly	Tyr	Ala	Arg	Gln	Ile	Gln	Leu	Gly	Ile	Glu	Arg	Val	Glu	Ala	Thr		
200								205								210	
ctt	cct	cgc	ctt	ggt	gag	ctg	gct	att	ggt	ggc	acc	gct	gct	ggt	acc	787	
Leu	Pro	Arg	Leu	Gly	Glu	Leu	Ala	Ile	Gly	Gly	Thr	Ala	Ala	Gly	Thr		
215								220								225	
ggt	atc	aac	acc	tcc	gct	gat	ttc	ggc	ggc	aag	gtt	gtt	gct	gaa	ctg	835	
Gly	Ile	Asn	Thr	Ser	Ala	Asp	Phe	Gly	Gly	Lys	Val	Val	Ala	Glu	Leu		
230								235								240	
atc	aac	ttg	acc	gac	gtc	aag	gag	ctc	aag	gaa	gct	gag	aac	cac	ttc	883	
Ile	Asn	Leu	Thr	Asp	Val	Lys	Glu	Leu	Lys	Glu	Ala	Glu	Asn	His	Phe		
250								255								260	
gag	gct	cag	gct	gca	cgc	gac	gct	ctt	gtt	gag	ttc	tcc	ggc	gca	atg	931	
Glu	Ala	Gln	Ala	Ala	Arg	Asp	Ala	Leu	Val	Glu	Phe	Ser	Gly	Ala	Met		
265								270								275	
cgc	gtt	atc	gct	gtc	tcc	ttg	tac	aag	atc	gct	aac	gat	atc	cgc	ctc	979	
Arg	Val	Ile	Ala	Val	Ser	Leu	Tyr	Lys	Ile	Ala	Asn	Asp	Ile	Arg	Leu		
280								285								290	
atg	ggc	tcc	ggc	cca	ctg	acc	ggt	ctt	ggc	gag	atc	cgt	ctc	cca	gac	1027	
Met	Gly	Ser	Gly	Pro	Leu	Thr	Gly	Leu	Gly	Glu	Ile	Arg	Leu	Pro	Asp		
295								300								305	
ctg	cag	cca	ggt	tcc	tcc	atc	atg	cca	ggc	aag	gtc	aac	cca	gtt	ctc	1075	
Leu	Gln	Pro	Gly	Ser	Ser	Ile	Met	Pro	Gly	Lys	Val	Asn	Pro	Val	Leu		
310								315								320	
tgt	gag	acc	gct	acc	cag	gtt	tcc	gct	cag	gtt	atc	ggc	aat	gac	gca	1123	
Cys	Glu	Thr	Ala	Thr	Gln	Val	Ser	Ala	Gln	Val	Ile	Gly	Asn	Asp	Ala		
330								335								340	

gct gtt gcg ttc tcc ggc acc cag ggc cag ttc gag ctc aac gtg ttc 1171
 Ala Val Ala Phe Ser Gly Thr Gln Gly Gln Phe Glu Leu Asn Val Phe
 345 350 355

 atc cca gtg atg gct cgc aac gtg ctt gag tcc gct cgc ctg ctg gct 1219
 Ile Pro Val Met Ala Arg Asn Val Leu Glu Ser Ala Arg Leu Leu Ala
 360 365 370

 aac act tcc cgc gtg ttc gca acc cgt ctc gtt gat ggc att gag cca 1267
 Asn Thr Ser Arg Val Phe Ala Thr Arg Leu Val Asp Gly Ile Glu Pro
 375 380 385

 aac gag gca cac atg aag gag ctc gct gag tct tca cct tcc atc gtt 1315
 Asn Glu Ala His Met Lys Glu Leu Ala Glu Ser Ser Pro Ser Ile Val
 390 395 400 405

 acc cca ctg aac tct gca atc ggc tac gaa gct gct gca aag gtg gct 1363
 Thr Pro Leu Asn Ser Ala Ile Gly Tyr Glu Ala Ala Ala Lys Val Ala
 410 415 420

 aag act gct ttg gct gag ggc aag acc atc cgc cag act gtc atc gat 1411
 Lys Thr Ala Leu Ala Glu Gly Lys Thr Ile Arg Gln Thr Val Ile Asp
 425 430 435

 ttg ggc ttg gtt gat ggc gag aag ctc acc gag gaa gag ctg gac aag 1459
 Leu Gly Leu Val Asp Gly Glu Lys Leu Thr Glu Glu Glu Leu Asp Lys
 440 445 450

 cgc ctc gac gtt ctt gct atg gct cac acc gag cgc gag aac aag ttc 1507
 Arg Leu Asp Val Leu Ala Met Ala His Thr Glu Arg Glu Asn Lys Phe
 455 460 465

 taaaactaga acccgataaa taa 1530

<210> 18
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 <212> PRT
 <213> Corynebacterium glutamicum

<400> 18
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 Glu Asn Phe Pro Ile Ser Gly Arg Gly Leu Glu Ser Ala Gln Ile Arg
 35 40 45

 Ala Met Gly Leu Leu Lys Ala Ala Cys Ala Gln Val Asn Lys Asp Ser
 50 55 60

 Gly Ala Leu Asp Ala Glu Lys Ala Asp Ala Ile Ile Ala Ala Gly Lys
 65 70 75 80

 Glu Ile Ala Ser Gly Lys His Asp Ala Glu Phe Pro Ile Asp Val Phe
 85 90 95

 Gln Thr Gly Ser Gly Thr Ser Ser Asn Met Asn Thr Asn Glu Val Ile

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Ala	Ser	Ile	Ala	Lys	Ala	Asn	Gly	Val	Glu	Val	His	Pro	Asn	Asp	His
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Val	Asn	Met	Gly	Gln	Ser	Ser	Asn	Asp	Thr	Phe	Pro	Thr	Ala	Thr	His
		130					135					140			
Val	Ala	Ala	Thr	Glu	Ala	Ala	Val	Asn	Asp	Leu	Ile	Pro	Gly	Leu	Lys
		145					150					155			160
Val	Leu	His	Glu	Ser	Leu	Ala	Lys	Lys	Ala	Asn	Glu	Trp	Ser	Glu	Val
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Val	Lys	Ser	Gly	Arg	Thr	His	Leu	Met	Asp	Ala	Val	Pro	Val	Thr	Leu
			180					185					190		
Gly	Gln	Glu	Phe	Gly	Gly	Tyr	Ala	Arg	Gln	Ile	Gln	Leu	Gly	Ile	Glu
		195					200					205			
Arg	Val	Glu	Ala	Thr	Leu	Pro	Arg	Leu	Gly	Glu	Leu	Ala	Ile	Gly	Gly
		210					215					220			
Thr	Ala	Ala	Gly	Thr	Gly	Ile	Asn	Thr	Ser	Ala	Asp	Phe	Gly	Gly	Lys
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Phe	Ser	Gly	Ala	Met	Arg	Val	Ile	Ala	Val	Ser	Leu	Tyr	Lys	Ile	Ala
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Val	Asn	Pro	Val	Leu	Cys	Glu	Thr	Ala	Thr	Gln	Val	Ser	Ala	Gln	Val
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Glu	Leu	Asn	Val	Phe	Ile	Pro	Val	Met	Ala	Arg	Asn	Val	Leu	Glu	Ser
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		370					375					380			
Asp	Gly	Ile	Glu	Pro	Asn	Glu	Ala	His	Met	Lys	Glu	Leu	Ala	Glu	Ser
		385					390					395			400
Ser	Pro	Ser	Ile	Val	Thr	Pro	Leu	Asn	Ser	Ala	Ile	Gly	Tyr	Glu	Ala
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Gln Thr Val Ile Asp Leu Gly Leu Val Asp Gly Glu Lys Leu Thr Glu
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<223> RXA00517

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Met Pro Glu Val Thr
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gtc aac gcc caa caa ctc act gtt ctc tgc aca gac atc ctc acc aaa 163
Val Asn Ala Gln Gln Leu Thr Val Leu Cys Thr Asp Ile Leu Thr Lys
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act gga gta cct gca gca gac gcc cat ctt gtc ggt gat agt ttg gtg 211
Thr Gly Val Pro Ala Ala Asp Ala His Leu Val Gly Asp Ser Leu Val
25 30 35
cag gct gat ctt tgg ggt cac ccc tcc cac ggt gtg ctt cga ctg cct 259
Gln Ala Asp Leu Trp Gly His Pro Ser His Gly Val Leu Arg Leu Pro
40 45 50
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Trp Tyr Val Arg Arg Leu His Ser Gly Ala Met Thr Thr His Ala His
55 60 65
gtg gag gtt ctc aat gat ttg ggt gcc gtg ttg gcg ttg gat gga cac 355
Val Glu Val Leu Asn Asp Leu Gly Ala Val Leu Ala Leu Asp Gly His
70 75 80 85
aat gga atc ggc caa gtt tta gct gat cat gct cgt aaa gaa gca gtg 403
Asn Gly Ile Gly Gln Val Leu Ala Asp His Ala Arg Lys Glu Ala Val
90 95 100
act agg gca atg atg ttc ggc atc ggt gcg gtg tcg gtg cgc aac tcc 451
Thr Arg Ala Met Met Phe Gly Ile Gly Ala Val Ser Val Arg Asn Ser
105 110 115
aat cat ttt gga act gcc atg tac tac acc cgg aaa gcg gca gcg caa 499
Asn His Phe Gly Thr Ala Met Tyr Tyr Thr Arg Lys Ala Ala Ala Gln
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gga tgt gtt tcc att ctc acc acc aat gca tct ccg gcg atg gcg ccc 547

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Trp	Gly	Gly	Arg	Glu	Lys	Arg	Ile	Gly	Thr	Asn	Pro	Trp	Ser	Ile	Ala		
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gca	cct	ttt	gga	gaa	acg	gct	acg	gta	gtc	gat	ata	gcc	aat	act	gcg	643	
Ala	Pro	Phe	Gly	Glu	Thr	Ala	Thr	Val	Val	Asp	Ile	Ala	Asn	Thr	Ala		
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Val	Ala	Arg	Gly	Lys	Ile	Tyr	His	Ala	Arg	Gln	Thr	Asn	Met	Pro	Ile		
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cct	gag	act	tgg	gcg	atc	acg	agt	gag	ggc	gca	ccc	acc	acg	gat	cct	739	
Pro	Glu	Thr	Trp	Ala	Ile	Thr	Ser	Glu	Gly	Ala	Pro	Thr	Thr	Asp	Pro		
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Ala	Glu	Ala	Ile	Asn	Gly	Val	Val	Leu	Pro	Met	Ala	Gly	His	Lys	Gly		
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tat	gcg	att	agc	ttc	atg	atg	gat	gtg	ctt	tct	gga	gtt	ctc	act	ggg	835	
Tyr	Ala	Ile	Ser	Phe	Met	Met	Asp	Val	Leu	Ser	Gly	Val	Leu	Thr	Gly		
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tcc	cag	cac	agc	acc	aag	gta	cat	ggg	ccg	tat	gat	ccc	act	ccc	cca	883	
Ser	Gln	His	Ser	Thr	Lys	Val	His	Gly	Pro	Tyr	Asp	Pro	Thr	Pro	Pro		
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ggg	gga	gct	ggc	cac	ttg	ttc	atc	gcg	ttg	gat	gtt	gca	gcg	ttt	cgc	931	
Gly	Gly	Ala	Gly	His	Leu	Phe	Ile	Ala	Leu	Asp	Val	Ala	Ala	Phe	Arg		
			265					270					275				
gat	cca	caa	gat	ttc	gat	gac	gca	ctc	agc	gat	ctg	gtt	ggg	gaa	gtt	979	
Asp	Pro	Gln	Asp	Phe	Asp	Asp	Ala	Leu	Ser	Asp	Leu	Val	Gly	Glu	Val		
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aaa	tcc	act	ccg	aaa	gca	caa	aac	acc	gag	gag	att	ttc	tac	ccc	ggg	1027	
Lys	Ser	Thr	Pro	Lys	Ala	Gln	Asn	Thr	Glu	Glu	Ile	Phe	Tyr	Pro	Gly		
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Glu	Ser	Glu	Asp	Arg	Ala	His	Arg	Lys	Asn	Ser	Ala	His	Gly	Ile	Ser		
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Leu	Pro	Glu	Lys	Thr	Trp	Met	Glu	Leu	Gln	Glu	Leu	Ala	Ile	Glu	Asn		
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<211> 347

<212> PRT

<213> Corynebacterium glutamicum

<400> 20

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Val  Leu  Arg  Leu  Pro  Trp  Tyr  Val  Arg  Arg  Leu  His  Ser  Gly  Ala  Met
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Thr  Thr  His  Ala  His  Val  Glu  Val  Leu  Asn  Asp  Leu  Gly  Ala  Val  Leu
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Ala  Leu  Asp  Gly  His  Asn  Gly  Ile  Gly  Gln  Val  Leu  Ala  Asp  His  Ala
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Arg  Lys  Glu  Ala  Val  Thr  Arg  Ala  Met  Met  Phe  Gly  Ile  Gly  Ala  Val
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Ser  Val  Arg  Asn  Ser  Asn  His  Phe  Gly  Thr  Ala  Met  Tyr  Tyr  Thr  Arg
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Pro  Ala  Met  Ala  Pro  Trp  Gly  Gly  Arg  Glu  Lys  Arg  Ile  Gly  Thr  Asn
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Pro  Trp  Ser  Ile  Ala  Ala  Pro  Phe  Gly  Glu  Thr  Ala  Thr  Val  Val  Asp
      165              170              175

Ile  Ala  Asn  Thr  Ala  Val  Ala  Arg  Gly  Lys  Ile  Tyr  His  Ala  Arg  Gln
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Thr  Asn  Met  Pro  Ile  Pro  Glu  Thr  Trp  Ala  Ile  Thr  Ser  Glu  Gly  Ala
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Pro  Thr  Thr  Asp  Pro  Ala  Glu  Ala  Ile  Asn  Gly  Val  Val  Leu  Pro  Met
      210              215              220

Ala  Gly  His  Lys  Gly  Tyr  Ala  Ile  Ser  Phe  Met  Met  Asp  Val  Leu  Ser
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Asp  Pro  Thr  Pro  Pro  Gly  Gly  Ala  Gly  His  Leu  Phe  Ile  Ala  Leu  Asp
      260              265              270

Val  Ala  Ala  Phe  Arg  Asp  Pro  Gln  Asp  Phe  Asp  Asp  Ala  Leu  Ser  Asp
      275              280              285

Leu  Val  Gly  Glu  Val  Lys  Ser  Thr  Pro  Lys  Ala  Gln  Asn  Thr  Glu  Glu
      290              295              300

Ile  Phe  Tyr  Pro  Gly  Glu  Ser  Glu  Asp  Arg  Ala  His  Arg  Lys  Asn  Ser
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 <223> RXA01350

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 Met Asn Ser Pro Gln
 1 5
 aac gtc tcc acc aag aag gtc acc gtc acc ggc gca gct ggt caa atc 163
 Asn Val Ser Thr Lys Lys Val Thr Val Thr Gly Ala Ala Gly Gln Ile
 10 15 20
 tct tat tca ctg ttg tgg cgc atc gcc aac ggt gaa gta ttc ggc acc 211
 Ser Tyr Ser Leu Leu Trp Arg Ile Ala Asn Gly Glu Val Phe Gly Thr
 25 30 35
 gac acc cct gta gaa ctg aaa ctt ctg gag atc cct cag gct ctt ggc 259
 Asp Thr Pro Val Glu Leu Lys Leu Leu Glu Ile Pro Gln Ala Leu Gly
 40 45 50
 ggg gca gag ggt gtg gct atg gaa ctt ctg gat tct gcc ttc ccc ctc 307
 Gly Ala Glu Gly Val Ala Met Glu Leu Leu Asp Ser Ala Phe Pro Leu
 55 60 65
 ctg cga aac atc acc atc acc gcg gat gcc aat gag gca ttc gac ggc 355
 Leu Arg Asn Ile Thr Ile Thr Ala Asp Ala Asn Glu Ala Phe Asp Gly
 70 75 80 85
 gct aat gcg gcg ttt ttg gtc ggt gcg aag cct cgc gga aaa ggc gaa 403
 Ala Asn Ala Ala Phe Leu Val Gly Ala Lys Pro Arg Gly Lys Gly Glu
 90 95 100
 gag cgc gca gat ttg ctg gct aac aac ggc aag att ttc gga cct caa 451
 Glu Arg Ala Asp Leu Leu Ala Asn Asn Gly Lys Ile Phe Gly Pro Gln
 105 110 115
 ggt aaa gct atc aat gac aac gcc gca gat gac att cgt gtc cta gtt 499
 Gly Lys Ala Ile Asn Asp Asn Ala Ala Asp Asp Ile Arg Val Leu Val
 120 125 130
 gtt gga aac cca gcg aac acc aac gcg ttg att gct tca gct gcg gcc 547
 Val Gly Asn Pro Ala Asn Thr Asn Ala Leu Ile Ala Ser Ala Ala Ala
 135 140 145
 cca gat gtt cca gca tcc cgc ttc aac gca atg atg cgc ctt gat cac 595

Pro Asp Val Pro Ala Ser Arg Phe Asn Ala Met Met Arg Leu Asp His
 150 155 160 165

aac cgt gcg atc tcc cag ctg gcc acc aag ctt ggc cgt gga tct gcg 643
 Asn Arg Ala Ile Ser Gln Leu Ala Thr Lys Leu Gly Arg Gly Ser Ala
 170 175 180

gaa ttt aac aac att gtg gtc tgg gga aat cac tcc gca acc cag ttc 691
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 185 190 195

cca gac atc acc tac gca acc gtt ggt gga gaa aag gtc act gac ctg 739
 Pro Asp Ile Thr Tyr Ala Thr Val Gly Gly Glu Lys Val Thr Asp Leu
 200 205 210

gtt gat cac gat tgg tat gtg gag gag ttc att cct cgc gtg gct aac 787
 Val Asp His Asp Trp Tyr Val Glu Glu Phe Ile Pro Arg Val Ala Asn
 215 220 225

cgt ggc gct gaa atc att gag gtc cgt gga aag tct tct gca gct tct 835
 Arg Gly Ala Glu Ile Ile Glu Val Arg Gly Lys Ser Ser Ala Ala Ser
 230 235 240 245

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 Ala Ala Ser Ser Ala Ile Asp His Met Arg Asp Trp Val Gln Gly Thr
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 Glu Ala Trp Ser Ser Ala Ala Ile Pro Ser Thr Gly Ala Tyr Gly Ile
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 Pro Glu Gly Ile Phe Val Gly Leu Pro Thr Val Ser Arg Asn Gly Glu
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 Trp Glu Ile Val Glu Gly Leu Glu Ile Ser Asp Phe Gln Arg Ala Arg
 295 300 305

atc gac gcg aat gct cag gaa ttg cag gcc gag cgc gag gca gtg cgc 1075
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<212> PRT

<213> Corynebacterium glutamicum

<400> 22

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35	40	45
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Glu Ala Phe Asp Gly Ala Asn Ala Ala Phe Leu Val Gly Ala Lys Pro 85 90 95		
Arg Gly Lys Gly Glu Glu Arg Ala Asp Leu Leu Ala Asn Asn Gly Lys 100 105 110		
Ile Phe Gly Pro Gln Gly Lys Ala Ile Asn Asp Asn Ala Ala Asp Asp 115 120 125		
Ile Arg Val Leu Val Val Gly Asn Pro Ala Asn Thr Asn Ala Leu Ile 130 135 140		
Ala Ser Ala Ala Ala Pro Asp Val Pro Ala Ser Arg Phe Asn Ala Met 145 150 155 160		
Met Arg Leu Asp His Asn Arg Ala Ile Ser Gln Leu Ala Thr Lys Leu 165 170 175		
Gly Arg Gly Ser Ala Glu Phe Asn Asn Ile Val Val Trp Gly Asn His 180 185 190		
Ser Ala Thr Gln Phe Pro Asp Ile Thr Tyr Ala Thr Val Gly Gly Glu 195 200 205		
Lys Val Thr Asp Leu Val Asp His Asp Trp Tyr Val Glu Glu Phe Ile 210 215 220		
Pro Arg Val Ala Asn Arg Gly Ala Glu Ile Ile Glu Val Arg Gly Lys 225 230 235 240		
Ser Ser Ala Ala Ser Ala Ala Ser Ser Ala Ile Asp His Met Arg Asp 245 250 255		
Trp Val Gln Gly Thr Glu Ala Trp Ser Ser Ala Ala Ile Pro Ser Thr 260 265 270		
Gly Ala Tyr Gly Ile Pro Glu Gly Ile Phe Val Gly Leu Pro Thr Val 275 280 285		
Ser Arg Asn Gly Glu Trp Glu Ile Val Glu Gly Leu Glu Ile Ser Asp 290 295 300		
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<212> DNA

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<222> (101)..(1069)

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                                         1 5

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                        10 15 20

ggg ctt gtc gac gaa tcc ggg cgc atc gtg acc agt ttg tcg gcg ccg 211
Gly Leu Val Asp Glu Ser Gly Arg Ile Val Thr Ser Leu Ser Ala Pro
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tcg ccg cgc acg acg cag gca atg gaa cag ggg att ttt gat cta gtc 259
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Leu Pro Trp Arg Asp Glu Pro Val Arg Glu Lys Leu Glu Asn Leu Leu
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Glu His Arg Phe Gly Ala Ala Gln Gly Ala Asp Asn Trp Val Leu Leu
                        120 125 130

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Ala Leu Gly Thr Gly Ile Gly Ala Ala Leu Ile Glu Lys Gly Glu Ile
                        135 140 145

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Tyr Arg Gly Ala Tyr Gly Thr Ala Pro Glu Phe Gly His Leu Arg Val
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Val Arg Gly Gly Arg Ala Cys Ala Cys Gly Lys Glu Gly Cys Leu Glu
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cgt tac tgt tcc ggt act gcc ttg gtt tac act gcg cgt gaa ttg gct 691
Arg Tyr Cys Ser Gly Thr Ala Leu Val Tyr Thr Ala Arg Glu Leu Ala
                        185 190 195

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 Asp Pro Asn Ser Ile Asn Gly Lys Thr Ile Thr Ala Ala Ala Arg Gln
 215 220 225
 gaa gac cca ctt gct ctc gcc gtt ctg gaa gat ttc agc gag tgg ctg 835
 Glu Asp Pro Leu Ala Leu Ala Val Leu Glu Asp Phe Ser Glu Trp Leu
 230 235 240 245
 ggc gaa act ttg gcg atc att gct gat gtc ctt gac cca ggc atg atc 883
 Gly Glu Thr Leu Ala Ile Ile Ala Asp Val Leu Asp Pro Gly Met Ile
 250 255 260
 atc att ggt ggc gga ctg tcc aat gct gcc gac ctt tat ttg gat cgc 931
 Ile Ile Gly Gly Gly Leu Ser Asn Ala Ala Asp Leu Tyr Leu Asp Arg
 265 270 275
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 Ser Val Asn His Tyr Ser Thr Arg Ile Val Gly Ala Gly Tyr Arg Pro
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 295 300 305
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<211> 323

<212> PRT

<213> Corynebacterium glutamicum

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 20 25 30

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 35 40 45

Ile Phe Asp Leu Val Glu Gln Leu Lys Ala Glu Tyr Pro Val Gly Ala
 50 55 60

Val Gly Leu Ala Val Ala Gly Phe Leu Asp Pro Glu Cys Glu Val Val
 65 70 75 80

Arg Phe Ala Pro His Leu Pro Trp Arg Asp Glu Pro Val Arg Glu Lys
 85 90 95

Leu Glu Asn Leu Leu Gly Leu Pro Val Arg Leu Glu His Asp Ala Asn
 100 105 110

Ser Ala Ala Trp Gly Glu His Arg Phe Gly Ala Ala Gln Gly Ala Asp
 115 120 125
 Asn Trp Val Leu Leu Ala Leu Gly Thr Gly Ile Gly Ala Ala Leu Ile
 130 135 140
 Glu Lys Gly Glu Ile Tyr Arg Gly Ala Tyr Gly Thr Ala Pro Glu Phe
 145 150 155 160
 Gly His Leu Arg Val Val Arg Gly Gly Arg Ala Cys Ala Cys Gly Lys
 165 170 175
 Glu Gly Cys Leu Glu Arg Tyr Cys Ser Gly Thr Ala Leu Val Tyr Thr
 180 185 190
 Ala Arg Glu Leu Ala Ser His Gly Ser Phe Arg Asn Ser Gly Leu Phe
 195 200 205
 Asp Lys Ile Lys Ala Asp Pro Asn Ser Ile Asn Gly Lys Thr Ile Thr
 210 215 220
 Ala Ala Ala Arg Gln Glu Asp Pro Leu Ala Leu Ala Val Leu Glu Asp
 225 230 235 240
 Phe Ser Glu Trp Leu Gly Glu Thr Leu Ala Ile Ile Ala Asp Val Leu
 245 250 255
 Asp Pro Gly Met Ile Ile Ile Gly Gly Gly Leu Ser Asn Ala Ala Asp
 260 265 270
 Leu Tyr Leu Asp Arg Ser Val Asn His Tyr Ser Thr Arg Ile Val Gly
 275 280 285
 Ala Gly Tyr Arg Pro Leu Ala Arg Val Ala Thr Ala Gln Leu Gly Ala
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 <222> (101)..(1762)
 <223> RXA01814

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 Met Ala His Glu Arg
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Ala Gly Gln Leu Ala Gln Pro Glu Asp Leu Ile Asp Val Ala Glu Leu	
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Val Thr Ala Tyr Phe Thr Arg Lys Pro Asp Val Asn Asn Pro Asp Gln	
25 30 35	
cag gtc gct ttc ggc acc tcc gga cac cgt ggc ttc gcg ctg gac agc	259
Gln Val Ala Phe Gly Thr Ser Gly His Arg Gly Phe Ala Leu Asp Ser	
40 45 50	
gct ttc aac gag gac cac atc ctg gca acc acc cag gcg atc gtc gac	307
Ala Phe Asn Glu Asp His Ile Leu Ala Thr Thr Gln Ala Ile Val Asp	
55 60 65	
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Tyr Arg Asn Gln Gln Pro Lys Asn Trp Val Gly Pro Leu Phe Ile Gly	
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Arg Asp Thr His Ala Leu Ser Glu Pro Ala Met Ile Ser Ala Leu Glu	
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Val Leu Ile Ala Asn Asp Val Glu Val Leu Val Asp Ala Asp Gly Arg	
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Tyr Thr Pro Thr Pro Ala Val Ser His Ala Ile Leu Arg His Asn Asp	
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Gly Ile Ile Leu Gly Thr Ala Gly Pro Ser Arg Pro Tyr Ala Asp Gly	
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Ile Val Ile Thr Pro Ser His Asn Pro Pro Arg Asp Gly Gly Phe Lys	
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Tyr Asn Pro Ala Asn Gly Gly Pro Ala Asp Thr Asp Ala Thr Asp Trp	
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atc gcc aac cgc gcc aac gat att ctg cgc ggc gac ctt gca gac gtg	691
Ile Ala Asn Arg Ala Asn Asp Ile Leu Arg Gly Asp Leu Ala Asp Val	
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Lys Arg Val Pro Val Ser Gly Val Leu Asp Glu Arg Thr Thr Ala Tyr	
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Asp Phe Lys Gly Ile Tyr Ile Ala Asp Leu Pro Asn Val Val Asn Ile	
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Asp Ala Ile Arg Glu Ala Gly Val Arg Ile Gly Ala Asp Pro Met Gly	
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Asn	Leu	Thr	Val	Val	Asn	Pro	His	Val	Asp	Ser	Thr	Phe	Arg	Phe	Met	
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Ala	Met	Ala	Ser	Leu	Ile	Asp	Asn	Arg	Asp	Lys	Phe	Asp	Val	Ala	Thr	
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Phe	Ala	His	Arg	Pro	Gly	Trp	Ser	Ala	Asp	Thr	Ala	Val	Gly	Lys	Thr	
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Leu	Val	Ser	Ser	Ser	Met	Ile	Asp	Arg	Val	Val	Ala	Gln	Leu	Gly	Arg	
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acc	ctc	gtt	gag	gtt	cca	gtc	gga	ttc	aag	tgg	ttt	gtc	cca	ggg	ttg	1267
Thr	Leu	Val	Glu	Val	Pro	Val	Gly	Phe	Lys	Trp	Phe	Val	Pro	Gly	Leu	
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Ile	Ser	Gly	Glu	Ile	Gly	Phe	Gly	Gly	Glu	Glu	Ser	Ala	Gly	Ala	Ser	
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Phe	Leu	Arg	Met	Asp	Gly	Thr	Thr	Trp	Ser	Thr	Asp	Lys	Asp	Gly	Leu	
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atc	ctt	gac	ctc	ctg	gca	gct	gag	atc	att	gca	gta	acc	ggc	aag	acc	1411
Ile	Leu	Asp	Leu	Leu	Ala	Ala	Glu	Ile	Ile	Ala	Val	Thr	Gly	Lys	Thr	
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Pro	Ser	Gln	Arg	Tyr	Ala	Glu	Leu	Ala	Glu	Glu	Phe	Gly	Ala	Pro	Ala	
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Tyr	Ala	Arg	Thr	Asp	Ala	Glu	Ala	Asn	Arg	Glu	Gln	Lys	Ala	Ile	Leu	
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Lys	Ala	Leu	Ser	Pro	Glu	Gln	Val	Thr	Ala	Thr	Glu	Leu	Ala	Gly	Glu	
470					475				480						485	
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Ser Gly Thr Glu Asp Lys Tyr Lys Ile Tyr Ala Glu Ser Phe Lys Gly				
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Glu Glu His Leu Ala Gln Val Gln Lys Glu Ala Gln Ala Leu Val Ser				
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<213> Corynebacterium glutamicum

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Phe	Ala	Leu	Asp	Ser	Ala	Phe	Asn	Glu	Asp	His	Ile	Leu	Ala	Thr	Thr
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Gln	Ala	Ile	Val	Asp	Tyr	Arg	Asn	Gln	Gln	Pro	Lys	Asn	Trp	Val	Gly
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Pro	Leu	Phe	Ile	Gly	Arg	Asp	Thr	His	Ala	Leu	Ser	Glu	Pro	Ala	Met
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Ile	Ser	Ala	Leu	Glu	Val	Leu	Ile	Ala	Asn	Asp	Val	Glu	Val	Leu	Val
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Asp	Ala	Asp	Gly	Arg	Tyr	Thr	Pro	Thr	Pro	Ala	Val	Ser	His	Ala	Ile
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Leu	Arg	His	Asn	Asp	Gly	Ile	Ile	Leu	Gly	Thr	Ala	Gly	Pro	Ser	Arg
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Pro	Tyr	Ala	Asp	Gly	Ile	Val	Ile	Thr	Pro	Ser	His	Asn	Pro	Pro	Arg
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 Arg Thr Thr Ala Tyr Asp Phe Lys Gly Ile Tyr Ile Ala Asp Leu Pro
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 225 230 235 240
 Ala Asp Pro Met Gly Gly Ala Ser Val Asp Tyr Trp Gly Ala Ile Ala
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 Glu Thr His Gly Leu Asn Leu Thr Val Val Asn Pro His Val Asp Ser
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 Thr Phe Arg Phe Met Thr Leu Asp Thr Asp Gly Lys Ile Arg Met Asp
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 Cys Ser Ser Pro His Ala Met Ala Ser Leu Ile Asp Asn Arg Asp Lys
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 Phe Asp Val Ala Thr Gly Asn Asp Ala Asp Ala Asp Arg His Gly Ile
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 Val Thr Pro Asp Ala Gly Leu Met Asn Pro Asn His Tyr Leu Ala Val
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 Ala Ile Glu Tyr Leu Phe Ala His Arg Pro Gly Trp Ser Ala Asp Thr
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 Ala Val Gly Lys Thr Leu Val Ser Ser Ser Met Ile Asp Arg Val Val
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 Ala Gln Leu Gly Arg Thr Leu Val Glu Val Pro Val Gly Phe Lys Trp
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 Phe Val Pro Gly Leu Ile Ser Gly Glu Ile Gly Phe Gly Gly Glu Glu
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 Ser Ala Gly Ala Ser Phe Leu Arg Met Asp Gly Thr Thr Trp Ser Thr
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Gln Gly Val Asp Val Ile Arg Val Gly Val Ile Pro Thr Pro Ala Val	
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Ala Phe Leu Thr Asp Asp Tyr Gly Ala Asp Met Gly Val Met Ile Ser	
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Ala Ser His Asn Pro Met Pro Asp Asn Gly Ile Lys Phe Phe Ser Ala	
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Gly Gly His Lys Leu Pro Asp His Val Glu Asp Glu Ile Glu Arg Val	
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Met Asp Ser Leu Pro Ala Glu Gly Pro Thr Gly His Gly Val Gly Arg	
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gtc atc gaa gaa gca acc gat gca cag gac cgt tac cta gag cac ctg	336
Val Ile Glu Glu Ala Thr Asp Ala Gln Asp Arg Tyr Leu Glu His Leu	
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Lys Glu Ala Val Pro Thr Ser Leu Glu Gly Ile Lys Ile Val Val Asp	
115 120 125	
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Ala Ala Asn Gly Ala Ala Ser Val Val Ala Pro Thr Ala Tyr Glu Ala	
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gcg ggt gca act gta att gct att cat aac aag cca gac tca tac aac	480
Ala Gly Ala Thr Val Ile Ala Ile His Asn Lys Pro Asp Ser Tyr Asn	
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Val Leu Lys His Gly Ala Asp Leu Gly Leu Ala His Asp Gly Asp Ala
      180                      185                      190

gac cgt tgt ttg gct gtg aac aag gat gcc aac ctt gtt gat ggt gac 624
Asp Arg Cys Leu Ala Val Asn Lys Asp Ala Asn Leu Val Asp Gly Asp
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Ala Ser His Asn Pro Met Pro Asp Asn Gly Ile Lys Phe Phe Ser Ala
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Gly Gly His Lys Leu Pro Asp His Val Glu Asp Glu Ile Glu Arg Val
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Met Asp Ser Leu Pro Ala Glu Gly Pro Thr Gly His Gly Val Gly Arg
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Val Ile Glu Glu Ala Thr Asp Ala Gln Asp Arg Tyr Leu Glu His Leu
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Lys Glu Ala Val Pro Thr Ser Leu Glu Gly Ile Lys Ile Val Val Asp
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Ala Ala Asn Gly Ala Ala Ser Val Val Ala Pro Thr Ala Tyr Glu Ala
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Ala Gly Ala Thr Val Ile Ala Ile His Asn Lys Pro Asp Ser Tyr Asn
      145         150         155         160

Ile Asn Met Asp Cys Gly Ser Thr His Ile Asp Gln Ala Gln Pro Pro
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Val Leu Lys His Gly Ala Asp Leu Gly Leu Ala His Asp Gly Asp Ala
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Asp Arg Cys Leu Ala Val Asn Lys Asp Ala Asn Leu Val Asp Gly Asp

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Gly Val Asp Val Ile Arg Val Gly Val Ile Pro Thr Pro Ala Val Ala	
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ttc ctc acc gat gat tat ggc gct gac atg ggc gtg atg att tct gca	144
Phe Leu Thr Asp Asp Tyr Gly Ala Asp Met Gly Val Met Ile Ser Ala	
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Ser His Asn Pro Met Pro Asp Asn Gly Ile Lys Phe Phe Ser Ala Gly	
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Gly His Lys Leu Pro Asp His Val Glu Asp Glu Ile Glu Arg Val Met	
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gac agc ttg cca gca gaa ggc cca aca ggg cat gga gtt ggc cgt gtc	288
Asp Ser Leu Pro Ala Glu Gly Pro Thr Gly His Gly Val Gly Arg Val	
85 90 95	
atc gaa gaa gca acc gat gca cag gac cgc tac cta gag cac ctg aag	336
Ile Glu Glu Ala Thr Asp Ala Gln Asp Arg Tyr Leu Glu His Leu Lys	
100 105 110	
gaa gct gtt cct acg tca ctt gaa ggc atc aag att gtt gtg gat gca	384
Glu Ala Val Pro Thr Ser Leu Glu Gly Ile Lys Ile Val Val Asp Ala	
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Ser His Asn Pro Met Pro Asp Asn Gly Ile Lys Phe Phe Ser Ala Gly	50	55	60
Gly His Lys Leu Pro Asp His Val Glu Asp Glu Ile Glu Arg Val Met	65	70	75
Asp Ser Leu Pro Ala Glu Gly Pro Thr Gly His Gly Val Gly Arg Val	85	90	95
Ile Glu Glu Ala Thr Asp Ala Gln Asp Arg Tyr Leu Glu His Leu Lys	100	105	110
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 1 5
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 Gln Leu Ser Phe Gly Thr Ala Gly Leu Arg Ala Pro Val Gly Pro Ala
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 Arg His Gln Met Asn Val Leu Gln Val Thr Arg Thr Thr Ala Gly Val
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 gct agt tgg ttg gca gaa cgt gcg gca cta aat cca gtg ccg cat ttg 259
 Ala Ser Trp Leu Ala Glu Arg Ala Ala Leu Asn Pro Val Pro His Leu
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 gtt cct gag gat gaa aca gga atc ggc agg gcg ttg tat ccc caa gat 307
 Val Pro Glu Asp Glu Thr Gly Ile Gly Arg Ala Leu Tyr Pro Gln Asp
 55 60 65
 ggt ccg ttg cgg gtc gtt gtg ggg tat gac gct cgc tat ggt tcg cat 355

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Thr	Phe	Ala	Ala	Thr	Thr	Ala	Glu	Val	Phe	Ala	Gly	Ala	Gly	Phe	Glu		
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Val	Thr	Leu	Leu	Pro	Thr	Pro	Ser	Pro	Thr	Pro	Leu	Ile	Pro	Trp	Leu		
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Asn	Gly	Ala	Ala	Asp	Asn	Gly	Tyr	Lys	Val	Phe	Leu	Ser	Asn	Gly	Arg		
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cag	ctt	tat	tct	gaa	ctg	gag	cct	gag	ctt	gag	gcg	cat	atc	aat	gct	595	
Gln	Leu	Tyr	Ser	Glu	Leu	Glu	Pro	Glu	Leu	Glu	Ala	His	Ile	Asn	Ala		
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Val	Val	Tyr	Thr	Ala	Leu	His	Gly	Val	Gly	Gly	Arg	Ala	Met	Ala	Asn		
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Gln	Tyr	Pro	Asp	Pro	Thr	Phe	Pro	Thr	Val	Ala	Phe	Pro	Asn	Pro	Glu		
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Glu	Pro	Ser	Ala	Ile	Glu	Leu	Leu	Leu	Glu	Arg	Ala	Lys	Glu	Lys	Asn		
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Ala	Asp	Ile	Leu	Phe	Ala	Leu	Asp	Pro	Asp	Ala	Asp	Arg	Cys	Ala	Val		
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Val	Gly	Thr	Leu	Leu	Ala	Thr	Arg	Leu	Val	Pro	Glu	Tyr	Ser	Gly	Glu		

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Gly Pro Arg Pro	Val Val Ala Thr	Thr Val Val Ser	Ser Gln Leu Leu	
	330	335	340	
ggt atc atc gcc	gag gat aaa ggg	tgg gat tat tcc	gag aca ctg acg	1171
Gly Ile Ile Ala	Glu Asp Lys Gly	Trp Asp Tyr Ser	Glu Thr Leu Thr	
	345	350	355	
gga ttc aaa aat	ctg tcg agg gct	gcc gat ggt ctc	gac gga ccg ctt	1219
Gly Phe Lys Asn	Leu Ser Arg Ala	Ala Asp Gly Leu	Asp Gly Pro Leu	
	360	365	370	
gct ttc gct tat	gag gaa gct gtg	ggc acc tgc ccg	gtt cca gat gtc	1267
Ala Phe Ala Tyr	Glu Glu Ala Val	Gly Thr Cys Pro	Val Pro Asp Val	
	375	380	385	
gtg ccg gat aag	gac ggc atc tct	aca gcg ttg ttc	atg gcg tcg tgg	1315
Val Pro Asp Lys	Asp Gly Ile Ser	Thr Ala Leu Phe	Met Ala Ser Trp	
	390	395	405	
gct gcc gaa ctg	aag gct cag ggc	gca agc ctg cag	caa aaa ctc aat	1363
Ala Ala Glu Leu	Lys Ala Gln Gly	Ala Ser Leu Gln	Gln Lys Leu Asn	
	410	415	420	
gag ttg tat cgc	cga tat ggg tat	ttt gcg tcc tcg	caa att gct gtg	1411
Glu Leu Tyr Arg	Arg Tyr Gly Tyr	Phe Ala Ser Ser	Gln Ile Ala Val	
	425	430	435	
cgc acg agc agt	cca cgc gag tta	gtt gat cac tgg	att gcg cat cct	1459
Arg Thr Ser Ser	Pro Arg Glu Leu	Val Asp His Trp	Ile Ala His Pro	
	440	445	450	
cag caa gaa ctc	att gga gtg tct	gtc acc cca cat	att ctt cct gaa	1507
Gln Gln Glu Leu	Ile Gly Val Ser	Val Thr Pro His	Ile Leu Pro Glu	
	455	460	465	
aaa cag ggc att	gct ttg cat ggc	cag gtg ggg cat	gtg cat atc cgt	1555
Lys Gln Gly Ile	Ala Leu His Gly	Gln Val Gly His	Val His Ile Arg	
	470	475	485	
gct att ggt cga	gtc tct gga act	gag gcg aaa gcc	aag ctc tat ttg	1603
Ala Ile Gly Arg	Val Ser Gly Thr	Glu Ala Lys Ala	Lys Leu Tyr Leu	
	490	495	500	
gaa gtt ggt cag	gcc agc tcc cat	gat gaa gca gct	cag ttg ttg cat	1651
Glu Val Gly Gln	Ala Ser Ser His	Asp Glu Ala Ala	Gln Leu Leu His	
	505	510	515	
cag ctg gag gat	gaa gtc caa agc	tgg ttg agc aag	ctt tagtttcctg	1700
Gln Leu Glu Asp	Glu Val Gln Ser	Trp Leu Ser Lys	Leu	
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<211> 530

<212> PRT

<213> Corynebacterium glutamicum

<400> 32

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 Thr Thr Ala Gly Val Ala Ser Trp Leu Ala Glu Arg Ala Ala Leu Asn
 35 40 45
 Pro Val Pro His Leu Val Pro Glu Asp Glu Thr Gly Ile Gly Arg Ala
 50 55 60
 Leu Tyr Pro Gln Asp Gly Pro Leu Arg Val Val Val Gly Tyr Asp Ala
 65 70 75 80
 Arg Tyr Gly Ser His Thr Phe Ala Ala Thr Thr Ala Glu Val Phe Ala
 85 90 95
 Gly Ala Gly Phe Glu Val Thr Leu Leu Pro Thr Pro Ser Pro Thr Pro
 100 105 110
 Leu Ile Pro Trp Leu Val Asn Lys His Gly Leu Asp Ala Gly Val Gln
 115 120 125
 Ile Thr Ala Ser His Asn Gly Ala Ala Asp Asn Gly Tyr Lys Val Phe
 130 135 140
 Leu Ser Asn Gly Arg Gln Leu Tyr Ser Glu Leu Glu Pro Glu Leu Glu
 145 150 155 160
 Ala His Ile Asn Ala Val Glu Asp Pro Ile Arg Val Pro Arg Val Thr
 165 170 175
 Val Arg Pro Thr Ala Asp Gln Leu Arg Arg Tyr Val Asp Glu Met Val
 180 185 190
 Ser Leu Val Thr Pro Asp Gln Ala Asp Leu Leu Arg Val Asn Ser Glu
 195 200 205
 Arg Gly Asn Leu Arg Val Val Tyr Thr Ala Leu His Gly Val Gly Gly
 210 215 220
 Arg Ala Met Ala Asn Ala Phe Gln Phe Ala Gly Phe Pro His Thr His
 225 230 235 240
 Gly Val Lys Ala Gln Gln Tyr Pro Asp Pro Thr Phe Pro Thr Val Ala
 245 250 255
 Phe Pro Asn Pro Glu Glu Pro Ser Ala Ile Glu Leu Leu Leu Glu Arg
 260 265 270
 Ala Lys Glu Lys Asn Ala Asp Ile Leu Phe Ala Leu Asp Pro Asp Ala
 275 280 285
 Asp Arg Cys Ala Val Gly Ile Arg Thr Ala Asp Gly Gly His Arg Met
 290 295 300
 Leu Ser Gly Asp Glu Val Gly Thr Leu Leu Ala Thr Arg Leu Val Pro
 305 310 315 320

Glu Tyr Ser Gly Glu Gly Pro Arg Pro Val Val Ala Thr Thr Val Val
 325 330 335
 Ser Ser Gln Leu Leu Gly Ile Ile Ala Glu Asp Lys Gly Trp Asp Tyr
 340 345 350
 Ser Glu Thr Leu Thr Gly Phe Lys Asn Leu Ser Arg Ala Ala Asp Gly
 355 360 365
 Leu Asp Gly Pro Leu Ala Phe Ala Tyr Glu Glu Ala Val Gly Thr Cys
 370 375 380
 Pro Val Pro Asp Val Val Pro Asp Lys Asp Gly Ile Ser Thr Ala Leu
 385 390 395 400
 Phe Met Ala Ser Trp Ala Ala Glu Leu Lys Ala Gln Gly Ala Ser Leu
 405 410 415
 Gln Gln Lys Leu Asn Glu Leu Tyr Arg Arg Tyr Gly Tyr Phe Ala Ser
 420 425 430
 Ser Gln Ile Ala Val Arg Thr Ser Ser Pro Arg Glu Leu Val Asp His
 435 440 445
 Trp Ile Ala His Pro Gln Gln Glu Leu Ile Gly Val Ser Val Thr Pro
 450 455 460
 His Ile Leu Pro Glu Lys Gln Gly Ile Ala Leu His Gly Gln Val Gly
 465 470 475 480
 His Val His Ile Arg Ala Ile Gly Arg Val Ser Gly Thr Glu Ala Lys
 485 490 495
 Ala Lys Leu Tyr Leu Glu Val Gly Gln Ala Ser Ser His Asp Glu Ala
 500 505 510
 Ala Gln Leu Leu His Gln Leu Glu Asp Glu Val Gln Ser Trp Leu Ser
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 Lys Leu
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<210> 33
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 <212> DNA
 <213> *Corynebacterium glutamicum*

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 <222> (101)..(1684)
 <223> FRXA02854

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 Met Asp Glu Ser Arg
 1 5

cag ctt agt ttc ggc aca gca ggg ttg cgt gca cca gtt ggc ccg gcg	163
Gln Leu Ser Phe Gly Thr Ala Gly Leu Arg Ala Pro Val Gly Pro Ala	
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cgc cat cag atg aat gtt ttg cag gta acc aga act aca gca ggt gtt	211
Arg His Gln Met Asn Val Leu Gln Val Thr Arg Thr Thr Ala Gly Val	
25 30 35	
gct agt tgg ttg gca gaa cgt gcg gca cta aat cca gtg ccg cat ttg	259
Ala Ser Trp Leu Ala Glu Arg Ala Ala Leu Asn Pro Val Pro His Leu	
40 45 50	
gtt cct gag gat gaa aca gga atc ggc agg gcg ttg tat ccc caa gat	307
Val Pro Glu Asp Glu Thr Gly Ile Gly Arg Ala Leu Tyr Pro Gln Asp	
55 60 65	
ggt ccg ttg cgg gtc gtt gtg ggg tat gac gct cgc tat ggt tcg cat	355
Gly Pro Leu Arg Val Val Val Gly Tyr Asp Ala Arg Tyr Gly Ser His	
70 75 80 85	
act ttt gct gca acc act gcg gag gtg ttc gcg ggt gct ggt ttt gag	403
Thr Phe Ala Ala Thr Thr Ala Glu Val Phe Ala Gly Ala Gly Phe Glu	
90 95 100	
gtg acg ttg ctc ccc acg cct agc cct acg ccg ttg att ccg tgg ttg	451
Val Thr Leu Leu Pro Thr Pro Ser Pro Thr Pro Leu Ile Pro Trp Leu	
105 110 115	
gtg aac aag cat ggg ttg gat gcg ggc gtt cag atc acg gct tcg cat	499
Val Asn Lys His Gly Leu Asp Ala Gly Val Gln Ile Thr Ala Ser His	
120 125 130	
aat ggt gcg gcg gac aat ggc tac aag gtg ttt ttg tct aat ggt cgc	547
Asn Gly Ala Ala Asp Asn Gly Tyr Lys Val Phe Leu Ser Asn Gly Arg	
135 140 145	
cag ctt tat tct gaa ctg gag cct gag ctt gag gcg cat atc aat gct	595
Gln Leu Tyr Ser Glu Leu Glu Pro Glu Leu Glu Ala His Ile Asn Ala	
150 155 160 165	
gtg gaa gat ccg att cgg gtt cct cgg gtg acg gtg cgc ccc act gct	643
Val Glu Asp Pro Ile Arg Val Pro Arg Val Thr Val Arg Pro Thr Ala	
170 175 180	
gat cag ctg cgt cga tat gtt gat gag atg gtg tcg ttg gtg act cct	691
Asp Gln Leu Arg Arg Tyr Val Asp Glu Met Val Ser Leu Val Thr Pro	
185 190 195	
gat cag gct gat ttg ttg cgg gtg aat tct gag cgg ggc aat ctt cgc	739
Asp Gln Ala Asp Leu Leu Arg Val Asn Ser Glu Arg Gly Asn Leu Arg	
200 205 210	
gtg gtg tat acc gct ctg cat ggt gtg ggt ggc cgc gcg atg gcc aat	787
Val Val Tyr Thr Ala Leu His Gly Val Gly Gly Arg Ala Met Ala Asn	
215 220 225	
gct ttc caa ttt gct ggt ttt ccc cat act cat ggc gtg aag gct cag	835
Ala Phe Gln Phe Ala Gly Phe Pro His Thr His Gly Val Lys Ala Gln	
230 235 240 245	
cag tat cct gat ccc acc ttc ccc act gtg gcg ttc ccc aat ccg gaa	883

Gln Tyr Pro Asp	Pro Thr Phe Pro Thr Val Ala Phe Pro Asn Pro Glu	
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Glu Pro Ser Ala Ile Glu Leu Leu Glu Arg Ala Lys Glu Lys Asn		
	265 270 275	
gct gac att ttg ttt gcg ctt gat cct gat gcc gat cgt tgt gct gtg	979	
Ala Asp Ile Leu Phe Ala Leu Asp Pro Asp Ala Asp Arg Cys Ala Val		
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ggc att cgt acc gct gat ggc ggc cac cga atg ctc tct ggc gat gag	1027	
Gly Ile Arg Thr Ala Asp Gly Gly His Arg Met Leu Ser Gly Asp Glu		
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gtg ggc aca ctt ttg gct act cgt ttg gtt ccg gag tat tcc ggt gaa	1075	
Val Gly Thr Leu Leu Ala Thr Arg Leu Val Pro Glu Tyr Ser Gly Glu		
	310 315 320 325	
ggc cca cgt ccc gtg gtt gcc acc acg gtg gtg tct tcg cag ctt ctg	1123	
Gly Pro Arg Pro Val Val Ala Thr Thr Val Val Ser Ser Gln Leu Leu		
	330 335 340	
ggc atc atc gcc gag gat aaa ggc tgg gat tat tcc gag aca ctg acg	1171	
Gly Ile Ile Ala Glu Asp Lys Gly Trp Asp Tyr Ser Glu Thr Leu Thr		
	345 350 355	
gga ttc aaa aat ctg tcg agg gct gcc gat ggt ctc gac gga ccg ctt	1219	
Gly Phe Lys Asn Leu Ser Arg Ala Ala Asp Gly Leu Asp Gly Pro Leu		
	360 365 370	
gct ttc gct tat gag gaa gct gtg ggc acc tgc ccg gtt cca gat gtc	1267	
Ala Phe Ala Tyr Glu Glu Ala Val Gly Thr Cys Pro Val Pro Asp Val		
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gtg ccg gat aag gac ggc atc tct aca gcg ttg ttc atg gcg tcg tgg	1315	
Val Pro Asp Lys Asp Gly Ile Ser Thr Ala Leu Phe Met Ala Ser Trp		
	390 395 400 405	
gct gcc gaa ctg aag gct cag ggc gca agc ctg cag caa aaa ctc aat	1363	
Ala Ala Glu Leu Lys Ala Gln Gly Ala Ser Leu Gln Gln Lys Leu Asn		
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Glu Leu Tyr Arg Arg Tyr Gly Tyr Phe Ala Ser Ser Gln Ile Ala Val		
	425 430 435	
cgc acg agc agt cca cgc gag tta gtt gat cac tgg att gcg cat cct	1459	
Arg Thr Ser Ser Pro Arg Glu Leu Val Asp His Trp Ile Ala His Pro		
	440 445 450	
cag caa gaa ctc att gga gtg tct gtc acc cca cat att ctt cct gaa	1507	
Gln Gln Glu Leu Ile Gly Val Ser Val Thr Pro His Ile Leu Pro Glu		
	455 460 465	
aaa cag ggc att gct ttg cat ggc cag gtg ggc cat gtg cat atc cgt	1555	
Lys Gln Gly Ile Ala Leu His Gly Gln Val Gly His Val His Ile Arg		
	470 475 480 485	
gct att ggt cga gtc tct gga act gag gcg aaa gcc aag ctc tat ttg	1603	
Ala Ile Gly Arg Val Ser Gly Thr Glu Ala Lys Ala Lys Leu Tyr Leu		

490										495					500					
gaa gtt ggt cag gcc agc tcc cat gat gaa gca gct cag ttg ttg cat																1651				
Glu Val Gly Gln Ala Ser Ser His Asp Glu Ala Ala Gln Leu Leu His																				
505											510						515			

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Gln Leu Glu Asp Glu Val Gln Ser Trp Leu Ser																	
520											525						

<210> 34
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 <212> PRT
 <213> Corynebacterium glutamicum

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 35 40 45
 Pro Val Pro His Leu Val Pro Glu Asp Glu Thr Gly Ile Gly Arg Ala
 50 55 60
 Leu Tyr Pro Gln Asp Gly Pro Leu Arg Val Val Val Gly Tyr Asp Ala
 65 70 75 80
 Arg Tyr Gly Ser His Thr Phe Ala Ala Thr Thr Ala Glu Val Phe Ala
 85 90 95
 Gly Ala Gly Phe Glu Val Thr Leu Leu Pro Thr Pro Ser Pro Thr Pro
 100 105 110
 Leu Ile Pro Trp Leu Val Asn Lys His Gly Leu Asp Ala Gly Val Gln
 115 120 125
 Ile Thr Ala Ser His Asn Gly Ala Ala Asp Asn Gly Tyr Lys Val Phe
 130 135 140
 Leu Ser Asn Gly Arg Gln Leu Tyr Ser Glu Leu Glu Pro Glu Leu Glu
 145 150 155 160
 Ala His Ile Asn Ala Val Glu Asp Pro Ile Arg Val Pro Arg Val Thr
 165 170 175
 Val Arg Pro Thr Ala Asp Gln Leu Arg Arg Tyr Val Asp Glu Met Val
 180 185 190
 Ser Leu Val Thr Pro Asp Gln Ala Asp Leu Leu Arg Val Asn Ser Glu
 195 200 205
 Arg Gly Asn Leu Arg Val Val Tyr Thr Ala Leu His Gly Val Gly Gly
 210 215 220
 Arg Ala Met Ala Asn Ala Phe Gln Phe Ala Gly Phe Pro His Thr His
 225 230 235 240

Gly Val Lys Ala Gln Gln Tyr Pro Asp Pro Thr Phe Pro Thr Val Ala
 245 250 255
 Phe Pro Asn Pro Glu Glu Pro Ser Ala Ile Glu Leu Leu Leu Glu Arg
 260 265 270
 Ala Lys Glu Lys Asn Ala Asp Ile Leu Phe Ala Leu Asp Pro Asp Ala
 275 280 285
 Asp Arg Cys Ala Val Gly Ile Arg Thr Ala Asp Gly Gly His Arg Met
 290 295 300
 Leu Ser Gly Asp Glu Val Gly Thr Leu Leu Ala Thr Arg Leu Val Pro
 305 310 315 320
 Glu Tyr Ser Gly Glu Gly Pro Arg Pro Val Val Ala Thr Thr Val Val
 325 330 335
 Ser Ser Gln Leu Leu Gly Ile Ile Ala Glu Asp Lys Gly Trp Asp Tyr
 340 345 350
 Ser Glu Thr Leu Thr Gly Phe Lys Asn Leu Ser Arg Ala Ala Asp Gly
 355 360 365
 Leu Asp Gly Pro Leu Ala Phe Ala Tyr Glu Glu Ala Val Gly Thr Cys
 370 375 380
 Pro Val Pro Asp Val Val Pro Asp Lys Asp Gly Ile Ser Thr Ala Leu
 385 390 395 400
 Phe Met Ala Ser Trp Ala Ala Glu Leu Lys Ala Gln Gly Ala Ser Leu
 405 410 415
 Gln Gln Lys Leu Asn Glu Leu Tyr Arg Arg Tyr Gly Tyr Phe Ala Ser
 420 425 430
 Ser Gln Ile Ala Val Arg Thr Ser Ser Pro Arg Glu Leu Val Asp His
 435 440 445
 Trp Ile Ala His Pro Gln Gln Glu Leu Ile Gly Val Ser Val Thr Pro
 450 455 460
 His Ile Leu Pro Glu Lys Gln Gly Ile Ala Leu His Gly Gln Val Gly
 465 470 475 480
 His Val His Ile Arg Ala Ile Gly Arg Val Ser Gly Thr Glu Ala Lys
 485 490 495
 Ala Lys Leu Tyr Leu Glu Val Gly Gln Ala Ser Ser His Asp Glu Ala
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 Ala Gln Leu Leu His Gln Leu Glu Asp Glu Val Gln Ser Trp Leu Ser
 515 520 525

<210> 35

<211> 536

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(513)

<223> RXA00511

<400> 35

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ttg aag att gct atg gat gaa gcc gga att aca ctg cgt acc acc aag      96
Leu Lys Ile Ala Met Asp Glu Ala Gly Ile Thr Leu Arg Thr Thr Lys
                20                      25                      30

gta gga gac cgc tac gtg ctg gaa gac ctc aat gca ggt gga ttc agc      144
Val Gly Asp Arg Tyr Val Leu Glu Asp Leu Asn Ala Gly Gly Phe Ser
                35                      40                      45

ctg ggc ggc gag caa tct ggc cac att gtt ctt cca gat cat ggc acc      192
Leu Gly Gly Glu Gln Ser Gly His Ile Val Leu Pro Asp His Gly Thr
  50                      55                      60

act ggc gat gga act ttg act ggt ctt tcc atc atg gcg cgc atg gct      240
Thr Gly Asp Gly Thr Leu Thr Gly Leu Ser Ile Met Ala Arg Met Ala
  65                      70                      75                      80

gaa acc gga aag tcc ttg ggc gag ttg gca caa gct atg acg gtg ctg      288
Glu Thr Gly Lys Ser Leu Gly Glu Leu Ala Gln Ala Met Thr Val Leu
                85                      90                      95

cca cag gtt ctg atc aat gtg cca gtt tgc gat aag tcc acc atc gtg      336
Pro Gln Val Leu Ile Asn Val Pro Val Ser Asp Lys Ser Thr Ile Val
                100                      105                      110

agc cac cca agc gtt gtg gct gcg atc gcg gaa gca gaa gct gag ttg      384
Ser His Pro Ser Val Val Ala Ala Ile Ala Glu Ala Glu Ala Glu Leu
                115                      120                      125

ggc gcc acc ggt cgc gtt ctt ctt cgt gct tct ggc acc gaa gag ctt      432
Gly Ala Thr Gly Arg Val Leu Leu Arg Ala Ser Gly Thr Glu Glu Leu
  130                      135                      140

ttc cgc gtg atg gtt gag gct gga gac aag gaa caa gct cgt cgt atc      480
Phe Arg Val Met Val Glu Ala Gly Asp Lys Glu Gln Ala Arg Arg Ile
  145                      150                      155                      160

gcg gga cgt ctt gct gca gtg gtt gca gaa gtc taattcactt cagtcacagc 533
Ala Gly Arg Leu Ala Ala Val Val Ala Glu Val
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gca

536

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<211> 171

<212> PRT

<213> Corynebacterium glutamicum

<400> 36

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 Val Gly Asp Arg Tyr Val Leu Glu Asp Leu Asn Ala Gly Gly Phe Ser
 35 40 45
 Leu Gly Gly Glu Gln Ser Gly His Ile Val Leu Pro Asp His Gly Thr
 50 55 60
 Thr Gly Asp Gly Thr Leu Thr Gly Leu Ser Ile Met Ala Arg Met Ala
 65 70 75 80
 Glu Thr Gly Lys Ser Leu Gly Glu Leu Ala Gln Ala Met Thr Val Leu
 85 90 95
 Pro Gln Val Leu Ile Asn Val Pro Val Ser Asp Lys Ser Thr Ile Val
 100 105 110
 Ser His Pro Ser Val Val Ala Ala Ile Ala Glu Ala Glu Ala Glu Leu
 115 120 125
 Gly Ala Thr Gly Arg Val Leu Leu Arg Ala Ser Gly Thr Glu Glu Leu
 130 135 140
 Phe Arg Val Met Val Glu Ala Gly Asp Lys Glu Gln Ala Arg Arg Ile
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 Ala Gly Arg Leu Ala Ala Val Val Ala Glu Val
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<210> 37

<211> 1497

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1474)

<223> RXN01365

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 Met Arg Thr Arg Glu
 1 5
 tct gtc aca gct gta att aag gcg tat gac gtc cgt ggt gtt gtt ggt 163
 Ser Val Thr Ala Val Ile Lys Ala Tyr Asp Val Arg Gly Val Val Gly
 10 15 20
 gtc gat att gat gct gat ttc att tct gag act ggc gct gcc ttt ggt 211
 Val Asp Ile Asp Ala Asp Phe Ile Ser Glu Thr Gly Ala Ala Phe Gly
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 cgg ctc atg cgt agt gag ggt gaa acc acc gtt gct att ggc cat gac 259

Arg	Leu	Met	Arg	Ser	Glu	Gly	Glu	Thr	Thr	Val	Ala	Ile	Gly	His	Asp	
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Met	Arg	Asp	Ser	Ser	Pro	Glu	Leu	Ala	Lys	Ala	Phe	Ala	Asp	Gly	Val	
	55					60				65						
act	gca	cag	ggg	ttg	gat	gtt	gtt	cat	ttg	gga	ctg	act	tct	act	gat	355
Thr	Ala	Gln	Gly	Leu	Asp	Val	Val	His	Leu	Gly	Leu	Thr	Ser	Thr	Asp	
	70				75					80					85	
gag	ctg	tac	ttt	gcg	tcc	gga	acc	ttg	aag	tgt	gct	ggg	gcg	atg	ttt	403
Glu	Leu	Tyr	Phe	Ala	Ser	Gly	Thr	Leu	Lys	Cys	Ala	Gly	Ala	Met	Phe	
				90					95					100		
act	gcg	tcg	cat	aac	ccc	gct	gag	tac	aac	ggc	atc	aag	ttg	tgt	cgt	451
Thr	Ala	Ser	His	Asn	Pro	Ala	Glu	Tyr	Asn	Gly	Ile	Lys	Leu	Cys	Arg	
			105					110					115			
gcg	ggg	gct	cgt	ccg	gtc	ggg	cag	gat	tct	ggg	ttg	gcc	aac	atc	att	499
Ala	Gly	Ala	Arg	Pro	Val	Gly	Gln	Asp	Ser	Gly	Leu	Ala	Asn	Ile	Ile	
		120					125					130				
gat	gat	ctg	gtt	gag	ggg	gtt	cca	gcg	ttt	gat	ggg	gag	tca	ggg	tcg	547
Asp	Asp	Leu	Val	Glu	Gly	Val	Pro	Ala	Phe	Asp	Gly	Glu	Ser	Gly	Ser	
	135				140						145					
gtt	tct	gag	cag	gat	ttg	ctg	agc	gca	tat	gcc	gag	tac	ctc	aat	gag	595
Val	Ser	Glu	Gln	Asp	Leu	Leu	Ser	Ala	Tyr	Ala	Glu	Tyr	Leu	Asn	Glu	
	150				155					160					165	
ctt	gtt	gat	ctg	aag	aac	atc	cgc	ccg	atg	aag	gtt	gct	gtg	gat	gcg	643
Leu	Val	Asp	Leu	Lys	Asn	Ile	Arg	Pro	Met	Lys	Val	Ala	Val	Asp	Ala	
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gca	aac	ggc	atg	ggg	ggg	ttc	act	gtc	cct	gag	gta	ttc	aag	ggg	ctg	691
Ala	Asn	Gly	Met	Gly	Gly	Phe	Thr	Val	Pro	Glu	Val	Phe	Lys	Gly	Leu	
			185					190					195			
cca	ctt	gat	gtt	gcg	cca	ctg	tat	ttt	gag	ctt	gac	ggc	aat	ttc	ccc	739
Pro	Leu	Asp	Val	Ala	Pro	Leu	Tyr	Phe	Glu	Leu	Asp	Gly	Asn	Phe	Pro	
		200					205					210				
aac	cat	gag	gcc	aat	cct	ctg	gag	cct	gcc	aac	ctg	gtt	gat	ttg	cag	787
Asn	His	Glu	Ala	Asn	Pro	Leu	Glu	Pro	Ala	Asn	Leu	Val	Asp	Leu	Gln	
	215					220					225					
aag	ttt	acc	gta	gag	acc	gga	tct	gat	atc	ggg	ttg	gcg	ttc	gac	ggc	835
Lys	Phe	Thr	Val	Glu	Thr	Gly	Ser	Asp	Ile	Gly	Leu	Ala	Phe	Asp	Gly	
	230				235					240					245	
gat	gcg	gat	cgt	tgc	ttc	gtg	gtc	gat	gag	aag	ggc	cag	cca	gtc	agc	883
Asp	Ala	Asp	Arg	Cys	Phe	Val	Val	Asp	Glu	Lys	Gly	Gln	Pro	Val	Ser	
				250					255					260		
cct	tcg	gcg	atc	tgt	gcg	atc	gta	gcg	gag	cgt	tac	ttg	gag	aag	ctt	931
Pro	Ser	Ala	Ile	Cys	Ala	Ile	Val	Ala	Glu	Arg	Tyr	Leu	Glu	Lys	Leu	
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ccg	ggg	tcc	acc	atc	atc	cac	aac	ctg	att	acc	tct	aag	gct	gtg	cct	979
Pro	Gly	Ser	Thr	Ile	Ile	His	Asn	Leu	Ile	Thr	Ser	Lys	Ala	Val	Pro	

280					285					290							
gag	gtg	att	gct	gaa	aac	ggt	ggc	act	gcg	gtg	cgt	act	cgc	gtg	ggt	1027	
Glu	Val	Ile	Ala	Glu	Asn	Gly	Gly	Thr	Ala	Val	Arg	Thr	Arg	Val	Gly		
295					300					305							
cac	tcc	ttc	atc	aag	gcg	aag	atg	gca	gag	acc	ggt	gcg	gcc	ttt	ggt	1075	
His	Ser	Phe	Ile	Lys	Ala	Lys	Met	Ala	Glu	Thr	Gly	Ala	Ala	Phe	Gly		
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Gly	Glu	His	Ser	Ala	His	Tyr	Tyr	Phe	Thr	Glu	Phe	Phe	Asn	Ala	Asp		
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Ser	Gly	Ile	Leu	Ala	Ala	Met	His	Val	Leu	Ala	Ala	Leu	Gly	Ser	Gln		
345					350					355							
gac	cag	cca	ctc	agt	gag	atg	atg	gct	agg	tat	aac	cgg	tac	gtt	gct	1219	
Asp	Gln	Pro	Leu	Ser	Glu	Met	Met	Ala	Arg	Tyr	Asn	Arg	Tyr	Val	Ala		
360					365					370							
tca	ggc	gag	ttg	aac	tcc	cgt	ttg	gct	aat	gca	gag	gcg	cag	caa	gag	1267	
Ser	Gly	Glu	Leu	Asn	Ser	Arg	Leu	Ala	Asn	Ala	Glu	Ala	Gln	Gln	Glu		
375					380					385							
cgc	acc	cag	gct	gtg	ctc	gat	gcg	ttc	gct	gat	cgc	acc	gag	tcc	gtg	1315	
Arg	Thr	Gln	Ala	Val	Leu	Asp	Ala	Phe	Ala	Asp	Arg	Thr	Glu	Ser	Val		
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gac	acc	ctt	gac	ggc	gtg	act	gtg	gaa	ctc	aag	gac	acc	tcc	gcg	tgg	1363	
Asp	Thr	Leu	Asp	Gly	Val	Thr	Val	Glu	Leu	Lys	Asp	Thr	Ser	Ala	Trp		
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Phe	Asn	Val	Arg	Ala	Ser	Asn	Thr	Glu	Pro	Leu	Leu	Arg	Leu	Asn	Val		
425					430					435							
gaa	gct	gca	tcg	aag	gaa	gaa	gtc	gat	gcg	ttg	gta	gcg	gag	att	cta	1459	
Glu	Ala	Ala	Ser	Lys	Glu	Glu	Val	Asp	Ala	Leu	Val	Ala	Glu	Ile	Leu		
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ggg	att	atc	cgc	gca	taatccatt	ttccggcg	ggg	cat								1497	
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<213> Corynebacterium glutamicum

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Gly	Ala	Ala	Phe	Gly	Arg	Leu	Met	Arg	Ser	Glu	Gly	Glu	Thr	Thr	Val
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Ala Ile Gly His Asp Met Arg Asp Ser Ser Pro Glu Leu Ala Lys Ala
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 Phe Ala Asp Gly Val Thr Ala Gln Gly Leu Asp Val Val His Leu Gly
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 Leu Thr Ser Thr Asp Glu Leu Tyr Phe Ala Ser Gly Thr Leu Lys Cys
 85 90 95
 Ala Gly Ala Met Phe Thr Ala Ser His Asn Pro Ala Glu Tyr Asn Gly
 100 105 110
 Ile Lys Leu Cys Arg Ala Gly Ala Arg Pro Val Gly Gln Asp Ser Gly
 115 120 125
 Leu Ala Asn Ile Ile Asp Asp Leu Val Glu Gly Val Pro Ala Phe Asp
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 Gly Glu Ser Gly Ser Val Ser Glu Gln Asp Leu Leu Ser Ala Tyr Ala
 145 150 155 160
 Glu Tyr Leu Asn Glu Leu Val Asp Leu Lys Asn Ile Arg Pro Met Lys
 165 170 175
 Val Ala Val Asp Ala Ala Asn Gly Met Gly Gly Phe Thr Val Pro Glu
 180 185 190
 Val Phe Lys Gly Leu Pro Leu Asp Val Ala Pro Leu Tyr Phe Glu Leu
 195 200 205
 Asp Gly Asn Phe Pro Asn His Glu Ala Asn Pro Leu Glu Pro Ala Asn
 210 215 220
 Leu Val Asp Leu Gln Lys Phe Thr Val Glu Thr Gly Ser Asp Ile Gly
 225 230 235 240
 Leu Ala Phe Asp Gly Asp Ala Asp Arg Cys Phe Val Val Asp Glu Lys
 245 250 255
 Gly Gln Pro Val Ser Pro Ser Ala Ile Cys Ala Ile Val Ala Glu Arg
 260 265 270
 Tyr Leu Glu Lys Leu Pro Gly Ser Thr Ile Ile His Asn Leu Ile Thr
 275 280 285
 Ser Lys Ala Val Pro Glu Val Ile Ala Glu Asn Gly Gly Thr Ala Val
 290 295 300
 Arg Thr Arg Val Gly His Ser Phe Ile Lys Ala Lys Met Ala Glu Thr
 305 310 315 320
 Gly Ala Ala Phe Gly Gly Glu His Ser Ala His Tyr Tyr Phe Thr Glu
 325 330 335
 Phe Phe Asn Ala Asp Ser Gly Ile Leu Ala Ala Met His Val Leu Ala
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 Ala Leu Gly Ser Gln Asp Gln Pro Leu Ser Glu Met Met Ala Arg Tyr
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Asn Arg Tyr Val Ala Ser Gly Glu Leu Asn Ser Arg Leu Ala Asn Ala
 370 375 380
 Glu Ala Gln Gln Glu Arg Thr Gln Ala Val Leu Asp Ala Phe Ala Asp
 385 390 395 400
 Arg Thr Glu Ser Val Asp Thr Leu Asp Gly Val Thr Val Glu Leu Lys
 405 410 415
 Asp Thr Ser Ala Trp Phe Asn Val Arg Ala Ser Asn Thr Glu Pro Leu
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 Met Arg Thr Arg Glu
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 tct gtc aca gct gta att aag gcg tat gac gtc cgt ggt gtt gtt ggt 163
 Ser Val Thr Ala Val Ile Lys Ala Tyr Asp Val Arg Gly Val Val Gly
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 Val Asp Ile Asp Ala Asp Phe Ile Ser Glu Thr Gly Ala Ala Phe Gly
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 cgg ctc atg cgt agt gag ggt gaa acc acc gtt gct att ggc cat gac 259
 Arg Leu Met Arg Ser Glu Gly Glu Thr Thr Val Ala Ile Gly His Asp
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 atg cgt gat tcc tcc cct gaa ttg gcc aag gcg ttt gcc gat ggc gtg 307
 Met Arg Asp Ser Ser Pro Glu Leu Ala Lys Ala Phe Ala Asp Gly Val
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 act gca cag ggt ttg gat gtt gtt cat ttg gga ctg act tct act gat 355
 Thr Ala Gln Gly Leu Asp Val Val His Leu Gly Leu Thr Ser Thr Asp
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 gag ctg tac ttt gcg tcc gga acc ttg aag tgt gct ggt gcg atg ttt 403
 Glu Leu Tyr Phe Ala Ser Gly Thr Leu Lys Cys Ala Gly Ala Met Phe
 90 95 100
 act gcg tcg cat aac ccc gct gag tac aac ggc atc aag ttg tgt cgt 451

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Ala	Gly	Ala	Arg	Pro	Val	Gly	Gln	Asp	Ser	Gly	Leu	Ala	Asn	Ile	Ile		
			120				125					130					
gat	gat	ctg	gtt	gag	ggt	gtt	cca	gcg	ttt	gat	ggt	gag	tca	ggt	tcg	547	
Asp	Asp	Leu	Val	Glu	Gly	Val	Pro	Ala	Phe	Asp	Gly	Glu	Ser	Gly	Ser		
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Val	Ser	Glu	Gln	Asp	Leu	Leu	Ser	Ala	Tyr	Ala	Glu	Tyr	Leu	Asn	Glu		
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Leu	Val	Asp	Leu	Lys	Asn	Ile	Arg	Pro	Met	Lys	Val	Ala	Val	Asp	Ala		
				170					175					180			
gca	aac	ggc	atg	ggt	ggg	ttc	act	gtc	cct	gag	gta	ttc	aag	ggt	ctg	691	
Ala	Asn	Gly	Met	Gly	Gly	Phe	Thr	Val	Pro	Glu	Val	Phe	Lys	Gly	Leu		
			185					190					195				
cca	ctt	gat	gtt	gcg	cca	ctg	tat	ttt	gag	ctt	gac	ggc	aat	ttc	ccc	739	
Pro	Leu	Asp	Val	Ala	Pro	Leu	Tyr	Phe	Glu	Leu	Asp	Gly	Asn	Phe	Pro		
			200				205					210					
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Asn	His	Glu	Ala	Asn	Pro	Leu	Glu	Pro	Ala	Asn	Leu	Val	Asp	Leu	Gln		
			215			220					225						
aag	ttt	acc	gta	gag	acc	gga	tct	gat	atc	ggt	ttg	gcg	ttc	gac	ggc	835	
Lys	Phe	Thr	Val	Glu	Thr	Gly	Ser	Asp	Ile	Gly	Leu	Ala	Phe	Asp	Gly		
230					235					240					245		
gat	gcg	gat	cgt	tgc	ttc	gtg	gtc	gat	gag	aag	ggc	cag	cca	gtc	agc	883	
Asp	Ala	Asp	Arg	Cys	Phe	Val	Val	Asp	Glu	Lys	Gly	Gln	Pro	Val	Ser		
				250					255					260			
cct	tcg	gcg	atc	tgt	gcg	atc	gta	gcg	gag	cgt	tac	ttg	gag	aag	ctt	931	
Pro	Ser	Ala	Ile	Cys	Ala	Ile	Val	Ala	Glu	Arg	Tyr	Leu	Glu	Lys	Leu		
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ccg	ggt	tcc	acc	atc	atc	cac	aac	ctg	att	acc	tct	aag	gct	gtg	cct	979	
Pro	Gly	Ser	Thr	Ile	Ile	His	Asn	Leu	Ile	Thr	Ser	Lys	Ala	Val	Pro		
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Glu	Val	Ile	Ala	Glu													
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<213> Corynebacterium glutamicum

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 35 40 45
 Ala Ile Gly His Asp Met Arg Asp Ser Ser Pro Glu Leu Ala Lys Ala
 50 55 60
 Phe Ala Asp Gly Val Thr Ala Gln Gly Leu Asp Val Val His Leu Gly
 65 70 75 80
 Leu Thr Ser Thr Asp Glu Leu Tyr Phe Ala Ser Gly Thr Leu Lys Cys
 85 90 95
 Ala Gly Ala Met Phe Thr Ala Ser His Asn Pro Ala Glu Tyr Asn Gly
 100 105 110
 Ile Lys Leu Cys Arg Ala Gly Ala Arg Pro Val Gly Gln Asp Ser Gly
 115 120 125
 Leu Ala Asn Ile Ile Asp Asp Leu Val Glu Gly Val Pro Ala Phe Asp
 130 135 140
 Gly Glu Ser Gly Ser Val Ser Glu Gln Asp Leu Leu Ser Ala Tyr Ala
 145 150 155 160
 Glu Tyr Leu Asn Glu Leu Val Asp Leu Lys Asn Ile Arg Pro Met Lys
 165 170 175
 Val Ala Val Asp Ala Ala Asn Gly Met Gly Gly Phe Thr Val Pro Glu
 180 185 190
 Val Phe Lys Gly Leu Pro Leu Asp Val Ala Pro Leu Tyr Phe Glu Leu
 195 200 205
 Asp Gly Asn Phe Pro Asn His Glu Ala Asn Pro Leu Glu Pro Ala Asn
 210 215 220
 Leu Val Asp Leu Gln Lys Phe Thr Val Glu Thr Gly Ser Asp Ile Gly
 225 230 235 240
 Leu Ala Phe Asp Gly Asp Ala Asp Arg Cys Phe Val Val Asp Glu Lys
 245 250 255
 Gly Gln Pro Val Ser Pro Ser Ala Ile Cys Ala Ile Val Ala Glu Arg
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 Ser Lys Ala Val Pro Glu Val Ile Ala Glu
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<223> RXA00098

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                                         Met Ala Asp Ile Ser
                                         1 5

acc acc cag gtt tgg caa gac ctg acc gat cat tac tca aac ttc cag 163
Thr Thr Gln Val Trp Gln Asp Leu Thr Asp His Tyr Ser Asn Phe Gln
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gca acc act ctg cgt gaa ctt ttc aag gaa gaa aac cgc gcc gag aag 211
Ala Thr Thr Leu Arg Glu Leu Phe Lys Glu Glu Asn Arg Ala Glu Lys
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tac acc ttc tcc gcg gct ggc ctc cac gtc gac ctg tcg aag aat ctg 259
Tyr Thr Phe Ser Ala Ala Gly Leu His Val Asp Leu Ser Lys Asn Leu
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ctt gac gac gcc acc ctc acc aag ctc ctt gca ctg acc gaa gaa tct 307
Leu Asp Asp Ala Thr Leu Thr Lys Leu Leu Ala Leu Thr Glu Glu Ser
                        55 60 65

ggc ctt cgc gaa cgc att gac gcg atg ttt gcc ggt gaa cac ctc aac 355
Gly Leu Arg Glu Arg Ile Asp Ala Met Phe Ala Gly Glu His Leu Asn
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aac acc gaa gac cgc gct gtc ctc cac acc gcg ctg cgc ctt cct gcc 403
Asn Thr Glu Asp Arg Ala Val Leu His Thr Ala Leu Arg Leu Pro Ala
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Glu Ala Asp Leu Ser Val Asp Gly Gln Asp Val Ala Ala Asp Val His
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Glu Val Leu Gly Arg Met Arg Asp Phe Ala Thr Ala Leu Arg Ser Gly
                        120 125 130

aac tgg ttg gga cac acc ggc cac acg atc aag aag atc gtc aac att 547
Asn Trp Leu Gly His Thr Gly His Thr Ile Lys Lys Ile Val Asn Ile
                        135 140 145

ggt atc ggt ggc tct gac ctc gga cca gcc atg gct acg aag gct ctg 595
Gly Ile Gly Gly Ser Asp Leu Gly Pro Ala Met Ala Thr Lys Ala Leu
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cgt gca tac gcg acc gct ggt atc tca gca gaa ttc gtc tcc aac gtc 643
Arg Ala Tyr Ala Thr Ala Gly Ile Ser Ala Glu Phe Val Ser Asn Val
                        170 175 180

gac cca gca gac ctc gtt tct gtg ttg gaa gac ctc gat gca gaa tcc 691
Asp Pro Ala Asp Leu Val Ser Val Leu Glu Asp Leu Asp Ala Glu Ser
                        185 190 195

aca ttg ttc gtg atc gct tcg aaa act ttc acc acc cag gag acg ctg 739
Thr Leu Phe Val Ile Ala Ser Lys Thr Phe Thr Thr Gln Glu Thr Leu

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Glu	Ala	Val	Ala	Lys	His	Phe	Val	Ala	Val	Ser	Thr	Asn	Ala	Glu	Lys	
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Val	Ala	Glu	Phe	Gly	Ile	Asp	Thr	Asp	Asn	Met	Phe	Gly	Phe	Trp	Asp	
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Trp	Val	Gly	Gly	Arg	Tyr	Ser	Val	Asp	Ser	Ala	Val	Gly	Leu	Ser	Leu	
			265					270					275			
atg	gca	gtg	atc	ggc	cct	cgc	gac	ttc	atg	cgt	ttc	ctc	ggt	gga	ttc	979
Met	Ala	Val	Ile	Gly	Pro	Arg	Asp	Phe	Met	Arg	Phe	Leu	Gly	Gly	Phe	
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His	Ala	Met	Asp	Glu	His	Phe	Arg	Thr	Thr	Lys	Phe	Glu	Glu	Asn	Val	
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Pro	Ile	Leu	Met	Ala	Leu	Leu	Gly	Val	Trp	Tyr	Ser	Asp	Phe	Tyr	Gly	
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Ala	Glu	Thr	His	Ala	Val	Leu	Pro	Tyr	Ser	Glu	Asp	Leu	Ser	Arg	Phe	
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gct	gct	tac	ctc	cag	cag	ctg	acc	atg	gaa	tca	aat	ggc	aag	tca	gtc	1171
Ala	Ala	Tyr	Leu	Gln	Gln	Leu	Thr	Met	Glu	Ser	Asn	Gly	Lys	Ser	Val	
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His	Arg	Asp	Gly	Ser	Pro	Val	Ser	Thr	Gly	Thr	Gly	Glu	Ile	Tyr	Trp	
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Gly	Glu	Pro	Gly	Thr	Asn	Gly	Gln	His	Ala	Phe	Phe	Gln	Leu	Ile	His	
	375					380					385					
cag	ggc	act	cgc	ctt	gtt	cca	gct	gat	ttc	att	ggt	ttc	gct	cgt	cca	1315
Gln	Gly	Thr	Arg	Leu	Val	Pro	Ala	Asp	Phe	Ile	Gly	Phe	Ala	Arg	Pro	
390					395					400					405	
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Lys	Gln	Asp	Leu	Pro	Ala	Gly	Glu	Arg	Thr	Met	His	Asp	Leu	Leu	Met	
				410					415					420		
agc	aac	ttc	ttc	gca	cag	acc	aag	gtt	ttg	gct	ttc	ggt	aag	aac	gct	1411
Ser	Asn	Phe	Phe	Ala	Gln	Thr	Lys	Val	Leu	Ala	Phe	Gly	Lys	Asn	Ala	
			425					430				435				
gaa	gag	atc	gct	gcg	gaa	ggt	gtc	gca	cct	gag	ctg	gtc	aac	cac	aag	1459
Glu	Glu	Ile	Ala	Ala	Glu	Gly	Val	Ala	Pro	Glu	Leu	Val	Asn	His	Lys	
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 Val Met Pro Gly Asn Arg Pro Thr Thr Thr Ile Leu Ala Glu Glu Leu
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 acc cct tct att ctc ggt gcg ttg atc gct ttg tac gaa cac atc gtg 1555
 Thr Pro Ser Ile Leu Gly Ala Leu Ile Ala Leu Tyr Glu His Ile Val
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 490 495 500
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 Val Glu Leu Gly Lys Gln Gln Ala Asn Asp Leu Ala Pro Ala Val Ser
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 Gly Glu Glu Asp Val Asp Ser Gly Asp Ser Ser Thr Asp Ser Leu Ile
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 35 40 45
 Leu Ser Lys Asn Leu Leu Asp Asp Ala Thr Leu Thr Lys Leu Leu Ala
 50 55 60
 Leu Thr Glu Glu Ser Gly Leu Arg Glu Arg Ile Asp Ala Met Phe Ala
 65 70 75 80
 Gly Glu His Leu Asn Asn Thr Glu Asp Arg Ala Val Leu His Thr Ala
 85 90 95
 Leu Arg Leu Pro Ala Glu Ala Asp Leu Ser Val Asp Gly Gln Asp Val
 100 105 110
 Ala Ala Asp Val His Glu Val Leu Gly Arg Met Arg Asp Phe Ala Thr
 115 120 125
 Ala Leu Arg Ser Gly Asn Trp Leu Gly His Thr Gly His Thr Ile Lys
 130 135 140
 Lys Ile Val Asn Ile Gly Ile Gly Gly Ser Asp Leu Gly Pro Ala Met
 145 150 155 160

Ala Thr Lys Ala Leu Arg Ala Tyr Ala Thr Ala Gly Ile Ser Ala Glu
 165 170 175
 Phe Val Ser Asn Val Asp Pro Ala Asp Leu Val Ser Val Leu Glu Asp
 180 185 190
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 195 200 205
 Thr Gln Glu Thr Leu Ser Asn Ala Arg Ala Ala Arg Ala Trp Leu Val
 210 215 220
 Glu Lys Leu Gly Glu Glu Ala Val Ala Lys His Phe Val Ala Val Ser
 225 230 235 240
 Thr Asn Ala Glu Lys Val Ala Glu Phe Gly Ile Asp Thr Asp Asn Met
 245 250 255
 Phe Gly Phe Trp Asp Trp Val Gly Gly Arg Tyr Ser Val Asp Ser Ala
 260 265 270
 Val Gly Leu Ser Leu Met Ala Val Ile Gly Pro Arg Asp Phe Met Arg
 275 280 285
 Phe Leu Gly Gly Phe His Ala Met Asp Glu His Phe Arg Thr Thr Lys
 290 295 300
 Phe Glu Glu Asn Val Pro Ile Leu Met Ala Leu Leu Gly Val Trp Tyr
 305 310 315 320
 Ser Asp Phe Tyr Gly Ala Glu Thr His Ala Val Leu Pro Tyr Ser Glu
 325 330 335
 Asp Leu Ser Arg Phe Ala Ala Tyr Leu Gln Gln Leu Thr Met Glu Ser
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 Asn Gly Lys Ser Val His Arg Asp Gly Ser Pro Val Ser Thr Gly Thr
 355 360 365
 Gly Glu Ile Tyr Trp Gly Glu Pro Gly Thr Asn Gly Gln His Ala Phe
 370 375 380
 Phe Gln Leu Ile His Gln Gly Thr Arg Leu Val Pro Ala Asp Phe Ile
 385 390 395 400
 Gly Phe Ala Arg Pro Lys Gln Asp Leu Pro Ala Gly Glu Arg Thr Met
 405 410 415
 His Asp Leu Leu Met Ser Asn Phe Phe Ala Gln Thr Lys Val Leu Ala
 420 425 430
 Phe Gly Lys Asn Ala Glu Glu Ile Ala Ala Glu Gly Val Ala Pro Glu
 435 440 445
 Leu Val Asn His Lys Val Met Pro Gly Asn Arg Pro Thr Thr Thr Ile
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 Leu Ala Glu Glu Leu Thr Pro Ser Ile Leu Gly Ala Leu Ile Ala Leu
 465 470 475 480

Tyr	Glu	His	Ile	Val	Met	Val	Gln	Gly	Val	Ile	Trp	Asp	Ile	Asn	Ser	
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Ala	Pro	Ala	Val	Ser	Gly	Glu	Glu	Asp	Val	Asp	Ser	Gly	Asp	Ser	Ser	
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<222> (1) .. (630)  
<223> RXA01989
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<400> 43																
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Val	Lys	Ser	Ile	His	Lys	Thr	Ile	His	Glu	Gly	Thr	Gly	Ala	Gly	Ser	
1				5					10					15		
gac	ttc	tta	ggc	tgg	ggt	gat	tta	cca	ggt	gat	tac	gac	aaa	gaa	gaa	96
Asp	Phe	Leu	Gly	Trp	Val	Asp	Leu	Pro	Val	Asp	Tyr	Asp	Lys	Glu	Glu	
			20					25					30			
ttt	tca	aga	att	ggt	gaa	gca	tca	aaa	cgc	att	aaa	gaa	aat	tct	gat	144
Phe	Ser	Arg	Ile	Val	Glu	Ala	Ser	Lys	Arg	Ile	Lys	Glu	Asn	Ser	Asp	
		35					40					45				
ggt	tta	gta	gtc	atc	ggg	att	ggg	ggg	tct	tac	tta	ggg	gca	cgt	gca	192
Val	Leu	Val	Val	Ile	Gly	Ile	Gly	Gly	Ser	Tyr	Leu	Gly	Ala	Arg	Ala	
	50					55					60					
gca	atc	gaa	atg	tta	acg	tca	tca	ttt	aga	aac	agc	aat	gaa	tac	cct	240
Ala	Ile	Glu	Met	Leu	Thr	Ser	Ser	Phe	Arg	Asn	Ser	Asn	Glu	Tyr	Pro	
65					70					75					80	
gaa	att	gta	ttt	ggt	ggg	aat	cac	tta	tca	tca	aca	tat	acg	aaa	gag	288
Glu	Ile	Val	Phe	Val	Gly	Asn	His	Leu	Ser	Ser	Thr	Tyr	Thr	Lys	Glu	
				85					90					95		
tta	ggt	gat	tat	tta	gca	gac	aaa	gat	ttc	tct	gta	aac	ggt	att	tct	336
Leu	Val	Asp	Tyr	Leu	Ala	Asp	Lys	Asp	Phe	Ser	Val	Asn	Val	Ile	Ser	
			100					105					110			
aaa	tct	ggg	aca	act	aca	gaa	cca	gca	ggt	gca	ttt	aga	ttg	ttc	aaa	384
Lys	Ser	Gly	Thr	Thr	Thr	Glu	Pro	Ala	Val	Ala	Phe	Arg	Leu	Phe	Lys	
		115					120					125				
caa	tta	ggt	gaa	gaa	aga	tac	ggg	aaa	gaa	gaa	gca	caa	aaa	cgt	ata	432
Gln	Leu	Val	Glu	Glu	Arg	Tyr	Gly	Lys	Glu	Glu	Ala	Gln	Lys	Arg	Ile	
	130					135					140					
ttt	gca	aca	acg	gat	aaa	gaa	aaa	ggg	gct	tta	aaa	cag	ttg	gct	aca	480

Phe Ala Thr Thr Asp Lys Glu Lys Gly Ala Leu Lys Gln Leu Ala Thr
 145 150 155 160
 aac gaa ggt tat gaa acg ttt atc gta cct gat gat gta ggt gga aga 528
 Asn Glu Gly Tyr Glu Thr Phe Ile Val Pro Asp Asp Val Gly Gly Arg
 165 170 175
 tat tct gtt tta aca gca gta gga tta tta cca att gca aca gct gga 576
 Tyr Ser Val Leu Thr Ala Val Gly Leu Leu Pro Ile Ala Thr Ala Gly
 180 185 190
 att aac atc gaa gct atg atg att ggt gct gca aaa gca cgt gaa gaa 624
 Ile Asn Ile Glu Ala Met Met Ile Gly Ala Ala Lys Ala Arg Glu Glu
 195 200 205
 tta tct
 Leu Ser
 210

<210> 44
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 <212> PRT
 <213> Corynebacterium glutamicum

<400> 44
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 20 25 30
 Phe Ser Arg Ile Val Glu Ala Ser Lys Arg Ile Lys Glu Asn Ser Asp
 35 40 45
 Val Leu Val Val Ile Gly Ile Gly Gly Ser Tyr Leu Gly Ala Arg Ala
 50 55 60
 Ala Ile Glu Met Leu Thr Ser Ser Phe Arg Asn Ser Asn Glu Tyr Pro
 65 70 75 80
 Glu Ile Val Phe Val Gly Asn His Leu Ser Ser Thr Tyr Thr Lys Glu
 85 90 95
 Leu Val Asp Tyr Leu Ala Asp Lys Asp Phe Ser Val Asn Val Ile Ser
 100 105 110
 Lys Ser Gly Thr Thr Thr Glu Pro Ala Val Ala Phe Arg Leu Phe Lys
 115 120 125
 Gln Leu Val Glu Glu Arg Tyr Gly Lys Glu Glu Ala Gln Lys Arg Ile
 130 135 140
 Phe Ala Thr Thr Asp Lys Glu Lys Gly Ala Leu Lys Gln Leu Ala Thr
 145 150 155 160
 Asn Glu Gly Tyr Glu Thr Phe Ile Val Pro Asp Asp Val Gly Gly Arg
 165 170 175
 Tyr Ser Val Leu Thr Ala Val Gly Leu Leu Pro Ile Ala Thr Ala Gly
 180 185 190

Ile Asn Ile Glu Ala Met Met Ile Gly Ala Ala Lys Ala Arg Glu Glu
 195 200 205

Leu Ser
 210

<210> 45
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 <213> Corynebacterium glutamicum

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 <222> (101)..(1246)
 <223> RXA00340

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 Val Lys Leu Val Ile
 1 5
 gag gcc gac ggc ggc tcc cgc gga aac ccc ggc gtc gcc ggc tcc ggc 163
 Glu Ala Asp Gly Gly Ser Arg Gly Asn Pro Gly Val Ala Gly Ser Gly
 10 15 20
 acc gtg gtg tac tcc gac aac aaa gca gaa gtt ctc aaa gaa atc gcc 211
 Thr Val Val Tyr Ser Asp Asn Lys Ala Glu Val Leu Lys Glu Ile Ala
 25 30 35
 tat gtt gtc gga aca aaa gcc acc aac aac gtc gcc gaa tac cgc gga 259
 Tyr Val Val Gly Thr Lys Ala Thr Asn Asn Val Ala Glu Tyr Arg Gly
 40 45 50
 cta ctc gaa ggc ctc aaa gca gcc cgc gag ctc ggc gct acc tcc gtg 307
 Leu Leu Glu Gly Leu Lys Ala Ala Arg Glu Leu Gly Ala Thr Ser Val
 55 60 65
 gat gtc tac atg gac tcc aaa ctt gtc gtt gaa caa atg tcc ggc cgg 355
 Asp Val Tyr Met Asp Ser Lys Leu Val Val Glu Gln Met Ser Gly Arg
 70 75 80 85
 tgg aaa atc aaa cac ccc gac atg aaa gtt cta gcg atc gaa gcc aag 403
 Trp Lys Ile Lys His Pro Asp Met Lys Val Leu Ala Ile Glu Ala Lys
 90 95 100
 gag att gct tcc gaa atc ggg tcc gtt tct tat acg tgg att ccg cgt 451
 Glu Ile Ala Ser Glu Ile Gly Ser Val Ser Tyr Thr Trp Ile Pro Arg
 105 110 115
 gag aaa aac aaa cga gct gac gca ttg tcc aac gtg gcg atg gat gct 499
 Glu Lys Asn Lys Arg Ala Asp Ala Leu Ser Asn Val Ala Met Asp Ala
 120 125 130
 gca gcg gca ggt aag ccg gta ggt gtt gta ggg gat tct gct tct gta 547
 Ala Ala Ala Gly Lys Pro Val Gly Val Val Gly Asp Ser Ala Ser Val
 135 140 145

tct tct gct tct tcg gtt gcg ggc tca gag aaa gaa gac ctc aac tgc	595
Ser Ser Ala Ser Ser Val Ala Gly Ser Glu Lys Glu Asp Leu Asn Cys	
150 155 160 165	
acc gaa acc aaa ccc acc aac tgg aac ggc gca acc aca gat ccc act	643
Thr Glu Thr Lys Pro Thr Asn Trp Asn Gly Ala Thr Thr Asp Pro Thr	
170 175 180	
cgt ttc ttg ttg ctt cgc cac ggc caa act gct atg tca gtg gca cgc	691
Arg Phe Leu Leu Leu Arg His Gly Gln Thr Ala Met Ser Val Ala Arg	
185 190 195	
ctt tac tcc ggt agg tcc aac cca gag ctg tct gaa ctt ggt gaa aaa	739
Leu Tyr Ser Gly Arg Ser Asn Pro Glu Leu Ser Glu Leu Gly Glu Lys	
200 205 210	
caa gca gca gcg gca gca cga cga ctc gct caa acc ggt ggc atc gac	787
Gln Ala Ala Ala Ala Ala Arg Arg Leu Ala Gln Thr Gly Gly Ile Asp	
215 220 225	
gct att gtg agt tct ccg ctc acc cgc acg atg caa acc gca gaa gca	835
Ala Ile Val Ser Ser Pro Leu Thr Arg Thr Met Gln Thr Ala Glu Ala	
230 235 240 245	
gca gcg gcc gca ctg gga atg aaa gta cgt gtt atc gat gat ctc atc	883
Ala Ala Ala Ala Leu Gly Met Lys Val Arg Val Ile Asp Asp Leu Ile	
250 255 260	
gaa act gac ttt gga ctg tgg gat gga aaa tca ttt tca gaa gcc cac	931
Glu Thr Asp Phe Gly Leu Trp Asp Gly Lys Ser Phe Ser Glu Ala His	
265 270 275	
gaa caa gat cca gaa ctg cac acc aag tgg ctc act gac tca tct gta	979
Glu Gln Asp Pro Glu Leu His Thr Lys Trp Leu Thr Asp Ser Ser Val	
280 285 290	
gcc cca ccc ggt ggt gag tcc ctg cag acg gtt aat cga cgt gtg aaa	1027
Ala Pro Pro Gly Gly Glu Ser Leu Gln Thr Val Asn Arg Arg Val Lys	
295 300 305	
aag gct cgt gaa agc ctc caa cgc gaa tac ggt gca gcg aat gtt ttg	1075
Lys Ala Arg Glu Ser Leu Gln Arg Glu Tyr Gly Ala Ala Asn Val Leu	
310 315 320 325	
gtg gtc agc cac gtc acc cca atc aaa gcc atc atg agg caa gca ttg	1123
Val Val Ser His Val Thr Pro Ile Lys Ala Ile Met Arg Gln Ala Leu	
330 335 340	
gac gca ggc cca tcc ttc ttt cag aag gca cac ctt gac ttg gcg tcg	1171
Asp Ala Gly Pro Ser Phe Phe Gln Lys Ala His Leu Asp Leu Ala Ser	
345 350 355	
ctg tcg atc gca gag ttt tac gaa gac ggc cca acc tgc gta aga ctg	1219
Leu Ser Ile Ala Glu Phe Tyr Glu Asp Gly Pro Thr Cys Val Arg Leu	
360 365 370	
ttc aac gac acc tca cac ctg gaa ggc tgacgacagt ctgacggaag	1266
Phe Asn Asp Thr Ser His Leu Glu Ala	
375 380	
ctc	1269

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 <211> 382
 <212> PRT
 <213> Corynebacterium glutamicum

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 Leu Lys Glu Ile Ala Tyr Val Val Gly Thr Lys Ala Thr Asn Asn Val
 35 40 45
 Ala Glu Tyr Arg Gly Leu Leu Glu Gly Leu Lys Ala Ala Arg Glu Leu
 50 55 60
 Gly Ala Thr Ser Val Asp Val Tyr Met Asp Ser Lys Leu Val Val Glu
 65 70 75 80
 Gln Met Ser Gly Arg Trp Lys Ile Lys His Pro Asp Met Lys Val Leu
 85 90 95
 Ala Ile Glu Ala Lys Glu Ile Ala Ser Glu Ile Gly Ser Val Ser Tyr
 100 105 110
 Thr Trp Ile Pro Arg Glu Lys Asn Lys Arg Ala Asp Ala Leu Ser Asn
 115 120 125
 Val Ala Met Asp Ala Ala Ala Ala Gly Lys Pro Val Gly Val Val Gly
 130 135 140
 Asp Ser Ala Ser Val Ser Ser Ala Ser Ser Val Ala Gly Ser Glu Lys
 145 150 155 160
 Glu Asp Leu Asn Cys Thr Glu Thr Lys Pro Thr Asn Trp Asn Gly Ala
 165 170 175
 Thr Thr Asp Pro Thr Arg Phe Leu Leu Leu Arg His Gly Gln Thr Ala
 180 185 190
 Met Ser Val Ala Arg Leu Tyr Ser Gly Arg Ser Asn Pro Glu Leu Ser
 195 200 205
 Glu Leu Gly Glu Lys Gln Ala Ala Ala Ala Ala Arg Arg Leu Ala Gln
 210 215 220
 Thr Gly Gly Ile Asp Ala Ile Val Ser Ser Pro Leu Thr Arg Thr Met
 225 230 235 240
 Gln Thr Ala Glu Ala Ala Ala Ala Ala Leu Gly Met Lys Val Arg Val
 245 250 255
 Ile Asp Asp Leu Ile Glu Thr Asp Phe Gly Leu Trp Asp Gly Lys Ser
 260 265 270
 Phe Ser Glu Ala His Glu Gln Asp Pro Glu Leu His Thr Lys Trp Leu
 275 280 285

Thr Asp Ser Ser Val Ala Pro Pro Gly Gly Glu Ser Leu Gln Thr Val
 290 295 300

Asn Arg Arg Val Lys Lys Ala Arg Glu Ser Leu Gln Arg Glu Tyr Gly
 305 310 315 320

Ala Ala Asn Val Leu Val Val Ser His Val Thr Pro Ile Lys Ala Ile
 325 330 335

Met Arg Gln Ala Leu Asp Ala Gly Pro Ser Phe Phe Gln Lys Ala His
 340 345 350

Leu Asp Leu Ala Ser Leu Ser Ile Ala Glu Phe Tyr Glu Asp Gly Pro
 355 360 365

Thr Cys Val Arg Leu Phe Asn Asp Thr Ser His Leu Glu Ala
 370 375 380

<210> 47
 <211> 840
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
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 <222> (101)..(817)
 <223> RXA02492

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aaacgcgcgt cgtggaacat aaagtggcaa actagtagcct atg act aac gga aaa 115
 Met Thr Asn Gly Lys
 1 5

ttg att ctt ctt cgt cac ggt cag agc gaa tgg aac gca tcc aac cag 163
 Leu Ile Leu Leu Arg His Gly Gln Ser Glu Trp Asn Ala Ser Asn Gln
 10 15 20

ttc act gga tgg gtc gac gtc aat ctg acc gaa cag ggt gag gct gag 211
 Phe Thr Gly Trp Val Asp Val Asn Leu Thr Glu Gln Gly Glu Ala Glu
 25 30 35

gcc aaa ggc gtc ctc cca ggc gtt gta tac acc tcc ttg ctg cgt cgc 259
 Ala Lys Gly Val Leu Pro Gly Val Val Tyr Thr Ser Leu Leu Arg Arg
 40 45 50

gcg atc cgc act gca aac atc gca ctg aac gct gca gac cgc cac tgg 307
 Ala Ile Arg Thr Ala Asn Ile Ala Leu Asn Ala Ala Asp Arg His Trp
 55 60 65

atc cca gtg atc cgc gac tgg cgc ctc aac gag cgt cac tac ggc gca 355
 Ile Pro Val Ile Arg Asp Trp Arg Leu Asn Glu Arg His Tyr Gly Ala
 70 75 80 85

ctg cag ggc ctt gac aag gct gca acc aag gaa aaa tac ggc gac gac 403
 Leu Gln Gly Leu Asp Lys Ala Ala Thr Lys Glu Lys Tyr Gly Asp Asp
 90 95 100

cag ttc atg gaa tgg cgc cgc tcc tac gac acc cca cca cca gag ctc 451
 Gln Phe Met Glu Trp Arg Arg Ser Tyr Asp Thr Pro Pro Pro Glu Leu
 105 110 115

 gcg gat gac gca gag tac tcc cag gca aat gac cct cgt tac gcg gac 499
 Ala Asp Asp Ala Glu Tyr Ser Gln Ala Asn Asp Pro Arg Tyr Ala Asp
 120 125 130

 ctc gac gta gtt cca cgc acc gaa tgc ctc aag gac gtt gtg gtt cgt 547
 Leu Asp Val Val Pro Arg Thr Glu Cys Leu Lys Asp Val Val Val Arg
 135 140 145

 ttt gtt cct tac ttc gag gaa gaa atc ctg cca cgc gca aag aag ggc 595
 Phe Val Pro Tyr Phe Glu Glu Glu Ile Leu Pro Arg Ala Lys Lys Gly
 150 155 160 165

 gaa acc gtc ctc atc gca gca cac ggc aac tcc ctg cgt gcg ctg gtt 643
 Glu Thr Val Leu Ile Ala Ala His Gly Asn Ser Leu Arg Ala Leu Val
 170 175 180

 aag cac ctt gac ggc atc tcc gat gct gat atc gca gag ctc aac atc 691
 Lys His Leu Asp Gly Ile Ser Asp Ala Asp Ile Ala Glu Leu Asn Ile
 185 190 195

 cca acc ggc atc cca ctg gtc tac gaa atc gcc gaa gac ggt tcc gta 739
 Pro Thr Gly Ile Pro Leu Val Tyr Glu Ile Ala Glu Asp Gly Ser Val
 200 205 210

 gta aac cca ggc ggc acc tac ctc gat cct gag gca gca gca gcc ggc 787
 Val Asn Pro Gly Gly Thr Tyr Leu Asp Pro Glu Ala Ala Ala Ala Gly
 215 220 225

 gca gca gca gta gca aac cag ggt aat aag tagctatttg taggtgagca 837
 Ala Ala Ala Val Ala Asn Gln Gly Asn Lys
 230 235

 ctc 840

<210> 48

<211> 239

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 48

Met Thr Asn Gly Lys Leu Ile Leu Leu Arg His Gly Gln Ser Glu Trp
 1 5 10 15

Asn Ala Ser Asn Gln Phe Thr Gly Trp Val Asp Val Asn Leu Thr Glu
 20 25 30

Gln Gly Glu Ala Glu Ala Lys Gly Val Leu Pro Gly Val Val Tyr Thr
 35 40 45

Ser Leu Leu Arg Arg Ala Ile Arg Thr Ala Asn Ile Ala Leu Asn Ala
 50 55 60

Ala Asp Arg His Trp Ile Pro Val Ile Arg Asp Trp Arg Leu Asn Glu
 65 70 75 80

Arg His Tyr Gly Ala Leu Gln Gly Leu Asp Lys Ala Ala Thr Lys Glu

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<210> 49
<211> 729
<212> DNA
<213> Corynebacterium glutamicum
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<220>  
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<223> RXA00381
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tcaagcccgc cgcacgtgca gcagcagaag cgaaggcatc													115		
										atg	acg	caa	acc	att	
										Met	Thr	Gln	Thr	Ile	
										1				5	
gtc cat cta gtt cgc cac ggc gaa gtc cac aac cca gag aaa atc ctg													163		
Val	His	Leu	Val	Arg	His	Gly	Glu	Val	His	Asn	Pro	Glu	Lys	Ile	Leu
				10					15					20	
tac gga cgc atg ccc gga tac agg ttg tct tcc cgt gga cgc agc caa													211		
Tyr	Gly	Arg	Met	Pro	Gly	Tyr	Arg	Leu	Ser	Ser	Arg	Gly	Arg	Ser	Gln
			25					30					35		
gcc gcc cgc act gca gct tct ttt gaa ggc cac gat gtc acc tac att													259		
Ala	Ala	Arg	Thr	Ala	Ala	Ser	Phe	Glu	Gly	His	Asp	Val	Thr	Tyr	Ile
		40					45					50			
gcg gcc tcc cca ttg cag cgt gtg cag gaa acc tcc gaa ccg ttc atc													307		
Ala	Ala	Ser	Pro	Leu	Gln	Arg	Val	Gln	Glu	Thr	Ser	Glu	Pro	Phe	Ile

55	60	65	
aag gtc aca ggc cta gaa ctg atc acc gac gag gat ctt ctg gaa gca			355
Lys Val Thr Gly Leu Glu Leu Ile Thr Asp Glu Asp Leu Leu Glu Ala			
70	75	80	85
ggc aac cgt ttc gaa ggc ctg cgc acc aaa ggt tgg cgt tcc cag ttg			403
Gly Asn Arg Phe Glu Gly Leu Arg Thr Lys Gly Trp Arg Ser Gln Leu			
	90	95	100
tgg aac ccc gtg cgt tgg cct ttg atg tac aac ccc acg ctt ccc agc			451
Trp Asn Pro Val Arg Trp Pro Leu Met Tyr Asn Pro Thr Leu Pro Ser			
	105	110	115
tgg ggc gaa cac tac acc gac att ttg gaa aga atg atg gcg gct gtg			499
Trp Gly Glu His Tyr Thr Asp Ile Leu Glu Arg Met Met Ala Ala Val			
	120	125	130
gaa cga gct cgg gtg gca gcg gaa gga cac gaa gca atc ctg gtg acc			547
Glu Arg Ala Arg Val Ala Ala Glu Gly His Glu Ala Ile Leu Val Thr			
	135	140	145
cac cag ttg ccg atc gtg tgc gtg caa cgc cac gcc cgc gga caa agc			595
His Gln Leu Pro Ile Val Cys Val Gln Arg His Ala Arg Gly Gln Ser			
	150	155	160
ctg tcc cat aac cca gcg acc agg caa tgc gac ctc gcc tca gtg aca			643
Leu Ser His Asn Pro Ala Thr Arg Gln Cys Asp Leu Ala Ser Val Thr			
	170	175	180
tcc ttg gtg ttc caa gac gat caa att gtc ggc gtg cat tac aac gaa			691
Ser Leu Val Phe Gln Asp Asp Gln Ile Val Gly Val His Tyr Asn Glu			
	185	190	195
cca gct cag gag att tgatcactcg tgcgtttgac caa			729
Pro Ala Gln Glu Ile			
200			

<210> 50

<211> 202

<212> PRT

<213> Corynebacterium glutamicum

<400> 50

Met Thr Gln Thr Ile Val His Leu Val Arg His Gly Glu Val His Asn
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Pro Glu Lys Ile Leu Tyr Gly Arg Met Pro Gly Tyr Arg Leu Ser Ser
20 25 30

Arg Gly Arg Ser Gln Ala Ala Arg Thr Ala Ala Ser Phe Glu Gly His
35 40 45

Asp Val Thr Tyr Ile Ala Ala Ser Pro Leu Gln Arg Val Gln Glu Thr
50 55 60

Ser Glu Pro Phe Ile Lys Val Thr Gly Leu Glu Leu Ile Thr Asp Glu
65 70 75 80

Asp Leu Leu Glu Ala Gly Asn Arg Phe Glu Gly Leu Arg Thr Lys Gly

<400> 51																
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ccttttttta agtgggcggt caggaatttt tcgcacaggt																
											atg	ctg	cat	gtc	atg	115
											Met	Leu	His	Val	Met	
											1				5	
aag ccg ggt tca cac gca gct gcc gaa aag act caa tcc act gtg gtt																163
Lys Pro Gly Ser His Ala Ala Ala Glu Lys Thr Gln Ser Thr Val Val																
											10				20	
tta ctc att cgg cat ggg caa acc cca aca act ggt cag gtt ctg cct																211
Leu Leu Ile Arg His Gly Gln Thr Pro Thr Thr Gly Gln Val Leu Pro																
											25			35		
ggt cag acg ccg ggt tta cac ctg tct gat aag ggt gaa gag cag gcg																259
Gly Gln Thr Pro Gly Leu His Leu Ser Asp Lys Gly Glu Glu Gln Ala																
											40			50		
cgg gag gtg gca cag cgt ctg gcg gag gtg ccg att acc gct gtg tat																307
Arg Glu Val Ala Gln Arg Leu Ala Glu Val Pro Ile Thr Ala Val Tyr																
											55			65		
tca tcg ccg atg gag cgt gcg cag gaa aca gca gca ccg acg gtc agc																355
Ser Ser Pro Met Glu Arg Ala Gln Glu Thr Ala Ala Pro Thr Val Ser																
											70			80		85

gct cat ggc ctc gag ttg acg gtg gaa cct ggg ctt att gaa tgc gat 403
 Ala His Gly Leu Glu Leu Thr Val Glu Pro Gly Leu Ile Glu Cys Asp
 90 95 100

ttc ggc gag tgg acg ggc cgg aaa cta act gag ctc aat gcc cta gag 451
 Phe Gly Glu Trp Thr Gly Arg Lys Leu Thr Glu Leu Asn Ala Leu Glu
 105 110 115

gag tgg aaa gcg gtg cag aag aca ccg tct acc ttc agg ttt cca ggt 499
 Glu Trp Lys Ala Val Gln Lys Thr Pro Ser Thr Phe Arg Phe Pro Gly
 120 125 130

ggt gag agt ttc gtg gaa atg cag gat cgg atg gtg gag gct atc ggc 547
 Gly Glu Ser Phe Val Glu Met Gln Asp Arg Met Val Glu Ala Ile Gly
 135 140 145

aac att gcg cag cag cat ccg gga gaa atc gtt gct gcg ttt agt cat 595
 Asn Ile Ala Gln Gln His Pro Gly Glu Ile Val Ala Ala Phe Ser His
 150 155 160 165

gcc gac acg atc aag gct gcg gtg gct cat ttt gta ggc act cca ctg 643
 Ala Asp Thr Ile Lys Ala Ala Val Ala His Phe Val Gly Thr Pro Leu
 170 175 180

gat tct ttt cag cgc att ttc atc gac acg gcg tca att tcc gca gtg 691
 Asp Ser Phe Gln Arg Ile Phe Ile Asp Thr Ala Ser Ile Ser Ala Val
 185 190 195

gaa ttt acc ggg aaa tct tca ggc gtc tcc tcc cat atg ctg ctg aca 739
 Glu Phe Thr Gly Lys Ser Ser Gly Val Ser Ser His Met Leu Leu Thr
 200 205 210

aat tcc aga aca gga tgc ttg gga tac ctt cga gac aaa ctt ccg aaa 787
 Asn Ser Arg Thr Gly Ser Leu Gly Tyr Leu Arg Asp Lys Leu Pro Lys
 215 220 225

gct ccg caa cca tgatcacctc accatttgag cgc 822
 Ala Pro Gln Pro
 230

<210> 52

<211> 233

<212> PRT

<213> Corynebacterium glutamicum

<400> 52

Met Leu His Val Met Lys Pro Gly Ser His Ala Ala Ala Glu Lys Thr
 1 5 10 15

Gln Ser Thr Val Val Leu Leu Ile Arg His Gly Gln Thr Pro Thr Thr
 20 25 30

Gly Gln Val Leu Pro Gly Gln Thr Pro Gly Leu His Leu Ser Asp Lys
 35 40 45

Gly Glu Glu Gln Ala Arg Glu Val Ala Gln Arg Leu Ala Glu Val Pro
 50 55 60

Ile Thr Ala Val Tyr Ser Ser Pro Met Glu Arg Ala Gln Glu Thr Ala
 65 70 75 80

Ala	Pro	Thr	Val	Ser 85	Ala	His	Gly	Leu	Glu 90	Leu	Thr	Val	Glu	Pro 95	Gly
Leu	Ile	Glu	Cys 100	Asp	Phe	Gly	Glu	Trp 105	Thr	Gly	Arg	Lys	Leu 110	Thr	Glu
Leu	Asn	Ala 115	Leu	Glu	Glu	Trp	Lys 120	Ala	Val	Gln	Lys	Thr 125	Pro	Ser	Thr
Phe	Arg 130	Phe	Pro	Gly	Gly	Glu 135	Ser	Phe	Val	Glu	Met 140	Gln	Asp	Arg	Met
Val 145	Glu	Ala	Ile	Gly	Asn 150	Ile	Ala	Gln	Gln	His 155	Pro	Gly	Glu	Ile	Val 160
Ala	Ala	Phe	Ser	His 165	Ala	Asp	Thr	Ile	Lys 170	Ala	Ala	Val	Ala	His 175	Phe
Val	Gly	Thr	Pro 180	Leu	Asp	Ser	Phe	Gln 185	Arg	Ile	Phe	Ile	Asp 190	Thr	Ala
Ser	Ile	Ser 195	Ala	Val	Glu	Phe	Thr 200	Gly	Lys	Ser	Ser	Gly 205	Val	Ser	Ser
His 210	Met	Leu	Leu	Thr	Asn	Ser 215	Arg	Thr	Gly	Ser	Leu 220	Gly	Tyr	Leu	Arg
Asp 225	Lys	Leu	Pro	Lys	Ala	Pro	Gln	Pro							

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<210> 53
<211> 1161
<212> DNA
<213> Corynebacterium glutamicum
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<221> CDS
<222> (101)..(1138)
<223> RXA00206
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                                         Met Glu Asp Met Arg
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att gct act ctc acg tca ggc ggc gac tgc ccc gga cta aac gcc gtc 163
Ile Ala Thr Leu Thr Ser Gly Gly Asp Cys Pro Gly Leu Asn Ala Val
                        10                               15                        20

atc cga gga atc gtc cgc aca gcc agc aat gaa ttt ggc tcc acc gtc 211
Ile Arg Gly Ile Val Arg Thr Ala Ser Asn Glu Phe Gly Ser Thr Val
                        25                               30                        35

gtt ggt tat caa gac ggt tgg gaa gga ctg tta ggc gat cgt cgc gta 259
Val Gly Tyr Gln Asp Gly Trp Glu Gly Leu Leu Gly Asp Arg Arg Val
                        40                               45                        50

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cag ctg tat gac gat gaa gat att gac cga atc ctc ctt cga ggc ggc	307
Gln Leu Tyr Asp Asp Glu Asp Ile Asp Arg Ile Leu Leu Arg Gly Gly	
55 60 65	
acc att ttg ggc act ggt cgc ctc cat ccg gac aag ttt aag gcc gga	355
Thr Ile Leu Gly Thr Gly Arg Leu His Pro Asp Lys Phe Lys Ala Gly	
70 75 80 85	
att gat cag att aag gcc aac tta gaa gac gcc ggc atc gat gcc ctt	403
Ile Asp Gln Ile Lys Ala Asn Leu Glu Asp Ala Gly Ile Asp Ala Leu	
90 95 100	
atc cca atc ggt ggc gaa gga acc ctg aag ggt gcc aag tgg ctg tct	451
Ile Pro Ile Gly Gly Glu Gly Thr Leu Lys Gly Ala Lys Trp Leu Ser	
105 110 115	
gat aac ggt atc cct gtt gtc ggt gtc cca aag acc att gac aat gac	499
Asp Asn Gly Ile Pro Val Val Gly Val Pro Lys Thr Ile Asp Asn Asp	
120 125 130	
gtg aat ggc act gac ttc acc ttc ggt ttc gat act gct gtg gca gtg	547
Val Asn Gly Thr Asp Phe Thr Phe Gly Phe Asp Thr Ala Val Ala Val	
135 140 145	
gct acc gac gct gtt gac cgc ctg cac acc acc gct gaa tct cac aac	595
Ala Thr Asp Ala Val Asp Arg Leu His Thr Thr Ala Glu Ser His Asn	
150 155 160 165	
cgt gtg atg atc gtg gag gtc atg ggc cgc cac gtg ggt tgg att gct	643
Arg Val Met Ile Val Glu Val Met Gly Arg His Val Gly Trp Ile Ala	
170 175 180	
ctg cac gca ggt atg gcc ggc ggt gct cac tac acc gtt att cca gaa	691
Leu His Ala Gly Met Ala Gly Gly Ala His Tyr Thr Val Ile Pro Glu	
185 190 195	
gta cct ttc gat att gca gag atc tgc aag gcg atg gaa cgt cgc ttc	739
Val Pro Phe Asp Ile Ala Glu Ile Cys Lys Ala Met Glu Arg Arg Phe	
200 205 210	
cag atg ggc gag aag tac ggc att atc gtc gtt gcg gaa ggt gcg ttg	787
Gln Met Gly Glu Lys Tyr Gly Ile Ile Val Val Ala Glu Gly Ala Leu	
215 220 225	
cca cgc gaa ggc acc atg gag ctt cgt gaa ggc cac att gac cag ttc	835
Pro Arg Glu Gly Thr Met Glu Leu Arg Glu Gly His Ile Asp Gln Phe	
230 235 240 245	
ggt cac aag acc ttc acg gga att gga cag cag atc gct gat gag atc	883
Gly His Lys Thr Phe Thr Gly Ile Gly Gln Gln Ile Ala Asp Glu Ile	
250 255 260	
cac gtg cgc ctc ggc cac gat gtt cgt acg acc gtt ctt ggc cac att	931
His Val Arg Leu Gly His Asp Val Arg Thr Thr Val Leu Gly His Ile	
265 270 275	
caa cgt ggt gga acc cca act gct ttc gac cgt gtt ctg gcc act cgt	979
Gln Arg Gly Gly Thr Pro Thr Ala Phe Asp Arg Val Leu Ala Thr Arg	
280 285 290	
tat ggt gtt cgt gca gct cgt gcg tgc cat gag gga agc ttt gac aag	1027

Tyr Gly Val Arg Ala Ala Arg Ala Cys His Glu Gly Ser Phe Asp Lys
 295 300 305
 gtt gtt gct ttg aag ggt gag agc att gag atg atc acc ttt gaa gaa 1075
 Val Val Ala Leu Lys Gly Glu Ser Ile Glu Met Ile Thr Phe Glu Glu
 310 315 320 325
 gca gtc gga acc ttg aag gaa gtt cca ttc gaa cgc tgg gtt act gcc 1123
 Ala Val Gly Thr Leu Lys Glu Val Pro Phe Glu Arg Trp Val Thr Ala
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 Gln Ala Met Phe Gly
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<210> 54
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 <212> PRT
 <213> Corynebacterium glutamicum

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 35 40 45
 Gly Asp Arg Arg Val Gln Leu Tyr Asp Asp Glu Asp Ile Asp Arg Ile
 50 55 60
 Leu Leu Arg Gly Gly Thr Ile Leu Gly Thr Gly Arg Leu His Pro Asp
 65 70 75 80
 Lys Phe Lys Ala Gly Ile Asp Gln Ile Lys Ala Asn Leu Glu Asp Ala
 85 90 95
 Gly Ile Asp Ala Leu Ile Pro Ile Gly Gly Glu Gly Thr Leu Lys Gly
 100 105 110
 Ala Lys Trp Leu Ser Asp Asn Gly Ile Pro Val Val Gly Val Pro Lys
 115 120 125
 Thr Ile Asp Asn Asp Val Asn Gly Thr Asp Phe Thr Phe Gly Phe Asp
 130 135 140
 Thr Ala Val Ala Val Ala Thr Asp Ala Val Asp Arg Leu His Thr Thr
 145 150 155 160
 Ala Glu Ser His Asn Arg Val Met Ile Val Glu Val Met Gly Arg His
 165 170 175
 Val Gly Trp Ile Ala Leu His Ala Gly Met Ala Gly Gly Ala His Tyr
 180 185 190
 Thr Val Ile Pro Glu Val Pro Phe Asp Ile Ala Glu Ile Cys Lys Ala
 195 200 205

Met Glu Arg Arg Phe Gln Met Gly Glu Lys Tyr Gly Ile Ile Val Val
 210 215 220

Ala Glu Gly Ala Leu Pro Arg Glu Gly Thr Met Glu Leu Arg Glu Gly
 225 230 235 240

His Ile Asp Gln Phe Gly His Lys Thr Phe Thr Gly Ile Gly Gln Gln
 245 250 255

Ile Ala Asp Glu Ile His Val Arg Leu Gly His Asp Val Arg Thr Thr
 260 265 270

Val Leu Gly His Ile Gln Arg Gly Gly Thr Pro Thr Ala Phe Asp Arg
 275 280 285

Val Leu Ala Thr Arg Tyr Gly Val Arg Ala Ala Arg Ala Cys His Glu
 290 295 300

Gly Ser Phe Asp Lys Val Val Ala Leu Lys Gly Glu Ser Ile Glu Met
 305 310 315 320

Ile Thr Phe Glu Glu Ala Val Gly Thr Leu Lys Glu Val Pro Phe Glu
 325 330 335

Arg Trp Val Thr Ala Gln Ala Met Phe Gly
 340 345

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 <212> DNA
 <213> Corynebacterium glutamicum

<220>
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 <222> (101)..(1060)
 <223> RXA01243

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agcagttgcg agaacgcgat gtagaagttg tgattgcaga atg att ctt aca gtc 115
 Met Ile Leu Thr Val
 1 5

act gca agt ccg tat ctg ttg agc acc aat gag ctt gac ggc acc atc 163
 Thr Ala Ser Pro Tyr Leu Leu Ser Thr Asn Glu Leu Asp Gly Thr Ile
 10 15 20

gaa att ggc gaa gca aac aaa atc cgg cag gtt tcc act gtt gcc ggt 211
 Glu Ile Gly Glu Ala Asn Lys Ile Arg Gln Val Ser Thr Val Ala Gly
 25 30 35

ggg ttt ggc acc ggt gtg gct gcc acc ttg ttt tat ggc ggc aat gaa 259
 Gly Phe Gly Thr Gly Val Ala Ala Thr Leu Phe Tyr Gly Gly Asn Glu
 40 45 50

act ttt gca gtt ttt ccc gct cca gaa atc tct cat tac atg cgc ctg 307
 Thr Phe Ala Val Phe Pro Ala Pro Glu Ile Ser His Tyr Met Arg Leu
 55 60 65

gtg acg ttt gct ggg ttg cct cat gaa att att ccg gtg gca ggt ccc	355
Val Thr Phe Ala Gly Leu Pro His Glu Ile Ile Pro Val Ala Gly Pro	
70 75 80 85	
atc ccc atg cat ttg acc atg cgt gat gca gag ggc aat gag act aag	403
Ile Pro Met His Leu Thr Met Arg Asp Ala Glu Gly Asn Glu Thr Lys	
90 95 100	
ttc aaa gac tcc ccc atg cct ttg gat gtg tcc cag ttg gca att ctt	451
Phe Lys Asp Ser Pro Met Pro Leu Asp Val Ser Gln Leu Ala Ile Leu	
105 110 115	
cgt gat cta gtg gtg cgt cga gcc gaa gat gcc gcg tgg gtg ttg ttg	499
Arg Asp Leu Val Val Arg Arg Ala Glu Asp Ala Ala Trp Val Leu Leu	
120 125 130	
ggg ggc aat ttg ccg tct atc gcg cct gct gcg tgg ttt gtg gat gtg	547
Gly Gly Asn Leu Pro Ser Ile Ala Pro Ala Ala Trp Phe Val Asp Val	
135 140 145	
gtg aga tca ctt cgc ttg tac cac cct cat gtg aag gta gct atc gca	595
Val Arg Ser Leu Arg Leu Tyr His Pro His Val Lys Val Ala Ile Ala	
150 155 160 165	
gca act ggt gct gcg ttg cgt gcg gtt att cga cag ctt gca gct acg	643
Ala Thr Gly Ala Ala Leu Arg Ala Val Ile Arg Gln Leu Ala Ala Thr	
170 175 180	
tcc ccg gat gcg ctg att gtg gct gcg gaa gaa atc gaa att gcc act	691
Ser Pro Asp Ala Leu Ile Val Ala Ala Glu Glu Ile Glu Ile Ala Thr	
185 190 195	
gga tta gaa ccc aaa acc ttg aga ggt cca tgg gta gag gga gat ctc	739
Gly Leu Glu Pro Lys Thr Leu Arg Gly Pro Trp Val Glu Gly Asp Leu	
200 205 210	
tcc ccg act gtg gcg gca gcg cgc gct tta att gat agc ggt gtc acc	787
Ser Pro Thr Val Ala Ala Ala Arg Ala Leu Ile Asp Ser Gly Val Thr	
215 220 225	
gag gtg ttg gtt acc aac aag cgg acg gaa tct ttg tat gtt tcc gag	835
Glu Val Leu Val Thr Asn Lys Arg Thr Glu Ser Leu Tyr Val Ser Glu	
230 235 240 245	
tct gaa tca ctg tta gcc agc tac gac agc acc cct ggt aag cag ggc	883
Ser Glu Ser Leu Leu Ala Ser Tyr Asp Ser Thr Pro Gly Lys Gln Gly	
250 255 260	
gtg aat tgg cgg gaa tct ttt act gca gga ttc ttg gca gca tcc aat	931
Val Asn Trp Arg Glu Ser Phe Thr Ala Gly Phe Leu Ala Ala Ser Asn	
265 270 275	
gat gga aaa tcc act gag gac agc gtg atc aac gcg gtt gct tac gcc	979
Asp Gly Lys Ser Thr Glu Asp Ser Val Ile Asn Ala Val Ala Tyr Ala	
280 285 290	
aac gct gaa ggc agt gag tgg gac aac tac att ccc aca ccc gat aag	1027
Asn Ala Glu Gly Ser Glu Trp Asp Asn Tyr Ile Pro Thr Pro Asp Lys	
295 300 305	
ctt cgg gcg gag cac gtg gtc atc aaa tcg ctt tagaccacgc aaaaagcctc	1080

Leu Arg Ala Glu His Val Val Ile Lys Ser Leu
310 315 320

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1083

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<212> PRT
<213> Corynebacterium glutamicum

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35 40 45
Tyr Gly Gly Asn Glu Thr Phe Ala Val Phe Pro Ala Pro Glu Ile Ser
50 55 60
His Tyr Met Arg Leu Val Thr Phe Ala Gly Leu Pro His Glu Ile Ile
65 70 75 80
Pro Val Ala Gly Pro Ile Pro Met His Leu Thr Met Arg Asp Ala Glu
85 90 95
Gly Asn Glu Thr Lys Phe Lys Asp Ser Pro Met Pro Leu Asp Val Ser
100 105 110
Gln Leu Ala Ile Leu Arg Asp Leu Val Val Arg Arg Ala Glu Asp Ala
115 120 125
Ala Trp Val Leu Leu Gly Gly Asn Leu Pro Ser Ile Ala Pro Ala Ala
130 135 140
Trp Phe Val Asp Val Val Arg Ser Leu Arg Leu Tyr His Pro His Val
145 150 155 160
Lys Val Ala Ile Ala Ala Thr Gly Ala Ala Leu Arg Ala Val Ile Arg
165 170 175
Gln Leu Ala Ala Thr Ser Pro Asp Ala Leu Ile Val Ala Ala Glu Glu
180 185 190
Ile Glu Ile Ala Thr Gly Leu Glu Pro Lys Thr Leu Arg Gly Pro Trp
195 200 205
Val Glu Gly Asp Leu Ser Pro Thr Val Ala Ala Ala Arg Ala Leu Ile
210 215 220
Asp Ser Gly Val Thr Glu Val Leu Val Thr Asn Lys Arg Thr Glu Ser
225 230 235 240
Leu Tyr Val Ser Glu Ser Glu Ser Leu Leu Ala Ser Tyr Asp Ser Thr
245 250 255
Pro Gly Lys Gln Gly Val Asn Trp Arg Glu Ser Phe Thr Ala Gly Phe

260	265	270
Leu Ala Ala Ser Asn Asp Gly Lys Ser Thr Glu Asp Ser Val Ile Asn		
275	280	285
Ala Val Ala Tyr Ala Asn Ala Glu Gly Ser Glu Trp Asp Asn Tyr Ile		
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		320

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 <223> RXA01882

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 Met Ile Ile Thr Phe
 1 5
 acc cca aac ccg agt att gat tcc acg ctg tcg ctc ggc gaa gag ctc 163
 Thr Pro Asn Pro Ser Ile Asp Ser Thr Leu Ser Leu Gly Glu Glu Leu
 10 15 20
 tcc cgt gga tcc gtc caa cga ctt gat tcc gtc acc gct gtc gca ggt 211
 Ser Arg Gly Ser Val Gln Arg Leu Asp Ser Val Thr Ala Val Ala Gly
 25 30 35
 ggt aaa ggc atc aat gtc gcc cac gct gtc ttg ctt gcg ggc ttt gaa 259
 Gly Lys Gly Ile Asn Val Ala His Ala Val Leu Leu Ala Gly Phe Glu
 40 45 50
 acc ttg gct gtg ttc cca gcc ggc aag ctc gac ccc ttc gtc cca ctg 307
 Thr Leu Ala Val Phe Pro Ala Gly Lys Leu Asp Pro Phe Val Pro Leu
 55 60 65
 gtc cgc gac atc ggc ttg ccc gtg gaa act gtt gtg atc aac aag aac 355
 Val Arg Asp Ile Gly Leu Pro Val Glu Thr Val Val Ile Asn Lys Asn
 70 75 80 85
 gtc cgc acc aac acc aca gtc acc gaa ccg gac ggc acc acc acc aag 403
 Val Arg Thr Asn Thr Thr Val Thr Glu Pro Asp Gly Thr Thr Thr Lys
 90 95 100
 ctc aac ggc ccc ggc gcg ccg ctc agc gag cag aag ctc cgt agc ttg 451
 Leu Asn Gly Pro Gly Ala Pro Leu Ser Glu Gln Lys Leu Arg Ser Leu
 105 110 115
 gaa aag gtg ctt atc gac gcg ctc cgc ccc gaa gtc acc tgg gtt gtc 499

Glu	Lys	Val	Leu	Ile	Asp	Ala	Leu	Arg	Pro	Glu	Val	Thr	Trp	Val	Val		
		120					125					130					
ctg	gcg	ggc	tcg	ctg	cca	cca	ggg	gca	cca	gtt	gac	tgg	tac	gcg	cgt	547	
Leu	Ala	Gly	Ser	Leu	Pro	Pro	Gly	Ala	Pro	Val	Asp	Trp	Tyr	Ala	Arg		
	135					140					145						
ctc	acc	gcg	ttg	atc	cat	tca	gca	cgc	cct	gac	gtt	cgc	gtg	gct	gtc	595	
Leu	Thr	Ala	Leu	Ile	His	Ser	Ala	Arg	Pro	Asp	Val	Arg	Val	Ala	Val		
150				155						160					165		
gat	acc	tca	gac	aag	cca	ctg	atg	gcg	ttg	ggc	gag	agc	ttg	gat	aca	643	
Asp	Thr	Ser	Asp	Lys	Pro	Leu	Met	Ala	Leu	Gly	Glu	Ser	Leu	Asp	Thr		
				170					175					180			
cct	ggc	gct	gct	ccg	aac	ctg	att	aag	cca	aat	ggc	ctg	gaa	ctg	ggc	691	
Pro	Gly	Ala	Ala	Pro	Asn	Leu	Ile	Lys	Pro	Asn	Gly	Leu	Glu	Leu	Gly		
			185					190					195				
cag	ctg	gct	aac	act	gat	ggc	gaa	gag	ctg	gag	gag	cgt	gct	gag	caa	739	
Gln	Leu	Ala	Asn	Thr	Asp	Gly	Glu	Glu	Leu	Glu	Ala	Arg	Ala	Ala	Gln		
	200						205					210					
ggc	gat	tac	gac	gcc	atc	atc	gca	gct	gag	gac	gta	ctg	gtt	aac	cgt	787	
Gly	Asp	Tyr	Asp	Ala	Ile	Ile	Ala	Ala	Ala	Asp	Val	Leu	Val	Asn	Arg		
	215				220						225						
ggc	atc	gaa	cag	gtg	ctt	gtc	acc	ttg	ggc	gcc	gca	gga	gag	gtg	ttg	835	
Gly	Ile	Glu	Gln	Val	Leu	Val	Thr	Leu	Gly	Ala	Ala	Gly	Ala	Val	Leu		
230					235				240						245		
gtc	aac	gca	gaa	ggc	gag	tgg	act	gct	act	tct	cca	aag	att	gat	gtt	883	
Val	Asn	Ala	Glu	Gly	Ala	Trp	Thr	Ala	Thr	Ser	Pro	Lys	Ile	Asp	Val		
				250					255					260			
gta	tcc	acc	gtt	gga	gct	gga	gac	tgt	gct	ctt	gca	ggc	ttt	gtt	atg	931	
Val	Ser	Thr	Val	Gly	Ala	Gly	Asp	Cys	Ala	Leu	Ala	Gly	Phe	Val	Met		
			265				270						275				
gca	cgt	tcc	cag	aag	aaa	aca	ctg	gag	gaa	tct	ctg	ctg	aat	gcc	gtg	979	
Ala	Arg	Ser	Gln	Lys	Lys	Thr	Leu	Glu	Glu	Ser	Leu	Leu	Asn	Ala	Val		
		280					285					290					
tct	tac	ggc	tcg	act	gag	gag	tct	ctt	cct	ggc	act	acc	att	cct	cgt	1027	
Ser	Tyr	Gly	Ser	Thr	Ala	Ala	Ser	Leu	Pro	Gly	Thr	Thr	Ile	Pro	Arg		
	295					300					305						
cct	gac	caa	ctc	gcc	aca	gct	ggc	gca	acg	gtc	acc	caa	gtc	aaa	gga	1075	
Pro	Asp	Gln	Leu	Ala	Thr	Ala	Gly	Ala	Thr	Val	Thr	Gln	Val	Lys	Gly		
310					315					320					325		
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Leu	Lys	Glu	Ser	Ala													
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<211> 330

<212> PRT

<213> Corynebacterium glutamicum

<400> 58

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Thr Ala Val Ala Gly Gly Lys Gly Ile Asn Val Ala His Ala Val Leu
      35           40           45

Leu Ala Gly Phe Glu Thr Leu Ala Val Phe Pro Ala Gly Lys Leu Asp
 50           55           60

Pro Phe Val Pro Leu Val Arg Asp Ile Gly Leu Pro Val Glu Thr Val
 65           70           75           80

Val Ile Asn Lys Asn Val Arg Thr Asn Thr Thr Val Thr Glu Pro Asp
          85           90           95

Gly Thr Thr Thr Lys Leu Asn Gly Pro Gly Ala Pro Leu Ser Glu Gln
      100           105           110

Lys Leu Arg Ser Leu Glu Lys Val Leu Ile Asp Ala Leu Arg Pro Glu
      115           120           125

Val Thr Trp Val Val Leu Ala Gly Ser Leu Pro Pro Gly Ala Pro Val
      130           135           140

Asp Trp Tyr Ala Arg Leu Thr Ala Leu Ile His Ser Ala Arg Pro Asp
145           150           155           160

Val Arg Val Ala Val Asp Thr Ser Asp Lys Pro Leu Met Ala Leu Gly
          165           170           175

Glu Ser Leu Asp Thr Pro Gly Ala Ala Pro Asn Leu Ile Lys Pro Asn
      180           185           190

Gly Leu Glu Leu Gly Gln Leu Ala Asn Thr Asp Gly Glu Glu Leu Glu
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Ala Arg Ala Ala Gln Gly Asp Tyr Asp Ala Ile Ile Ala Ala Ala Asp
      210           215           220

Val Leu Val Asn Arg Gly Ile Glu Gln Val Leu Val Thr Leu Gly Ala
225           230           235           240

Ala Gly Ala Val Leu Val Asn Ala Glu Gly Ala Trp Thr Ala Thr Ser
          245           250           255

Pro Lys Ile Asp Val Val Ser Thr Val Gly Ala Gly Asp Cys Ala Leu
      260           265           270

Ala Gly Phe Val Met Ala Arg Ser Gln Lys Lys Thr Leu Glu Glu Ser
      275           280           285

Leu Leu Asn Ala Val Ser Tyr Gly Ser Thr Ala Ala Ser Leu Pro Gly
      290           295           300

Thr Thr Ile Pro Arg Pro Asp Gln Leu Ala Thr Ala Gly Ala Thr Val
305           310           315           320

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 <223> RXA01702

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 Met Pro Ile Ala Thr
 1 5
 ccc gag gtc tat aac gag atg ctg gat cgt gct aag gaa ggc gga ttc 163
 Pro Glu Val Tyr Asn Glu Met Leu Asp Arg Ala Lys Glu Gly Phe
 10 15 20
 gcc ttc cca gcc atc aac tgc acc tcc tcg gaa acc atc aac gca gct 211
 Ala Phe Pro Ala Ile Asn Cys Thr Ser Ser Glu Thr Ile Asn Ala Ala
 25 30 35
 ctg aag ggc ttc gca gag gct gaa tct gac gga atc atc cag ttc tcc 259
 Leu Lys Gly Phe Ala Glu Ala Glu Ser Asp Gly Ile Ile Gln Phe Ser
 40 45 50
 acc ggt ggt gca gag ttc ggt tcc ggc ctg gca gta aag aac aag gtc 307
 Thr Gly Gly Ala Glu Phe Gly Ser Gly Leu Ala Val Lys Asn Lys Val
 55 60 65
 aag ggc gca gtt gcg ctt gca gcc ttc gcc cac gag gca gca aag agc 355
 Lys Gly Ala Val Ala Leu Ala Ala Phe Ala His Glu Ala Ala Lys Ser
 70 75 80 85
 tac ggc atc aac gtt gct ctg cac act gac cac tgc cag aag gaa gtc 403
 Tyr Gly Ile Asn Val Ala Leu His Thr Asp His Cys Gln Lys Glu Val
 90 95 100
 ctg gac gag tac gtc cgc cca ctg ctg gct atc tcc cag gag cgc gtc 451
 Leu Asp Glu Tyr Val Arg Pro Leu Leu Ala Ile Ser Gln Glu Arg Val
 105 110 115
 gac cgc ggc gag ctt cca ctg ttc cag tcc cac atg tgg gat ggt tcc 499
 Asp Arg Gly Glu Leu Pro Leu Phe Gln Ser His Met Trp Asp Gly Ser
 120 125 130
 gct gtc cca atc gac gag aac ctg gaa atc gca cag gag ctg ctg gct 547
 Ala Val Pro Ile Asp Glu Asn Leu Glu Ile Ala Gln Glu Leu Leu Ala
 135 140 145
 aag gcc aag gca gcg aac atc atc ttg gaa gtt gag atc ggt gtt gtc 595
 Lys Ala Lys Ala Ala Asn Ile Ile Leu Glu Val Glu Ile Gly Val Val
 150 155 160 165

ggt ggc gaa gaa gac ggc gtt gag gct aag gct ggc gca aac ctc tac 643
 Gly Gly Glu Glu Asp Gly Val Glu Ala Lys Ala Gly Ala Asn Leu Tyr
 170 175 180
 acc tcc cca gaa gac ttt gag aag acc atc gat gca atc ggc acc ggt 691
 Thr Ser Pro Glu Asp Phe Glu Lys Thr Ile Asp Ala Ile Gly Thr Gly
 185 190 195
 gag aag ggc cgc tac ctg cta gca gct acc ttc ggt aac gtc cac ggc 739
 Glu Lys Gly Arg Tyr Leu Leu Ala Ala Thr Phe Gly Asn Val His Gly
 200 205 210
 gtt tac aag cca ggc aac gtc aag ctg cgc cca gag gtc ctc ctt gag 787
 Val Tyr Lys Pro Gly Asn Val Lys Leu Arg Pro Glu Val Leu Leu Glu
 215 220 225
 ggc cag cag gtt gca cgc aag aag ctt gga ctt gca gac gac gca ctt 835
 Gly Gln Gln Val Ala Arg Lys Lys Leu Gly Leu Ala Asp Asp Ala Leu
 230 235 240 245
 cca ttc gac ttc gtc ttc cac ggt ggc tca ggc tcc gag aag gaa aag 883
 Pro Phe Asp Phe Val Phe His Gly Gly Ser Gly Ser Glu Lys Glu Lys
 250 255 260
 atc gaa gag gcg ctg acc tac ggc gtc atc aag atg aac gtt gat act 931
 Ile Glu Glu Ala Leu Thr Tyr Gly Val Ile Lys Met Asn Val Asp Thr
 265 270 275
 gac acc cag tac gca ttc acc cgc cca atc gtc tcc cac atg ttt gag 979
 Asp Thr Gln Tyr Ala Phe Thr Arg Pro Ile Val Ser His Met Phe Glu
 280 285 290
 aac tac aac ggc gtt ctc aag atc gac ggc gag gtc gga aac aag aag 1027
 Asn Tyr Asn Gly Val Leu Lys Ile Asp Gly Glu Val Gly Asn Lys Lys
 295 300 305
 gct tac gac cca cgc tct tac atg aag aag gct gag cag agc atg tct 1075
 Ala Tyr Asp Pro Arg Ser Tyr Met Lys Lys Ala Glu Gln Ser Met Ser
 310 315 320 325
 gag cgc att atc gag tct tgc cag gac ctc aag tct gtt gga aag acc 1123
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<211> 344

<212> PRT

<213> Corynebacterium glutamicum

<400> 60

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Thr Ile Asn Ala Ala Leu Lys Gly Phe Ala Glu Ala Glu Ser Asp Gly
 35 40 45
 Ile Ile Gln Phe Ser Thr Gly Gly Ala Glu Phe Gly Ser Gly Leu Ala
 50 55 60
 Val Lys Asn Lys Val Lys Gly Ala Val Ala Leu Ala Ala Phe Ala His
 65 70 75 80
 Glu Ala Ala Lys Ser Tyr Gly Ile Asn Val Ala Leu His Thr Asp His
 85 90 95
 Cys Gln Lys Glu Val Leu Asp Glu Tyr Val Arg Pro Leu Leu Ala Ile
 100 105 110
 Ser Gln Glu Arg Val Asp Arg Gly Glu Leu Pro Leu Phe Gln Ser His
 115 120 125
 Met Trp Asp Gly Ser Ala Val Pro Ile Asp Glu Asn Leu Glu Ile Ala
 130 135 140
 Gln Glu Leu Leu Ala Lys Ala Lys Ala Ala Asn Ile Ile Leu Glu Val
 145 150 155 160
 Glu Ile Gly Val Val Gly Gly Glu Glu Asp Gly Val Glu Ala Lys Ala
 165 170 175
 Gly Ala Asn Leu Tyr Thr Ser Pro Glu Asp Phe Glu Lys Thr Ile Asp
 180 185 190
 Ala Ile Gly Thr Gly Glu Lys Gly Arg Tyr Leu Leu Ala Ala Thr Phe
 195 200 205
 Gly Asn Val His Gly Val Tyr Lys Pro Gly Asn Val Lys Leu Arg Pro
 210 215 220
 Glu Val Leu Leu Glu Gly Gln Gln Val Ala Arg Lys Lys Leu Gly Leu
 225 230 235 240
 Ala Asp Asp Ala Leu Pro Phe Asp Phe Val Phe His Gly Gly Ser Gly
 245 250 255
 Ser Glu Lys Glu Lys Ile Glu Glu Ala Leu Thr Tyr Gly Val Ile Lys
 260 265 270
 Met Asn Val Asp Thr Asp Thr Gln Tyr Ala Phe Thr Arg Pro Ile Val
 275 280 285
 Ser His Met Phe Glu Asn Tyr Asn Gly Val Leu Lys Ile Asp Gly Glu
 290 295 300
 Val Gly Asn Lys Lys Ala Tyr Asp Pro Arg Ser Tyr Met Lys Lys Ala
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 Glu Gln Ser Met Ser Glu Arg Ile Ile Glu Ser Cys Gln Asp Leu Lys
 325 330 335
 Ser Val Gly Lys Thr Thr Ser Lys
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<220>
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 <222> (101)..(877)
 <223> RXA02258

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 Met Ala Arg Lys Pro
 1 5

ctt atc gct ggt aac tgg aag atg aac ctg gat cac cag cag gca atc 163
 Leu Ile Ala Gly Asn Trp Lys Met Asn Leu Asp His Gln Gln Ala Ile
 10 15 20

ggc act gtt cag aag ctt gca ttc gcc ctt cca aag gaa tac ttc gag 211
 Gly Thr Val Gln Lys Leu Ala Phe Ala Leu Pro Lys Glu Tyr Phe Glu
 25 30 35

aag gtt gac gtt gca gtc acc gtt cct ttc act gac atc cgc tcc gtc 259
 Lys Val Asp Val Ala Val Thr Val Pro Phe Thr Asp Ile Arg Ser Val
 40 45 50

cag act ctc gtt gag ggc gac aag ctt gag gtc act ttc ggt gct cag 307
 Gln Thr Leu Val Glu Gly Asp Lys Leu Glu Val Thr Phe Gly Ala Gln
 55 60 65

gac gtc tcc cag cac gag tcc ggt gcg tac acc ggt gaa gtt tct gca 355
 Asp Val Ser Gln His Glu Ser Gly Ala Tyr Thr Gly Glu Val Ser Ala
 70 75 80 85

agc atg ctg gca aag ttg aac tgc tct tgg gtt gtc gtt gga cac tcc 403
 Ser Met Leu Ala Lys Leu Asn Cys Ser Trp Val Val Val Gly His Ser
 90 95 100

gag cgc cgc gag tac cac aac gag tct gat gag ttg gtt gct gcg aag 451
 Glu Arg Arg Glu Tyr His Asn Glu Ser Asp Glu Leu Val Ala Ala Lys
 105 110 115

gca aag gca gct ctg tcc aac ggc atc agc ccg atc gtc tgc gtt ggt 499
 Ala Lys Ala Ala Leu Ser Asn Gly Ile Ser Pro Ile Val Cys Val Gly
 120 125 130

gag cca ctg gaa atc cgt gaa gct ggc acc cac gtt gag tac gtc gtc 547
 Glu Pro Leu Glu Ile Arg Glu Ala Gly Thr His Val Glu Tyr Val Val
 135 140 145

gag cag acc cgt aag tcc ctt gct ggc ctg gat gct gct gag ctg gcc 595
 Glu Gln Thr Arg Lys Ser Leu Ala Gly Leu Asp Ala Ala Glu Leu Ala
 150 155 160 165

aac acc gtt atc gcg tat gag cca gtg tgg gct atc ggc acc ggt aag 643
 Asn Thr Val Ile Ala Tyr Glu Pro Val Trp Ala Ile Gly Thr Gly Lys
 170 175 180

gtt gct tcc gca gct gac gct cag gaa gtg tgc aag gct atc cgc ggt 691
 Val Ala Ser Ala Ala Asp Ala Gln Glu Val Cys Lys Ala Ile Arg Gly
 185 190 195
 ctg atc gtg gag ctt gca ggc gac gag gtc gct gag ggc ctg cgt att 739
 Leu Ile Val Glu Leu Ala Gly Asp Glu Val Ala Glu Gly Leu Arg Ile
 200 205 210
 ctt tac ggt ggt tct gtt aag gca gaa acc gtc gct gag atc gtc ggt 787
 Leu Tyr Gly Gly Ser Val Lys Ala Glu Thr Val Ala Glu Ile Val Gly
 215 220 225
 cag cct gac gtc gac ggc gga ctt gtc ggt ggc gct tcc ctc gac ggt 835
 Gln Pro Asp Val Asp Gly Gly Leu Val Gly Gly Ala Ser Leu Asp Gly
 230 235 240 245
 gaa gca ttc gcc aag ctg gct gcc aac gct gcg agc gtt gct 877
 Glu Ala Phe Ala Lys Leu Ala Ala Asn Ala Ala Ser Val Ala
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 <211> 259
 <212> PRT
 <213> Corynebacterium glutamicum

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 His Gln Gln Ala Ile Gly Thr Val Gln Lys Leu Ala Phe Ala Leu Pro
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 Lys Glu Tyr Phe Glu Lys Val Asp Val Ala Val Thr Val Pro Phe Thr
 35 40 45
 Asp Ile Arg Ser Val Gln Thr Leu Val Glu Gly Asp Lys Leu Glu Val
 50 55 60
 Thr Phe Gly Ala Gln Asp Val Ser Gln His Glu Ser Gly Ala Tyr Thr
 65 70 75 80
 Gly Glu Val Ser Ala Ser Met Leu Ala Lys Leu Asn Cys Ser Trp Val
 85 90 95
 Val Val Gly His Ser Glu Arg Arg Glu Tyr His Asn Glu Ser Asp Glu
 100 105 110
 Leu Val Ala Ala Lys Ala Lys Ala Ala Leu Ser Asn Gly Ile Ser Pro
 115 120 125
 Ile Val Cys Val Gly Glu Pro Leu Glu Ile Arg Glu Ala Gly Thr His
 130 135 140
 Val Glu Tyr Val Val Glu Gln Thr Arg Lys Ser Leu Ala Gly Leu Asp
 145 150 155 160
 Ala Ala Glu Leu Ala Asn Thr Val Ile Ala Tyr Glu Pro Val Trp Ala
 165 170 175

Ile Gly Thr Gly Lys Val Ala Ser Ala Ala Asp Ala Gln Glu Val Cys
 180 185 190

Lys Ala Ile Arg Gly Leu Ile Val Glu Leu Ala Gly Asp Glu Val Ala
 195 200 205

Glu Gly Leu Arg Ile Leu Tyr Gly Gly Ser Val Lys Ala Glu Thr Val
 210 215 220

Ala Glu Ile Val Gly Gln Pro Asp Val Asp Gly Gly Leu Val Gly Gly
 225 230 235 240

Ala Ser Leu Asp Gly Glu Ala Phe Ala Lys Leu Ala Ala Asn Ala Ala
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Ser Val Ala

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 <211> 1563
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 <213> Corynebacterium glutamicum

<220>
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 <222> (101)..(1540)
 <223> RXN01225

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cccggttaa cccacgcct aagtcagtga aggacttttt atg acg cac aac cac 115
 Met Thr His Asn His
 1 5

aag gac tgg aac gat cgc att gca gtt gcg gag gaa atg gtg ccg ttg 163
 Lys Asp Trp Asn Asp Arg Ile Ala Val Ala Glu Glu Met Val Pro Leu
 10 15 20

atc ggg cgc ctg cac cgc aac aac aac gtg gtg gtt tcc gta ttc ggt 211
 Ile Gly Arg Leu His Arg Asn Asn Asn Val Val Val Ser Val Phe Gly
 25 30 35

cgt ctc ctt gtg aat gtc tca gac atc gat atc atc aag tct cac cgc 259
 Arg Leu Leu Val Asn Val Ser Asp Ile Asp Ile Ile Lys Ser His Arg
 40 45 50

tac gcc cgc cac atc ata tcc aag gaa ctt cca ctg gaa agc tcc ttg 307
 Tyr Ala Arg His Ile Ile Ser Lys Glu Leu Pro Leu Glu Ser Ser Leu
 55 60 65

gat att ttg cgc gaa ctg gta gat atg aac ctt ggt acc gca tcg atc 355
 Asp Ile Leu Arg Glu Leu Val Asp Met Asn Leu Gly Thr Ala Ser Ile
 70 75 80 85

gac ctg gga cag ctg gcc tac agc ttc gaa gaa tcc gaa agc acc gac 403
 Asp Leu Gly Gln Leu Ala Tyr Ser Phe Glu Glu Ser Glu Ser Thr Asp
 90 95 100

ctg	cgt	gcc	ttc	ctg	gag	gac	gct	ctc	gcg	ccg	gtc	att	ggg	gcg	gaa	451
Leu	Arg	Ala	Phe	Leu	Glu	Asp	Ala	Leu	Ala	Pro	Val	Ile	Gly	Ala	Glu	
			105					110					115			
acc	gac	atc	aac	cca	act	gat	atc	gtg	ctg	tac	ggg	ttc	ggc	cgc	atc	499
Thr	Asp	Ile	Asn	Pro	Thr	Asp	Ile	Val	Leu	Tyr	Gly	Phe	Gly	Arg	Ile	
			120				125					130				
ggg	cgc	ctg	ctg	gcc	cgc	atc	ctg	gtt	tcc	cgc	gag	gca	ctg	tat	gac	547
Gly	Arg	Leu	Leu	Ala	Arg	Ile	Leu	Val	Ser	Arg	Glu	Ala	Leu	Tyr	Asp	
			135				140				145					
ggg	gct	cgt	ctg	cgc	gcc	atc	gtg	gtc	cgc	aaa	aat	ggg	gaa	gaa	gac	595
Gly	Ala	Arg	Leu	Arg	Ala	Ile	Val	Val	Arg	Lys	Asn	Gly	Glu	Glu	Asp	
150					155					160					165	
ctg	gtc	aag	cgc	gca	tcc	ttg	ctg	cgt	cgt	gat	tct	gtc	cac	ggg	gga	643
Leu	Val	Lys	Arg	Ala	Ser	Leu	Leu	Arg	Arg	Asp	Ser	Val	His	Gly	Gly	
				170					175					180		
ttc	gat	ggc	acc	atc	acc	acc	gat	tat	gac	aac	aac	atc	atc	tgg	gcc	691
Phe	Asp	Gly	Thr	Ile	Thr	Thr	Asp	Tyr	Asp	Asn	Asn	Ile	Ile	Trp	Ala	
			185					190					195			
aac	ggc	acc	cca	atc	aag	gtc	atc	tac	tcc	aat	gac	cca	gcc	acc	att	739
Asn	Gly	Thr	Pro	Ile	Lys	Val	Ile	Tyr	Ser	Asn	Asp	Pro	Ala	Thr	Ile	
			200				205					210				
gat	tac	acc	gaa	tac	ggc	atc	aat	gac	gcc	gtc	gtg	gta	gac	aac	acc	787
Asp	Tyr	Thr	Glu	Tyr	Gly	Ile	Asn	Asp	Ala	Val	Val	Val	Asp	Asn	Thr	
			215			220					225					
ggc	cgc	tgg	cgt	gac	cgc	gaa	ggc	ctg	tcc	cag	cac	ctc	aag	tcc	aag	835
Gly	Arg	Trp	Arg	Asp	Arg	Glu	Gly	Leu	Ser	Gln	His	Leu	Lys	Ser	Lys	
230					235					240					245	
ggc	gtt	gcc	aag	gtt	gta	ctc	acc	gcg	ccg	ggc	aag	ggc	gat	ctg	aag	883
Gly	Val	Ala	Lys	Val	Val	Leu	Thr	Ala	Pro	Gly	Lys	Gly	Asp	Leu	Lys	
				250					255					260		
aac	atc	gtg	tac	ggc	atc	aac	cac	acc	gac	atc	acc	gca	gat	gat	cag	931
Asn	Ile	Val	Tyr	Gly	Ile	Asn	His	Thr	Asp	Ile	Thr	Ala	Asp	Asp	Gln	
			265					270					275			
atc	gtt	tcc	gca	gca	tca	tgc	acc	acc	aat	gcc	att	acc	cca	gtg	ctc	979
Ile	Val	Ser	Ala	Ala	Ser	Cys	Thr	Thr	Asn	Ala	Ile	Thr	Pro	Val	Leu	
			280				285					290				
aag	gtg	atc	aat	gat	cgc	tac	ggc	gtg	gaa	ttc	ggc	cac	gta	gaa	acc	1027
Lys	Val	Ile	Asn	Asp	Arg	Tyr	Gly	Val	Glu	Phe	Gly	His	Val	Glu	Thr	
			295			300					305					
gtt	cac	tcc	ttc	acc	aat	gac	cag	aac	ctg	atc	gac	aac	ttc	cac	aag	1075
Val	His	Ser	Phe	Thr	Asn	Asp	Gln	Asn	Leu	Ile	Asp	Asn	Phe	His	Lys	
310					315					320					325	
ggg	tct	cgc	cgt	ggg	cgc	gca	gca	ggg	ctg	aat	atg	gtt	ctc	acc	gaa	1123
Gly	Ser	Arg	Arg	Gly	Arg	Ala	Ala	Gly	Leu	Asn	Met	Val	Leu	Thr	Glu	
				330					335					340		
acc	ggc	gct	gca	aag	gct	gta	tcc	aag	gcg	ctt	cca	gag	ctg	gaa	ggc	1171

Thr Gly Ala Ala Lys Ala Val Ser Lys Ala Leu Pro Glu Leu Glu Gly
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 aag ctc acc ggc aat gcc atc cgc gtt cct acc cct gac gtg tcc atg 1219
 Lys Leu Thr Gly Asn Ala Ile Arg Val Pro Thr Pro Asp Val Ser Met
 360 365 370
 gct gtg ctc aac ttg acc ctg aac acg gag gtg gac cgc gat gag gtc 1267
 Ala Val Leu Asn Leu Thr Leu Asn Thr Glu Val Asp Arg Asp Glu Val
 375 380 385
 aac gag ttc ctc cgc cgt gtg tcc ctg cac tct gac ttg cgc cag caa 1315
 Asn Glu Phe Leu Arg Arg Val Ser Leu His Ser Asp Leu Arg Gln Gln
 390 395 400 405
 atc gac tgg atc cgt tcc cca gag gtt gtt tcc act gac ttc gtg ggc 1363
 Ile Asp Trp Ile Arg Ser Pro Glu Val Val Ser Thr Asp Phe Val Gly
 410 415 420
 acc acc cac gcg ggc atc gtt gat ggt cta gcc acc atc gca acc ggt 1411
 Thr Thr His Ala Gly Ile Val Asp Gly Leu Ala Thr Ile Ala Thr Gly
 425 430 435
 cgc cac ctg gtg ctt tac gtg tgg tac gac aac gag ttc ggc tac tcc 1459
 Arg His Leu Val Leu Tyr Val Trp Tyr Asp Asn Glu Phe Gly Tyr Ser
 440 445 450
 aac cag gtc att cgc atc gtc gag gag atc gcc ggc gtg cgt cct cgc 1507
 Asn Gln Val Ile Arg Ile Val Glu Glu Ile Ala Gly Val Arg Pro Arg
 455 460 465
 gtg tac ccg gag cgc agg cag cca gcc gta cta taggttatcc aagcctaata 1560
 Val Tyr Pro Glu Arg Arg Gln Pro Ala Val Leu
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 cac 1563

<210> 64
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 <212> PRT
 <213> *Corynebacterium glutamicum*

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 20 25 30
 Val Ser Val Phe Gly Arg Leu Leu Val Asn Val Ser Asp Ile Asp Ile
 35 40 45
 Ile Lys Ser His Arg Tyr Ala Arg His Ile Ile Ser Lys Glu Leu Pro
 50 55 60
 Leu Glu Ser Ser Leu Asp Ile Leu Arg Glu Leu Val Asp Met Asn Leu
 65 70 75 80
 Gly Thr Ala Ser Ile Asp Leu Gly Gln Leu Ala Tyr Ser Phe Glu Glu
 85 90 95

Ser Glu Ser Thr Asp Leu Arg Ala Phe Leu Glu Asp Ala Leu Ala Pro
 100 105 110
 Val Ile Gly Ala Glu Thr Asp Ile Asn Pro Thr Asp Ile Val Leu Tyr
 115 120 125
 Gly Phe Gly Arg Ile Gly Arg Leu Leu Ala Arg Ile Leu Val Ser Arg
 130 135 140
 Glu Ala Leu Tyr Asp Gly Ala Arg Leu Arg Ala Ile Val Val Arg Lys
 145 150 155 160
 Asn Gly Glu Glu Asp Leu Val Lys Arg Ala Ser Leu Leu Arg Arg Asp
 165 170 175
 Ser Val His Gly Gly Phe Asp Gly Thr Ile Thr Thr Asp Tyr Asp Asn
 180 185 190
 Asn Ile Ile Trp Ala Asn Gly Thr Pro Ile Lys Val Ile Tyr Ser Asn
 195 200 205
 Asp Pro Ala Thr Ile Asp Tyr Thr Glu Tyr Gly Ile Asn Asp Ala Val
 210 215 220
 Val Val Asp Asn Thr Gly Arg Trp Arg Asp Arg Glu Gly Leu Ser Gln
 225 230 235 240
 His Leu Lys Ser Lys Gly Val Ala Lys Val Val Leu Thr Ala Pro Gly
 245 250 255
 Lys Gly Asp Leu Lys Asn Ile Val Tyr Gly Ile Asn His Thr Asp Ile
 260 265 270
 Thr Ala Asp Asp Gln Ile Val Ser Ala Ala Ser Cys Thr Thr Asn Ala
 275 280 285
 Ile Thr Pro Val Leu Lys Val Ile Asn Asp Arg Tyr Gly Val Glu Phe
 290 295 300
 Gly His Val Glu Thr Val His Ser Phe Thr Asn Asp Gln Asn Leu Ile
 305 310 315 320
 Asp Asn Phe His Lys Gly Ser Arg Arg Gly Arg Ala Ala Gly Leu Asn
 325 330 335
 Met Val Leu Thr Glu Thr Gly Ala Ala Lys Ala Val Ser Lys Ala Leu
 340 345 350
 Pro Glu Leu Glu Gly Lys Leu Thr Gly Asn Ala Ile Arg Val Pro Thr
 355 360 365
 Pro Asp Val Ser Met Ala Val Leu Asn Leu Thr Leu Asn Thr Glu Val
 370 375 380
 Asp Arg Asp Glu Val Asn Glu Phe Leu Arg Arg Val Ser Leu His Ser
 385 390 395 400
 Asp Leu Arg Gln Gln Ile Asp Trp Ile Arg Ser Pro Glu Val Val Ser
 405 410 415

Thr Asp Phe Val Gly Thr Thr His Ala Gly Ile Val Asp Gly Leu Ala
 420 425 430

Thr Ile Ala Thr Gly Arg His Leu Val Leu Tyr Val Trp Tyr Asp Asn
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Glu Phe Gly Tyr Ser Asn Gln Val Ile Arg Ile Val Glu Glu Ile Ala
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Gly Val Arg Pro Arg Val Tyr Pro Glu Arg Arg Gln Pro Ala Val Leu
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 <213> Corynebacterium glutamicum

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 <223> FRXA01225

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 Met Thr His Asn His
 1 5

aag gac tgg aac gat cgc att gca gtt gcg gag gaa atg gtg ccg ttg 163
 Lys Asp Trp Asn Asp Arg Ile Ala Val Ala Glu Glu Met Val Pro Leu
 10 15 20

atc ggg cgc ctg cac cgc aac aac aac gtg gtg gtt tcc gta ttc ggt 211
 Ile Gly Arg Leu His Arg Asn Asn Asn Val Val Val Ser Val Phe Gly
 25 30 35

cgt ctc ctt gtg aat gtc tca gac atc gat atc atc aag tct cac cgc 259
 Arg Leu Leu Val Asn Val Ser Asp Ile Asp Ile Ile Lys Ser His Arg
 40 45 50

tac gcc cgc cac atc ata tcc aag gaa ctt cca ctg gaa agc tcc ttg 307
 Tyr Ala Arg His Ile Ile Ser Lys Glu Leu Pro Leu Glu Ser Ser Leu
 55 60 65

gat att ttg cgc gaa ctg gta gat atg aac ctt ggt acc gca tcg atc 355
 Asp Ile Leu Arg Glu Leu Val Asp Met Asn Leu Gly Thr Ala Ser Ile
 70 75 80 85

gac ctg gga cag ctg gcc tac agc ttc gaa gaa tcc gaa agc acc gac 403
 Asp Leu Gly Gln Leu Ala Tyr Ser Phe Glu Glu Ser Glu Ser Thr Asp
 90 95 100

ctg cgt gcc ttc ctg gag gac gct ctc gcg ccg gtc att ggt gcg gaa 451
 Leu Arg Ala Phe Leu Glu Asp Ala Leu Ala Pro Val Ile Gly Ala Glu
 105 110 115

acc gac atc aac cca act gat atc gtg ctg tac ggt ttc ggc cgc atc	499
Thr Asp Ile Asn Pro Thr Asp Ile Val Leu Tyr Gly Phe Gly Arg Ile	
120 125 130	
ggt cgc ctg ctg gcc cgc atc ctg gtt tcc cgc gag gca ctg tat gac	547
Gly Arg Leu Leu Ala Arg Ile Leu Val Ser Arg Glu Ala Leu Tyr Asp	
135 140 145	
ggt gct cgt ctg cgc gcc atc gtg gtc cgc aaa aat ggt gaa gaa gac	595
Gly Ala Arg Leu Arg Ala Ile Val Val Arg Lys Asn Gly Glu Glu Asp	
150 155 160 165	
ctg gtc aag cgc gca tcc ttg ctg cgt cgt gat tct gtc cac ggt gga	643
Leu Val Lys Arg Ala Ser Leu Leu Arg Arg Asp Ser Val His Gly Gly	
170 175 180	
ttc gat ggc acc atc acc acc gat tat gac aac aac atc atc tgg gcc	691
Phe Asp Gly Thr Ile Thr Thr Asp Tyr Asp Asn Asn Ile Ile Trp Ala	
185 190 195	
aac ggc acc cca atc aag gtc atc tac tcc aat gac cca gcc acc att	739
Asn Gly Thr Pro Ile Lys Val Ile Tyr Ser Asn Asp Pro Ala Thr Ile	
200 205 210	
gat tac acc gaa tac ggc atc aat gac gcc gtc gtg gta gac aac acc	787
Asp Tyr Thr Glu Tyr Gly Ile Asn Asp Ala Val Val Val Asp Asn Thr	
215 220 225	
ggc cgc tgg cgt gac cgc gaa ggc ctg tcc cag cac ctc aag tcc aag	835
Gly Arg Trp Arg Asp Arg Glu Gly Leu Ser Gln His Leu Lys Ser Lys	
230 235 240 245	
ggc gtt gcc aag gtt gta ctc acc gcg ccg ggc aag ggc gat ctg aag	883
Gly Val Ala Lys Val Val Leu Thr Ala Pro Gly Lys Gly Asp Leu Lys	
250 255 260	
aac atc gtg tac ggc atc aac cac acc gac atc acc gca gat gat cag	931
Asn Ile Val Tyr Gly Ile Asn His Thr Asp Ile Thr Ala Asp Asp Gln	
265 270 275	
atc gtt tcc gca gca tca tgc acc acc aat gcc att acc cca gtg ctc	979
Ile Val Ser Ala Ala Ser Cys Thr Thr Asn Ala Ile Thr Pro Val Leu	
280 285 290	
aag gtg atc aat gat cgc tac ggc gtg gaa ttc ggc cac gta gaa acc	1027
Lys Val Ile Asn Asp Arg Tyr Gly Val Glu Phe Gly His Val Glu Thr	
295 300 305	
gtt cac tcc ttc acc aat gac cag aac ctg atc gac aac ttc cac aag	1075
Val His Ser Phe Thr Asn Asp Gln Asn Leu Ile Asp Asn Phe His Lys	
310 315 320 325	
ggt tct cgc cgt ggt cgc gca gca ggt ctg aat atg gtt ctc acc gaa	1123
Gly Ser Arg Arg Gly Arg Ala Ala Gly Leu Asn Met Val Leu Thr Glu	
330 335 340	
acc ggc gct gca aag gct gta tcc aag gcg ctt cca gag ctg gaa ggc	1171
Thr Gly Ala Ala Lys Ala Val Ser Lys Ala Leu Pro Glu Leu Glu Gly	
345 350 355	
aag ctc acc ggc aat gcc atc cgc gtt cct acc cct gac gtg tcc atg	1219

Lys Leu Thr Gly Asn Ala Ile Arg Val Pro Thr Pro Asp Val Ser Met
 360 365 370
 gct gtg ctc aac ttg acc ctg aac acg gag gtg gac cgc gat gag gtc 1267
 Ala Val Leu Asn Leu Thr Leu Asn Thr Glu Val Asp Arg Asp Glu Val
 375 380 385
 aac gag ttc ctc cgc cgt gtg tcc ctg cac tct gac ttg cgc cag caa 1315
 Asn Glu Phe Leu Arg Arg Val Ser Leu His Ser Asp Leu Arg Gln Gln
 390 395 400 405
 atc gac tgg atc cgt tcc cca gag gtt gtt tcc act gac ttc gtg ggc 1363
 Ile Asp Trp Ile Arg Ser Pro Glu Val Val Ser Thr Asp Phe Val Gly
 410 415 420
 acc acc cac gcg ggc atc gtt gat ggt cta gcc acc atc gca acc ggt 1411
 Thr Thr His Ala Gly Ile Val Asp Gly Leu Ala Thr Ile Ala Thr Gly
 425 430 435
 cgc cac ctg gtg ctt tac gtg tgg tac gac aac gag ttc ggc tac tcc 1459
 Arg His Leu Val Leu Tyr Val Trp Tyr Asp Asn Glu Phe Gly Tyr Ser
 440 445 450
 aac cag gtc att cgc atc gtc gag gag atc gcc ggc gtg cgt cct cgc 1507
 Asn Gln Val Ile Arg Ile Val Glu Glu Ile Ala Gly Val Arg Pro Arg
 455 460 465
 gtg tac ccg gag cgc agg cag cca gcc gta cta taggttatcc aagcctaata 1560
 Val Tyr Pro Glu Arg Arg Gln Pro Ala Val Leu
 470 475 480
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<210> 66

<211> 480

<212> PRT

<213> Corynebacterium glutamicum

<400> 66

Met Thr His Asn His Lys Asp Trp Asn Asp Arg Ile Ala Val Ala Glu
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 Glu Met Val Pro Leu Ile Gly Arg Leu His Arg Asn Asn Asn Val Val
 20 25 30
 Val Ser Val Phe Gly Arg Leu Leu Val Asn Val Ser Asp Ile Asp Ile
 35 40 45
 Ile Lys Ser His Arg Tyr Ala Arg His Ile Ile Ser Lys Glu Leu Pro
 50 55 60
 Leu Glu Ser Ser Leu Asp Ile Leu Arg Glu Leu Val Asp Met Asn Leu
 65 70 75 80
 Gly Thr Ala Ser Ile Asp Leu Gly Gln Leu Ala Tyr Ser Phe Glu Glu
 85 90 95
 Ser Glu Ser Thr Asp Leu Arg Ala Phe Leu Glu Asp Ala Leu Ala Pro
 100 105 110

Val Ile Gly Ala Glu Thr Asp Ile Asn Pro Thr Asp Ile Val Leu Tyr
 115 120 125
 Gly Phe Gly Arg Ile Gly Arg Leu Leu Ala Arg Ile Leu Val Ser Arg
 130 135 140
 Glu Ala Leu Tyr Asp Gly Ala Arg Leu Arg Ala Ile Val Val Arg Lys
 145 150 155 160
 Asn Gly Glu Glu Asp Leu Val Lys Arg Ala Ser Leu Leu Arg Arg Asp
 165 170 175
 Ser Val His Gly Gly Phe Asp Gly Thr Ile Thr Thr Asp Tyr Asp Asn
 180 185 190
 Asn Ile Ile Trp Ala Asn Gly Thr Pro Ile Lys Val Ile Tyr Ser Asn
 195 200 205
 Asp Pro Ala Thr Ile Asp Tyr Thr Glu Tyr Gly Ile Asn Asp Ala Val
 210 215 220
 Val Val Asp Asn Thr Gly Arg Trp Arg Asp Arg Glu Gly Leu Ser Gln
 225 230 235 240
 His Leu Lys Ser Lys Gly Val Ala Lys Val Val Leu Thr Ala Pro Gly
 245 250 255
 Lys Gly Asp Leu Lys Asn Ile Val Tyr Gly Ile Asn His Thr Asp Ile
 260 265 270
 Thr Ala Asp Asp Gln Ile Val Ser Ala Ala Ser Cys Thr Thr Asn Ala
 275 280 285
 Ile Thr Pro Val Leu Lys Val Ile Asn Asp Arg Tyr Gly Val Glu Phe
 290 295 300
 Gly His Val Glu Thr Val His Ser Phe Thr Asn Asp Gln Asn Leu Ile
 305 310 315 320
 Asp Asn Phe His Lys Gly Ser Arg Arg Gly Arg Ala Ala Gly Leu Asn
 325 330 335
 Met Val Leu Thr Glu Thr Gly Ala Ala Lys Ala Val Ser Lys Ala Leu
 340 345 350
 Pro Glu Leu Glu Gly Lys Leu Thr Gly Asn Ala Ile Arg Val Pro Thr
 355 360 365
 Pro Asp Val Ser Met Ala Val Leu Asn Leu Thr Leu Asn Thr Glu Val
 370 375 380
 Asp Arg Asp Glu Val Asn Glu Phe Leu Arg Arg Val Ser Leu His Ser
 385 390 395 400
 Asp Leu Arg Gln Gln Ile Asp Trp Ile Arg Ser Pro Glu Val Val Ser
 405 410 415
 Thr Asp Phe Val Gly Thr Thr His Ala Gly Ile Val Asp Gly Leu Ala
 420 425 430
 Thr Ile Ala Thr Gly Arg His Leu Val Leu Tyr Val Trp Tyr Asp Asn

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gacacattgc atttcctaca atcttttagag gagacacaac						atg	acc	att	cgt	gtt	115										
						Met	Thr	Ile	Arg	Val											
						1				5											
ggt	att	aac	gga	ttt	ggc	cgt	atc	gga	cgt	aac	ttc	ttc	cgc	gca	gtt	163					
Gly	Ile	Asn	Gly	Phe	Gly	Arg	Ile	Gly	Arg	Asn	Phe	Phe	Arg	Ala	Val						
				10					15					20							
ctg	gag	cgc	agc	gac	gat	ctc	gag	gta	gtt	gca	gtc	aac	gac	ctc	acc	211					
Leu	Glu	Arg	Ser	Asp	Asp	Leu	Glu	Val	Val	Ala	Val	Asn	Asp	Leu	Thr						
				25					30					35							
gac	aac	aag	acc	ctt	tcc	acc	ctt	ctc	aag	ttc	gac	tcc	atc	atg	ggc	259					
Asp	Asn	Lys	Thr	Leu	Ser	Thr	Leu	Leu	Lys	Phe	Asp	Ser	Ile	Met	Gly						
				40					45					50							
cgc	ctt	ggc	cag	gaa	gtt	gaa	tac	gac	gat	gac	tcc	atc	acc	gtt	ggt	307					
Arg	Leu	Gly	Gln	Glu	Val	Glu	Tyr	Asp	Asp	Asp	Ser	Ile	Thr	Val	Gly						
		55					60					65									
ggc	aag	cgc	atc	gct	gtt	tac	gca	gag	cgc	gat	cca	aag	aac	ctg	gac	355					
Gly	Lys	Arg	Ile	Ala	Val	Tyr	Ala	Glu	Arg	Asp	Pro	Lys	Asn	Leu	Asp						
		70					75					80					85				
tgg	gct	gca	cac	aac	gtt	gac	atc	gtg	atc	gag	tcc	acc	ggc	ttc	ttc	403					
Trp	Ala	Ala	His	Asn	Val	Asp	Ile	Val	Ile	Glu	Ser	Thr	Gly	Phe	Phe						
				90					95					100							
acc	gat	gca	aac	gcg	gct	aag	gct	cac	atc	gaa	gca	ggt	gcc	aag	aag	451					
Thr	Asp	Ala	Asn	Ala	Ala	Lys	Ala	His	Ile	Glu	Ala	Gly	Ala	Lys	Lys						
				105					110					115							
gtc	atc	atc	tcc	gca	cca	gca	agc	aac	gaa	gac	gca	acc	ttc	gtt	tac	499					
Val	Ile	Ile	Ser	Ala	Pro	Ala	Ser	Asn	Glu	Asp	Ala	Thr	Phe	Val	Tyr						
				120					125					130							

ggt gtg aac cac gag tcc tac gat cct gag aac cac aac gtg atc tcc	547
Gly Val Asn His Glu Ser Tyr Asp Pro Glu Asn His Asn Val Ile Ser	
135 140 145	
ggc gca tct tgc acc acc aac tgc ctc gca cca atg gca aag gtc cta	595
Gly Ala Ser Cys Thr Thr Asn Cys Leu Ala Pro Met Ala Lys Val Leu	
150 155 160 165	
aac gac aag ttc ggc atc gag aac ggc ctc atg acc acc gtt cac gca	643
Asn Asp Lys Phe Gly Ile Glu Asn Gly Leu Met Thr Thr Val His Ala	
170 175 180	
tac act ggc gac cag cgc ctg cac gat gca cct cac cgc gac ctg cgt	691
Tyr Thr Gly Asp Gln Arg Leu His Asp Ala Pro His Arg Asp Leu Arg	
185 190 195	
cgt gca cgt gca gca gca gtc aac atc gtt cct acc tcc acc ggt gca	739
Arg Ala Arg Ala Ala Ala Val Asn Ile Val Pro Thr Ser Thr Gly Ala	
200 205 210	
gct aag gct gtt gct ctg gtt ctc cca gag ctc aag ggc aag ctt gac	787
Ala Lys Ala Val Ala Leu Val Leu Pro Glu Leu Lys Gly Lys Leu Asp	
215 220 225	
ggc tac gca ctt cgc gtt cca gtt atc acc ggt tcc gca acc gac ctg	835
Gly Tyr Ala Leu Arg Val Pro Val Ile Thr Gly Ser Ala Thr Asp Leu	
230 235 240 245	
acc ttc aac acc aag tct gag gtc acc gtt gag tcc atc aac gct gca	883
Thr Phe Asn Thr Lys Ser Glu Val Thr Val Glu Ser Ile Asn Ala Ala	
250 255 260	
atc aag gaa gct gca gtc ggc gag ttc ggc gag acc ctg gct tac tcc	931
Ile Lys Glu Ala Ala Val Gly Glu Phe Gly Glu Thr Leu Ala Tyr Ser	
265 270 275	
gaa gag cca ctg gtt tcc acc gac atc gtc cac gat tcc cac ggc tcc	979
Glu Glu Pro Leu Val Ser Thr Asp Ile Val His Asp Ser His Gly Ser	
280 285 290	
atc ttc gac gct ggc ctg acc aag gtc tcc ggc aac acc gtc aag gtt	1027
Ile Phe Asp Ala Gly Leu Thr Lys Val Ser Gly Asn Thr Val Lys Val	
295 300 305	
gtt tcc tgg tac gac aac gag tgg ggc tac acc tgc cag ctc ctg cgt	1075
Val Ser Trp Tyr Asp Asn Glu Trp Gly Tyr Thr Cys Gln Leu Leu Arg	
310 315 320 325	
ctg acc gag ctc gta gct tcc aag ctc taattagttc acatcgctaa	1122
Leu Thr Glu Leu Val Ala Ser Lys Leu	
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cgt	1125

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<211> 334

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 68

Met Thr Ile Arg Val Gly Ile Asn Gly Phe Gly Arg Ile Gly Arg Asn
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 Phe Phe Arg Ala Val Leu Glu Arg Ser Asp Asp Leu Glu Val Val Ala
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 Val Asn Asp Leu Thr Asp Asn Lys Thr Leu Ser Thr Leu Leu Lys Phe
 35 40 45
 Asp Ser Ile Met Gly Arg Leu Gly Gln Glu Val Glu Tyr Asp Asp Asp
 50 55 60
 Ser Ile Thr Val Gly Gly Lys Arg Ile Ala Val Tyr Ala Glu Arg Asp
 65 70 75 80
 Pro Lys Asn Leu Asp Trp Ala Ala His Asn Val Asp Ile Val Ile Glu
 85 90 95
 Ser Thr Gly Phe Phe Thr Asp Ala Asn Ala Ala Lys Ala His Ile Glu
 100 105 110
 Ala Gly Ala Lys Lys Val Ile Ile Ser Ala Pro Ala Ser Asn Glu Asp
 115 120 125
 Ala Thr Phe Val Tyr Gly Val Asn His Glu Ser Tyr Asp Pro Glu Asn
 130 135 140
 His Asn Val Ile Ser Gly Ala Ser Cys Thr Thr Asn Cys Leu Ala Pro
 145 150 155 160
 Met Ala Lys Val Leu Asn Asp Lys Phe Gly Ile Glu Asn Gly Leu Met
 165 170 175
 Thr Thr Val His Ala Tyr Thr Gly Asp Gln Arg Leu His Asp Ala Pro
 180 185 190
 His Arg Asp Leu Arg Arg Ala Arg Ala Ala Val Asn Ile Val Pro
 195 200 205
 Thr Ser Thr Gly Ala Ala Lys Ala Val Ala Leu Val Leu Pro Glu Leu
 210 215 220
 Lys Gly Lys Leu Asp Gly Tyr Ala Leu Arg Val Pro Val Ile Thr Gly
 225 230 235 240
 Ser Ala Thr Asp Leu Thr Phe Asn Thr Lys Ser Glu Val Thr Val Glu
 245 250 255
 Ser Ile Asn Ala Ala Ile Lys Glu Ala Ala Val Gly Glu Phe Gly Glu
 260 265 270
 Thr Leu Ala Tyr Ser Glu Glu Pro Leu Val Ser Thr Asp Ile Val His
 275 280 285
 Asp Ser His Gly Ser Ile Phe Asp Ala Gly Leu Thr Lys Val Ser Gly
 290 295 300
 Asn Thr Val Lys Val Val Ser Trp Tyr Asp Asn Glu Trp Gly Tyr Thr
 305 310 315 320
 Cys Gln Leu Leu Arg Leu Thr Glu Leu Val Ala Ser Lys Leu

330

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gaagaatttt ttaaacaatc aaatctccaa ggagtacggc															atg gct gtt aag acc	115
															Met Ala Val Lys Thr	
															1 5	
ctc aag gac ttg ctc gac gaa ggc gta gac gga cgc cac gtc atc gtt															163	
Leu Lys Asp Leu Leu Asp Glu Gly Val Asp Gly Arg His Val Ile Val																
															10 15 20	
cga tct gac ttc aat gtt ccc ctc aac gat gac cgc gag atc acc gat															211	
Arg Ser Asp Phe Asn Val Pro Leu Asn Asp Asp Arg Glu Ile Thr Asp																
															25 30 35	
aag ggc cga atc att gcc tcc cta cca acc ctt aaa gca ctg agc gaa															259	
Lys Gly Arg Ile Ile Ala Ser Leu Pro Thr Leu Lys Ala Leu Ser Glu																
															40 45 50	
ggt ggc gca aag gtc atc gtc atg gct cac ctt ggc cgc cca aag ggc															307	
Gly Gly Ala Lys Val Ile Val Met Ala His Leu Gly Arg Pro Lys Gly																
															55 60 65	
gag gtc aac gag aag tac tcc ctc gca cct gtc gct gag gca ctc tcc															355	
Glu Val Asn Glu Lys Tyr Ser Leu Ala Pro Val Ala Glu Ala Leu Ser																
															70 75 80 85	
gat gag ctt ggc cag tac gtt gca ctt gcc gca gac gtt gtt ggc gaa															403	
Asp Glu Leu Gly Gln Tyr Val Ala Leu Ala Ala Asp Val Val Gly Glu																
															90 95 100	
gac gca cac gag cgc gca aac ggc ctg acc gag ggc gac atc ctg ctc															451	
Asp Ala His Glu Arg Ala Asn Gly Leu Thr Glu Gly Asp Ile Leu Leu																
															105 110 115	
ctg gag aac gtg cgc ttc gac cca cgc gaa acc tcc aag gac gag gca															499	
Leu Glu Asn Val Arg Phe Asp Pro Arg Glu Thr Ser Lys Asp Glu Ala																
															120 125 130	
gag cgc acc gct ttc gct cag gag ctc gca gct ctt gca gca gac aac															547	
Glu Arg Thr Ala Phe Ala Gln Glu Leu Ala Ala Leu Ala Ala Asp Asn																
															135 140 145	
ggc gca ttc gtt tct gac ggc ttc ggt gtt gtc cac cgc gca cag acc															595	
Gly Ala Phe Val Ser Asp Gly Phe Gly Val Val His Arg Ala Gln Thr																
															150 155 160 165	
tcc gtc tac gac att gca aag ttg ctg cca cac tac gct ggc gga ctg															643	

Ser	Val	Tyr	Asp	Ile	Ala	Lys	Leu	Leu	Pro	His	Tyr	Ala	Gly	Gly	Leu	
				170					175						180	
gta	gag	acc	gag	att	tcc	gtt	ctg	gaa	aag	atc	gca	gaa	tca	cca	gag	691
Val	Glu	Thr	Glu	Ile	Ser	Val	Leu	Glu	Lys	Ile	Ala	Glu	Ser	Pro	Glu	
			185					190					195			
gca	cca	tac	gta	gtg	gtt	ctc	ggg	gga	tcc	aag	gtc	tct	gac	aag	atc	739
Ala	Pro	Tyr	Val	Val	Val	Leu	Gly	Gly	Ser	Lys	Val	Ser	Asp	Lys	Ile	
		200					205					210				
ggg	gtt	att	gag	gcg	ctg	gct	gcc	aag	gct	gac	aag	atc	atc	gtc	ggg	787
Gly	Val	Ile	Glu	Ala	Leu	Ala	Ala	Lys	Ala	Asp	Lys	Ile	Ile	Val	Gly	
	215					220				225						
ggc	ggc	atg	tgc	tac	acc	ttc	ctc	gca	gct	cag	gga	cac	aac	gtt	cag	835
Gly	Gly	Met	Cys	Tyr	Thr	Phe	Leu	Ala	Ala	Gln	Gly	His	Asn	Val	Gln	
230					235					240					245	
cag	tcc	ctc	ctg	cag	gaa	gaa	atg	aag	gct	acc	tgc	acc	gac	ctg	ctc	883
Gln	Ser	Leu	Leu	Gln	Glu	Glu	Met	Lys	Ala	Thr	Cys	Thr	Asp	Leu	Leu	
				250					255					260		
gca	cgc	ttc	ggg	gac	aag	atc	gtt	ctc	cca	gtt	gac	ctg	gtt	gca	gca	931
Ala	Arg	Phe	Gly	Asp	Lys	Ile	Val	Leu	Pro	Val	Asp	Leu	Val	Ala	Ala	
			265					270					275			
tcc	gaa	ttt	aac	aag	gac	gca	gag	aag	cag	atc	gtt	gac	ctg	gac	tcc	979
Ser	Glu	Phe	Asn	Lys	Asp	Ala	Glu	Lys	Gln	Ile	Val	Asp	Leu	Asp	Ser	
		280					285					290				
atc	cca	gaa	ggc	tgg	atg	tct	ctt	gac	atc	gga	cca	gag	tcc	gtc	aag	1027
Ile	Pro	Glu	Gly	Trp	Met	Ser	Leu	Asp	Ile	Gly	Pro	Glu	Ser	Val	Lys	
	295					300					305					
aac	ttc	ggg	gag	gtt	ctc	agc	acc	gct	aag	acc	atc	ttc	tgg	aac	ggc	1075
Asn	Phe	Gly	Glu	Val	Leu	Ser	Thr	Ala	Lys	Thr	Ile	Phe	Trp	Asn	Gly	
310					315					320					325	
cca	atg	ggc	gtg	ttc	gag	ttc	gca	gca	ttc	tct	gaa	ggc	acc	cgc	ggc	1123
Pro	Met	Gly	Val	Phe	Glu	Phe	Ala	Ala	Phe	Ser	Glu	Gly	Thr	Arg	Gly	
				330					335					340		
atc	gcc	cag	gcc	atc	atc	gat	gca	act	gca	ggc	aac	gac	gca	ttc	tcc	1171
Ile	Ala	Gln	Ala	Ile	Ile	Asp	Ala	Thr	Ala	Gly	Asn	Asp	Ala	Phe	Ser	
			345					350					355			
gtt	gtt	ggc	ggg	ggc	gac	tcc	gca	gca	tcc	gtt	cgc	gtg	ctc	ggc	ctg	1219
Val	Val	Gly	Gly	Gly	Asp	Ser	Ala	Ala	Ser	Val	Arg	Val	Leu	Gly	Leu	
		360					365				370					
aac	gaa	gac	ggc	ttc	tcc	cac	atc	tcc	acc	ggg	ggg	ggc	gca	tcc	ctc	1267
Asn	Glu	Asp	Gly	Phe	Ser	His	Ile	Ser	Thr	Gly	Gly	Gly	Ala	Ser	Leu	
	375					380				385						
gag	tac	ctt	gaa	ggc	aag	gaa	ctc	cca	ggc	gtt	gca	att	ctc	gct	cag	1315
Glu	Tyr	Leu	Glu	Gly	Lys	Glu	Leu	Pro	Gly	Val	Ala	Ile	Leu	Ala	Gln	
390					395				400						405	
taa	atc	cgac	acg	gcc	cttt	gtt										1338

<210> 70
 <211> 405
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 70

Met	Ala	Val	Lys	Thr	Leu	Lys	Asp	Leu	Leu	Asp	Glu	Gly	Val	Asp	Gly	1	5	10	15
Arg	His	Val	Ile	Val	Arg	Ser	Asp	Phe	Asn	Val	Pro	Leu	Asn	Asp	Asp	20	25	30	
Arg	Glu	Ile	Thr	Asp	Lys	Gly	Arg	Ile	Ile	Ala	Ser	Leu	Pro	Thr	Leu	35	40	45	
Lys	Ala	Leu	Ser	Glu	Gly	Gly	Ala	Lys	Val	Ile	Val	Met	Ala	His	Leu	50	55	60	
Gly	Arg	Pro	Lys	Gly	Glu	Val	Asn	Glu	Lys	Tyr	Ser	Leu	Ala	Pro	Val	65	70	75	80
Ala	Glu	Ala	Leu	Ser	Asp	Glu	Leu	Gly	Gln	Tyr	Val	Ala	Leu	Ala	Ala	85	90	95	
Asp	Val	Val	Gly	Glu	Asp	Ala	His	Glu	Arg	Ala	Asn	Gly	Leu	Thr	Glu	100	105	110	
Gly	Asp	Ile	Leu	Leu	Leu	Glu	Asn	Val	Arg	Phe	Asp	Pro	Arg	Glu	Thr	115	120	125	
Ser	Lys	Asp	Glu	Ala	Glu	Arg	Thr	Ala	Phe	Ala	Gln	Glu	Leu	Ala	Ala	130	135	140	
Leu	Ala	Ala	Asp	Asn	Gly	Ala	Phe	Val	Ser	Asp	Gly	Phe	Gly	Val	Val	145	150	155	160
His	Arg	Ala	Gln	Thr	Ser	Val	Tyr	Asp	Ile	Ala	Lys	Leu	Leu	Pro	His	165	170	175	
Tyr	Ala	Gly	Gly	Leu	Val	Glu	Thr	Glu	Ile	Ser	Val	Leu	Glu	Lys	Ile	180	185	190	
Ala	Glu	Ser	Pro	Glu	Ala	Pro	Tyr	Val	Val	Val	Leu	Gly	Gly	Ser	Lys	195	200	205	
Val	Ser	Asp	Lys	Ile	Gly	Val	Ile	Glu	Ala	Leu	Ala	Ala	Lys	Ala	Asp	210	215	220	
Lys	Ile	Ile	Val	Gly	Gly	Gly	Met	Cys	Tyr	Thr	Phe	Leu	Ala	Ala	Gln	225	230	235	240
Gly	His	Asn	Val	Gln	Gln	Ser	Leu	Leu	Gln	Glu	Glu	Met	Lys	Ala	Thr	245	250	255	
Cys	Thr	Asp	Leu	Leu	Ala	Arg	Phe	Gly	Asp	Lys	Ile	Val	Leu	Pro	Val	260	265	270	
Asp	Leu	Val	Ala	Ala	Ser	Glu	Phe	Asn	Lys	Asp	Ala	Glu	Lys	Gln	Ile	275	280	285	

Val Asp Leu Asp Ser Ile Pro Glu Gly Trp Met Ser Leu Asp Ile Gly
 290 295 300

Pro Glu Ser Val Lys Asn Phe Gly Glu Val Leu Ser Thr Ala Lys Thr
 305 310 315 320

Ile Phe Trp Asn Gly Pro Met Gly Val Phe Glu Phe Ala Ala Phe Ser
 325 330 335

Glu Gly Thr Arg Gly Ile Ala Gln Ala Ile Ile Asp Ala Thr Ala Gly
 340 345 350

Asn Asp Ala Phe Ser Val Val Gly Gly Gly Asp Ser Ala Ala Ser Val
 355 360 365

Arg Val Leu Gly Leu Asn Glu Asp Gly Phe Ser His Ile Ser Thr Gly
 370 375 380

Gly Gly Ala Ser Leu Glu Tyr Leu Glu Gly Lys Glu Leu Pro Gly Val
 385 390 395 400

Ala Ile Leu Ala Gln
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 <213> *Corynebacterium glutamicum*

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 <223> RXA00235

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 Val Ala Glu Ile Met
 1 5

cac gta ttc gct cgc gaa att ctc gac tcc cgc ggt aac cca acc gtc 163
 His Val Phe Ala Arg Glu Ile Leu Asp Ser Arg Gly Asn Pro Thr Val
 10 15 20

gag gca gag gtt ttc ctg gat gac ggt tcc cac ggt gtc gca ggt gtt 211
 Glu Ala Glu Val Phe Leu Asp Asp Gly Ser His Gly Val Ala Gly Val
 25 30 35

cca tcc ggc gca tcc acc ggc gtc cac gag gct cat gag ctg cgt gac 259
 Pro Ser Gly Ala Ser Thr Gly Val His Glu Ala His Glu Leu Arg Asp
 40 45 50

ggt ggc gat cgc tac ctg ggc aag ggc gtt ttg aag gca gtt gaa aac 307
 Gly Gly Asp Arg Tyr Leu Gly Lys Gly Val Leu Lys Ala Val Glu Asn
 55 60 65

gtc aac gaa gaa atc ggc gac gag ctc gct ggc cta gag gct gac gat 355
 Val Asn Glu Glu Ile Gly Asp Glu Leu Ala Gly Leu Glu Ala Asp Asp
 70 75 80 85

cag cgc ctc atc gac gaa gca atg atc aag ctt gat ggc acc gcc aac	403
Gln Arg Leu Ile Asp Glu Ala Met Ile Lys Leu Asp Gly Thr Ala Asn	
90 95 100	
aag tcc cgc ctg ggt gca aac gca atc ctt ggt gtt tcc atg gct gtt	451
Lys Ser Arg Leu Gly Ala Asn Ala Ile Leu Gly Val Ser Met Ala Val	
105 110 115	
gca aag gct gct gct gat tcc gca ggc ctc cca ctg ttc cgc tac atc	499
Ala Lys Ala Ala Ala Asp Ser Ala Gly Leu Pro Leu Phe Arg Tyr Ile	
120 125 130	
ggt gga cca aac gca cac gtt ctt cca gtt cca atg atg aac atc atc	547
Gly Gly Pro Asn Ala His Val Leu Pro Val Pro Met Met Asn Ile Ile	
135 140 145	
acc ggt ggc gct cac gct gac tcc ggt gtt gac gtt cag gaa ttc atg	595
Thr Gly Gly Ala His Ala Asp Ser Gly Val Asp Val Gln Glu Phe Met	
150 155 160 165	
atc gct cca atc ggt gca gag acc ttc tct gag gct ctc cgc aac ggc	643
Ile Ala Pro Ile Gly Ala Glu Thr Phe Ser Glu Ala Leu Arg Asn Gly	
170 175 180	
gcg gag gtc tac cac gca ctg aag tcc gtc atc aag gaa aag ggc ctg	691
Ala Glu Val Tyr His Ala Leu Lys Ser Val Ile Lys Glu Lys Gly Leu	
185 190 195	
tcc acc gga ctt ggc gat gag ggc ggc ttc gct cct tcc gtc ggc tcc	739
Ser Thr Gly Leu Gly Asp Glu Gly Phe Ala Pro Ser Val Gly Ser	
200 205 210	
acc cgt gag gct ctt gac ctt atc gtt gag gca atc gag aag gct ggc	787
Thr Arg Glu Ala Leu Asp Leu Ile Val Glu Ala Ile Glu Lys Ala Gly	
215 220 225	
ttc acc cca ggc aag gac atc gct ctt gct ctg gac gtt gct tcc tct	835
Phe Thr Pro Gly Lys Asp Ile Ala Leu Ala Leu Asp Val Ala Ser Ser	
230 235 240 245	
gag ttc ttc aag gac ggc acc tac cac ttc gaa ggt ggc cag cac tcc	883
Glu Phe Phe Lys Asp Gly Thr Tyr His Phe Glu Gly Gly Gln His Ser	
250 255 260	
gca gct gag atg gca aac gtt tac gct gag ctc gtt gac gcg tac cca	931
Ala Ala Glu Met Ala Asn Val Tyr Ala Glu Leu Val Asp Ala Tyr Pro	
265 270 275	
atc gtc tcc atc gag gac cca ctg cag gaa gat gac tgg gag ggt tac	979
Ile Val Ser Ile Glu Asp Pro Leu Gln Glu Asp Asp Trp Glu Gly Tyr	
280 285 290	
acc aac ctc acc gca acc atc ggc gac aag gtt cag atc gtt ggc gac	1027
Thr Asn Leu Thr Ala Thr Ile Gly Asp Lys Val Gln Ile Val Gly Asp	
295 300 305	
gac ttc ttc gtc acc aac cct gag cgc ctg aag gag ggc atc gct aag	1075
Asp Phe Phe Val Thr Asn Pro Glu Arg Leu Lys Glu Gly Ile Ala Lys	
310 315 320 325	

aag gct gcc aac tcc atc ctg gtt aag gtg aac cag atc ggt acc ctc 1123
 Lys Ala Ala Asn Ser Ile Leu Val Lys Val Asn Gln Ile Gly Thr Leu
 330 335 340

 acc gag acc ttc gac gct gtc gac atg gct cac cgc gca ggc tac acc 1171
 Thr Glu Thr Phe Asp Ala Val Asp Met Ala His Arg Ala Gly Tyr Thr
 345 350 355

 tcc atg atg tcc cac cgt tcc ggt gag acc gag gac acc acc att gct 1219
 Ser Met Met Ser His Arg Ser Gly Glu Thr Glu Asp Thr Thr Ile Ala
 360 365 370

 gac ctc gca gtt gca ctc aac tgt ggc cag atc aag act ggt gct cca 1267
 Asp Leu Ala Val Ala Leu Asn Cys Gly Gln Ile Lys Thr Gly Ala Pro
 375 380 385

 gca cgt tcc gac cgt gtc gca aag tac aac cag ctt ctc cgc atc gag 1315
 Ala Arg Ser Asp Arg Val Ala Lys Tyr Asn Gln Leu Leu Arg Ile Glu
 390 395 400 405

 cag ctg ctt ggc gac gcc ggc gtc tac gca ggt cgc agc gca ttc cca 1363
 Gln Leu Leu Gly Asp Ala Gly Val Tyr Ala Gly Arg Ser Ala Phe Pro
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 Arg Phe Gln Gly
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<210> 72

<211> 425

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 72

Val Ala Glu Ile Met His Val Phe Ala Arg Glu Ile Leu Asp Ser Arg
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 Gly Asn Pro Thr Val Glu Ala Glu Val Phe Leu Asp Asp Gly Ser His
 20 25 30

 Gly Val Ala Gly Val Pro Ser Gly Ala Ser Thr Gly Val His Glu Ala
 35 40 45

 His Glu Leu Arg Asp Gly Gly Asp Arg Tyr Leu Gly Lys Gly Val Leu
 50 55 60

 Lys Ala Val Glu Asn Val Asn Glu Glu Ile Gly Asp Glu Leu Ala Gly
 65 70 75 80

 Leu Glu Ala Asp Asp Gln Arg Leu Ile Asp Glu Ala Met Ile Lys Leu
 85 90 95

 Asp Gly Thr Ala Asn Lys Ser Arg Leu Gly Ala Asn Ala Ile Leu Gly
 100 105 110

 Val Ser Met Ala Val Ala Lys Ala Ala Ala Asp Ser Ala Gly Leu Pro
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 Val Gln Glu Phe Met Ile Ala Pro Ile Gly Ala Glu Thr Phe Ser Glu
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 Ala Leu Arg Asn Gly Ala Glu Val Tyr His Ala Leu Lys Ser Val Ile
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 Gly Gly Gln His Ser Ala Ala Glu Met Ala Asn Val Tyr Ala Glu Leu
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 Val Asp Ala Tyr Pro Ile Val Ser Ile Glu Asp Pro Leu Gln Glu Asp
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<220>

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<222> (101)..(1531)

<223> RXA01093

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Phe Ser His Gly Asp His Pro Asp His Glu Gln Asn Tyr Lys Trp Val
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Leu Gln Gly Pro Lys Ile Arg Leu Gly Arg Phe Thr Asp Gly Ala Thr
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gtg tgg gaa aac ggc gag acc att cgg atc acc gtt gac gat gta gag 403
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Phe	Thr	Thr	Ser	Gly	Asp	Thr	Ala	Lys	Arg	Val	Ala	Arg	Leu	His	Ser	
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Pro	Glu	Tyr	Asn	Lys	Gly	Asp	Met	Met	Val	Val	Val	Ala	Gly	Ser	Pro	

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 Asn Tyr Lys Trp Val Arg Glu Ala Ala Glu Lys Thr Gly Arg Ala Val
 50 55 60
 Gly Ile Leu Ala Asp Leu Gln Gly Pro Lys Ile Arg Leu Gly Arg Phe
 65 70 75 80
 Thr Asp Gly Ala Thr Val Trp Glu Asn Gly Glu Thr Ile Arg Ile Thr
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 Val Asp Asp Val Glu Gly Thr His Asp Arg Val Ser Thr Thr Tyr Lys
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 Asn Leu Ala Lys Asp Ala Lys Pro Gly Asp Arg Leu Leu Val Asp Asp
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 Gly Lys Val Gly Leu Val Cys Val Ser Val Glu Gly Asn Asp Val Ile
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 Cys Glu Val Val Glu Gly Gly Pro Val Ser Asn Asn Lys Gly Val Ser
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 Leu Pro Gly Met Asp Ile Ser Val Pro Ala Leu Ser Glu Lys Asp Ile
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 Arg Asp Leu Arg Phe Ala Leu Lys Leu Gly Val Asp Phe Ile Ala Leu
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 Ser Phe Val Arg Ser Pro Ala Asp Ala Glu Leu Val His Lys Ile Met
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 Asp Glu Glu Gly Arg Arg Val Pro Val Ile Ala Lys Leu Glu Lys Pro
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 Glu Ala Val Thr Ser Leu Glu Pro Ile Val Leu Ala Phe Asp Ala Val
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Arg Pro Thr Arg Ala Glu Ala Ser Asp Val Ala Asn Ala Val Leu Asp
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Gly Ala Asp Ala Val Met Leu Ser Gly Glu Thr Ser Val Gly Lys Asp
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Pro His Asn Val Val Arg Thr Met Ser Arg Ile Val Arg Phe Ala Glu
 325 330 335

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Gly Val Ile Ser Tyr Ser Ala Arg Asp Ile Ala Glu Arg Leu Asn Ala
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Arg Ala Leu Val Ala Phe Thr Thr Ser Gly Asp Thr Ala Lys Arg Val
 370 375 380

Ala Arg Leu His Ser His Leu Pro Leu Leu Val Phe Thr Pro Asn Glu
 385 390 395 400

Ala Val Arg Ser Glu Leu Ala Leu Thr Trp Gly Ala Thr Thr Phe Leu
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Cys Pro Pro Val Ser Asp Thr Asp Asp Met Met Arg Glu Val Asp Arg
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Ala Leu Leu Ala Met Pro Glu Tyr Asn Lys Gly Asp Met Met Val Val
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<210> 75

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<212> DNA

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<222> (101)..(1957)

<223> RXN02675

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Ser	Pro	Thr	His	Tyr	Val	Gly	Ala	Arg	Asn	Leu	Met	His	Tyr	Ala	His						
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Leu	Arg	Thr	Lys	Asp	Leu	Arg	Gly	Leu	Gln	Gln	Arg	Leu	Ser	Ser	Val						
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Tyr	Pro	Pro	Ser	Asp	Val	Val	Asp	Ala	Phe	Glu	Asp	Ala	Asp	Glu	Ile						
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Pro	Ser	Cys	Ile	Met	Val	Thr	Leu	Pro	Thr	Glu	Ala	Ala	Thr	Asp	Ile						
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<213> Corynebacterium glutamicum

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 50 55 60
 Arg Leu Ser Ser Val Gly Ala Thr Arg Leu Thr Thr Thr Glu Pro Ala
 65 70 75 80
 Val Gln Ala Arg Leu Lys Ala Ala Arg Asn Val Ile Gly Ala Phe Ala
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Gly Glu Gly Pro Leu Tyr Pro Pro Ser Asp Val Val Asp Ala Phe Glu
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 Pro Leu Pro Asp Thr Pro Ser Cys Ile Met Val Thr Leu Pro Thr Glu
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 Gln Met Ile Asp Asn Val His Thr Val Ala Glu Glu Val Gly Arg Glu
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 Thr Gly Lys Val Leu Thr Pro Ala Lys Leu Trp Ile Thr Ala His Gly
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Ala Tyr Lys Gly Ile Asn Leu Pro Asp Ser Glu Leu Pro Leu Pro Ser
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Ala Gln Ile Leu Leu Thr Gly Met Arg His Glu Asn Phe Gly Ile Met
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Ile Ala Arg Gly Asp Leu Ala Val Glu Leu Gly Phe Asp Arg Met Ala
515 520 525

Glu Val Pro Gln Leu Ile Met Ala Leu Ala Glu Ala Ala His Val Pro
530 535 540

Thr Ile Leu Ala Thr Gln Val Leu Glu Asn Met Ala Lys Asn Gly Leu
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Pro Ser Arg Ala Glu Ile Thr Asp Ala Ala Met Ala Leu Arg Ala Glu
565 570 575

Cys Val Met Leu Asn Lys Gly Pro His Ile Asn Asp Ala Ile Lys Val
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610 615

<210> 77

<211> 386

<212> DNA

<213> *Corynebacterium glutamicum*

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<221> CDS

<222> (1)..(363)

<223> FRXA02675

<400> 77

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Pro	Gln	Leu	Ile	Met	Ala	Leu	Ala	Glu	Ala	Ala	His	Val	Pro	Thr	Ile	

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Leu Ala Thr Gln Val Leu Glu Asn Met Ala Lys Asn Gly Leu Pro Ser			
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Arg Ala Glu Ile Thr Asp Ala Ala Met Ala Leu Arg Ala Glu Cys Val			
65	70	75	80
atg ctg aac aag gga cca cac atc aac gac gcc atc aag gtc ctc acc			288
Met Leu Asn Lys Gly Pro His Ile Asn Asp Ala Ile Lys Val Leu Thr			
85	90	95	
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Glu Met Ser Arg Lys Leu Gly Ala Ser Gln Arg Lys Ser Arg Leu Leu			
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cgt			386

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<213> Corynebacterium glutamicum

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Gln His Trp Pro Thr Val Phe Lys Pro Phe Glu Thr Ile Gly Gly Glu
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Glu	Lys	Glu	Arg 340	Val	Val	Glu	Glu	Tyr 345	Arg	Asp	Leu	Leu	Asp 350	Gly	Glu				
Gln	Leu	Ala 355	Gln	Phe	Asp	Ala	Lys 360	Cys	Gly	Leu	Ala	Ala 365	Thr	Ala	Tyr				
Pro	Tyr 370	Val	Glu	Asn	His	Asn 375	Phe	Tyr	Ile	Glu	His 380	Trp	Thr	Met	Ser				
Val 385	Phe	Trp	Arg	Lys	Val 390	Arg	Glu	Leu	Ser	Arg 395	Thr	Leu	Gln	Gly	Tyr 400				

Gly Phe Trp Glu Asn Glu Asp Asp Met Leu Tyr Leu Asn Arg Thr Glu
 405 410 415
 Val Arg Asp Val Leu Phe Asp Leu Ala Thr Ala Trp Gly Val Gly Ala
 420 425 430
 Pro Gly Gly Pro Ile Gly Thr Ile Ile Trp Pro Glu Glu Ile Glu Arg
 435 440 445
 Arg Lys Ala Ile Val Thr Ala Leu Lys Thr Ala Arg Pro Ala Pro Ala
 450 455 460
 Leu Asn Thr Pro Pro Glu Ser Ile Thr Glu Pro Phe Thr Arg Met Leu
 465 470 475 480
 Trp Gly Ile Thr Thr Glu Gln Val Gln Ser Trp Leu Gly Asn Asp Glu
 485 490 495
 Asp Ala Glu Glu Gly Thr Leu Lys Gly Met Ala Ala Ser Pro Gly Val
 500 505 510
 Val Glu Gly Tyr Ala Arg Val Ile Leu Ser Ala Asp Asp Leu Ser Glu
 515 520 525
 Ile Gln Gln Asp Glu Ile Leu Val Ala Pro Val Thr Ala Pro Ser Trp
 530 535 540
 Gly Pro Ile Phe Gly Lys Ile Lys Ala Thr Val Thr Asp Ile Gly Gly
 545 550 555 560
 Met Met Ser His Ala Ala Ile Val Cys Arg Glu Tyr Gly Leu Pro Ala
 565 570 575
 Val Thr Gly Thr Gly Ala Ala Ser Thr Thr Ile Lys Thr Gly Asp Tyr
 580 585 590
 Leu Lys Val Asp Gly Thr Lys Gly Lys Val Val Ile Val Asp Pro Asp
 595 600 605
 Ala Pro Arg Ile Glu Gly Pro Gly Ala His Ser His Ala His Ser Val
 610 615 620
 Ala Ala His Gly Val Asp Thr His Ala
 625 630

<210> 83

<211> 1215

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(1192)

<223> RXA00683

<400> 83

ggacaaagct atcgggttcc gggagaacct ctccttcgc gtcctccatt ctgttccgt 60

gacttgaac gcttaacgct ttattaaata aggagacacc atg acc aac agt ttg 115

125

230	235	240	245	
gtc tcc gaa cac att gga agc aaa cac gct gaa ctc atc ccc gat gcc	883			
Val Ser Glu His Ile Gly Ser Lys His Ala Glu Leu Ile Pro Asp Ala				
250 255 260				
acc agt gga agc ctc gtg gaa aag ccc gtt gat gaa gaa cgc gca aac	931			
Thr Ser Gly Ser Leu Val Glu Lys Pro Val Asp Glu Glu Arg Ala Asn				
265 270 275				
cgc cgc agt ctg act gat gag gaa atg ctc gct gtg gca caa atg gct	979			
Arg Arg Ser Leu Thr Asp Glu Glu Met Leu Ala Val Ala Gln Met Ala				
280 285 290				
aag cgt gca gaa aaa cac tac aag tgc cca caa gat atc gaa tgg gcg	1027			
Lys Arg Ala Glu Lys His Tyr Lys Cys Pro Gln Asp Ile Glu Trp Ala				
295 300 305				
ctg gac gct gat ctg cca gat gga gaa aac ctt ctg tta ttg caa tcc	1075			
Leu Asp Ala Asp Leu Pro Asp Gly Glu Asn Leu Leu Leu Leu Gln Ser				
310 315 320 325				
cgc ccg gaa act atc cac tcc aac ggt gtg aag aag gaa acc cca act	1123			
Arg Pro Glu Thr Ile His Ser Asn Gly Val Lys Lys Glu Thr Pro Thr				
330 335 340				
ccg cag gct gcc aaa acc ata ggc acc ttc gat ttc agc tca atc acc	1171			
Pro Gln Ala Ala Lys Thr Ile Gly Thr Phe Asp Phe Ser Ser Ile Thr				
345 350 355				
gtc gca atg acc ggc acg aag taaaaccacc gcatcttttc gtc	1215			
Val Ala Met Thr Gly Thr Lys				
360				

<210> 84

<211> 364

<212> PRT

<213> Corynebacterium glutamicum

<400> 84

Met Thr Asn Ser Leu Asn Ile Pro Phe Val Gln Arg Phe Asp Glu Gly
1 5 10 15

Leu Asp Pro Val Leu Glu Val Leu Gly Gly Lys Gly Ala Ser Leu Val
20 25 30

Thr Met Thr Asp Ala Gly Met Pro Val Pro Pro Gly Phe Val Val Thr
35 40 45

Thr Ala Ser Phe Asp Glu Phe Ile Arg Glu Ala Gly Val Ala Glu His
50 55 60

Ile Asp Lys Phe Leu Asn Asp Leu Asp Ala Glu Asp Val Lys Glu Val
65 70 75 80

Asp Arg Val Ser Ala Ile Ile Arg Asp Glu Leu Cys Ser Leu Asp Val
85 90 95

Pro Glu Asn Ala Arg Phe Ala Val His Gln Ala Tyr Arg Asp Leu Met
100 105 110

Glu Arg Cys Gly Gly Asp Val Pro Val Ala Val Arg Ser Ser Ala Thr
 115 120 125
 Ala Glu Asp Leu Pro Asp Ala Ser Phe Ala Gly Gln Gln Asp Thr Tyr
 130 135 140
 Leu Trp Gln Val Gly Leu Ser Ala Val Thr Glu His Ile Arg Lys Cys
 145 150 155 160
 Trp Ala Ser Leu Phe Thr Ser Arg Ala Ile Ile Tyr Arg Leu Lys Asn
 165 170 175
 Asn Ile Pro Asn Glu Gly Leu Ser Met Ala Val Val Val Gln Lys Met
 180 185 190
 Val Asn Ser Arg Val Ala Gly Val Ala Ile Thr Met Asn Pro Ser Asn
 195 200 205
 Gly Asp Arg Ser Lys Ile Thr Ile Asp Ser Ser Trp Gly Val Gly Glu
 210 215 220
 Met Val Val Ser Gly Glu Val Thr Pro Asp Asn Ile Leu Leu Asp Lys
 225 230 235 240
 Ile Thr Leu Gln Val Val Ser Glu His Ile Gly Ser Lys His Ala Glu
 245 250 255
 Leu Ile Pro Asp Ala Thr Ser Gly Ser Leu Val Glu Lys Pro Val Asp
 260 265 270
 Glu Glu Arg Ala Asn Arg Arg Ser Leu Thr Asp Glu Glu Met Leu Ala
 275 280 285
 Val Ala Gln Met Ala Lys Arg Ala Glu Lys His Tyr Lys Cys Pro Gln
 290 295 300
 Asp Ile Glu Trp Ala Leu Asp Ala Asp Leu Pro Asp Gly Glu Asn Leu
 305 310 315 320
 Leu Leu Leu Gln Ser Arg Pro Glu Thr Ile His Ser Asn Gly Val Lys
 325 330 335
 Lys Glu Thr Pro Thr Pro Gln Ala Ala Lys Thr Ile Gly Thr Phe Asp
 340 345 350
 Phe Ser Ser Ile Thr Val Ala Met Thr Gly Thr Lys
 355 360

<210> 85
 <211> 1860
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1837)
 <223> RXN00635

<400> 85

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aagttaggca acacaatagc cataacgttg aggagttcag atg gca cac agc tac 115
Met Ala His Ser Tyr
1 5

gca gaa caa tta att gac act ttg gaa gct caa ggt gtg aag cga att 163
Ala Glu Gln Leu Ile Asp Thr Leu Glu Ala Gln Gly Val Lys Arg Ile
10 15 20

tat ggt ttg gtg ggt gac agc ctt aat ccg atc gtg gat gct gtc cgc 211
Tyr Gly Leu Val Gly Asp Ser Leu Asn Pro Ile Val Asp Ala Val Arg
25 30 35

caa tca gat att gag tgg gtg cac gtt cga aat gag gaa gcg gcg gcg 259
Gln Ser Asp Ile Glu Trp Val His Val Arg Asn Glu Glu Ala Ala Ala
40 45 50

ttt gca gcc ggt gcg gaa tcg ttg atc act ggg gag ctg gca gta tgt 307
Phe Ala Ala Gly Ala Glu Ser Leu Ile Thr Gly Glu Leu Ala Val Cys
55 60 65

gct gct tct tgt ggt cct gga aac aca cac ctg att cag ggt ctt tat 355
Ala Ala Ser Cys Gly Pro Gly Asn Thr His Leu Ile Gln Gly Leu Tyr
70 75 80 85

gat tcg cat cga aat ggt gcg aag gtg ttg gcc atc gct agc cat att 403
Asp Ser His Arg Asn Gly Ala Lys Val Leu Ala Ile Ala Ser His Ile
90 95 100

ccg agt gcc cag att ggt tcg acg ttc ttc cag gaa acg cat ccg gag 451
Pro Ser Ala Gln Ile Gly Ser Thr Phe Phe Gln Glu Thr His Pro Glu
105 110 115

att ttg ttt aag gaa tgc tct ggt tac tgc gag atg gtg aat ggt ggt 499
Ile Leu Phe Lys Glu Cys Ser Gly Tyr Cys Glu Met Val Asn Gly Gly
120 125 130

gag cag ggt gaa cgc att ttg cat cac gcg att cag tcc acc atg gcg 547
Glu Gln Gly Glu Arg Ile Leu His His Ala Ile Gln Ser Thr Met Ala
135 140 145

ggt aaa ggt gtg tcg gtg gta gtg att cct ggt gat atc gct aag gaa 595
Gly Lys Gly Val Ser Val Val Val Ile Pro Gly Asp Ile Ala Lys Glu
150 155 160 165

gac gca ggt gac ggt act tat tcc aat tcc act att tct tct ggc act 643
Asp Ala Gly Asp Gly Thr Tyr Ser Asn Ser Thr Ile Ser Ser Gly Thr
170 175 180

cct gtg gtg ttc ccg gat cct act gag gct gca gcg ctg gtg gag gcg 691
Pro Val Val Phe Pro Asp Pro Thr Glu Ala Ala Ala Leu Val Glu Ala
185 190 195

att aac aac gct aag tct gtc act ttg ttc tgc ggt gcg ggc gtg aag 739
Ile Asn Asn Ala Lys Ser Val Thr Leu Phe Cys Gly Ala Gly Val Lys
200 205 210

aat gct cgc gcg cag gtg ttg gag ttg gcg gag aag att aaa tca ccg 787
Asn Ala Arg Ala Gln Val Leu Glu Leu Ala Glu Lys Ile Lys Ser Pro
215 220 225

atc ggg cat gcg ctg ggt ggt aag cag tac atc cag cat gag aat ccg	835
Ile Gly His Ala Leu Gly Gly Lys Gln Tyr Ile Gln His Glu Asn Pro	
230 235 240 245	
ttt gag gtc ggc atg tct ggc ctg ctt ggt tac ggc gcc tgc gtg gat	883
Phe Glu Val Gly Met Ser Gly Leu Leu Gly Tyr Gly Ala Cys Val Asp	
250 255 260	
gcg tcc aat gag gcg gat ctg ctg att cta ttg ggt acg gat ttc cct	931
Ala Ser Asn Glu Ala Asp Leu Leu Ile Leu Leu Gly Thr Asp Phe Pro	
265 270 275	
tat tct gat ttc ctt cct aaa gac aac gtt gcc cag gtg gat atc aac	979
Tyr Ser Asp Phe Leu Pro Lys Asp Asn Val Ala Gln Val Asp Ile Asn	
280 285 290	
ggt gcg cac att ggt cga cgt acc acg gtg aag tat ccg gtg acc ggt	1027
Gly Ala His Ile Gly Arg Arg Thr Thr Val Lys Tyr Pro Val Thr Gly	
295 300 305	
gat gtt gct gca aca atc gaa aat att ttg cct cat gtg aag gaa aaa	1075
Asp Val Ala Ala Thr Ile Glu Asn Ile Leu Pro His Val Lys Glu Lys	
310 315 320 325	
aca gat cgt tcc ttc ctt gat cgg atg ctc aag gca cac gag cgt aag	1123
Thr Asp Arg Ser Phe Leu Asp Arg Met Leu Lys Ala His Glu Arg Lys	
330 335 340	
ttg agc tcg gtg gta gag acg tac aca cat aac gtc gag aag cat gtg	1171
Leu Ser Ser Val Val Glu Thr Tyr Thr His Asn Val Glu Lys His Val	
345 350 355	
cct att cac cct gaa tac gtt gcc tct att ttg aac gag ctg gcg gat	1219
Pro Ile His Pro Glu Tyr Val Ala Ser Ile Leu Asn Glu Leu Ala Asp	
360 365 370	
aag gat gcg gtg ttt act gtg gat acc ggc atg tgc aat gtg tgg cat	1267
Lys Asp Ala Val Phe Thr Val Asp Thr Gly Met Cys Asn Val Trp His	
375 380 385	
gcg agg tac atc gag aat ccg gag gga acg cgc gac ttt gtg ggt tca	1315
Ala Arg Tyr Ile Glu Asn Pro Glu Gly Thr Arg Asp Phe Val Gly Ser	
390 395 400 405	
ttc cgc cac ggc acg atg gct aat gcg ttg cct cat gcg att ggt gcg	1363
Phe Arg His Gly Thr Met Ala Asn Ala Leu Pro His Ala Ile Gly Ala	
410 415 420	
caa agt gtt gat cga aac cgc cag gtg atc gcg atg tgt ggc gat ggt	1411
Gln Ser Val Asp Arg Asn Arg Gln Val Ile Ala Met Cys Gly Asp Gly	
425 430 435	
ggt ttg ggc atg ctg ctg ggt gag ctt ctg acc gtt aag ctg cac caa	1459
Gly Leu Gly Met Leu Leu Gly Glu Leu Leu Thr Val Lys Leu His Gln	
440 445 450	
ctt ccg ctg aag gct gtg gtg ttt aac aac agt tct ttg ggc atg gtg	1507
Leu Pro Leu Lys Ala Val Val Phe Asn Asn Ser Ser Leu Gly Met Val	
455 460 465	

aag ttg gag atg ctc gtg gag gga cag cca gaa ttt ggt act gac cat 1555
 Lys Leu Glu Met Leu Val Glu Gly Gln Pro Glu Phe Gly Thr Asp His
 470 475 480 485

 gag gaa gtg aat ttc gca gag att gcg gcg gct gcg ggt atc aaa tcg 1603
 Glu Glu Val Asn Phe Ala Glu Ile Ala Ala Ala Gly Ile Lys Ser
 490 495 500

 gta cgc atc acc gat ccg aag aaa gtt cgc gag cag cta gct gag gca 1651
 Val Arg Ile Thr Asp Pro Lys Lys Val Arg Glu Gln Leu Ala Glu Ala
 505 510 515

 ttg gca tat cct gga cct gta ctg atc gat atc gtc acg gat cct aat 1699
 Leu Ala Tyr Pro Gly Pro Val Leu Ile Asp Ile Val Thr Asp Pro Asn
 520 525 530

 gcg ctg tcg atc cca cca acc atc acg tgg gaa cag gtc atg gga ttc 1747
 Ala Leu Ser Ile Pro Pro Thr Ile Thr Trp Glu Gln Val Met Gly Phe
 535 540 545

 agc aag gcg gcc acc cga acc gtc ttt ggt gga gga gta gga gcg atg 1795
 Ser Lys Ala Ala Thr Arg Thr Val Phe Gly Gly Val Gly Ala Met
 550 555 560 565

 atc gat ctg gcc cgt tcg aac ata agg aat att cct act cca 1837
 Ile Asp Leu Ala Arg Ser Asn Ile Arg Asn Ile Pro Thr Pro
 570 575

 tgatgattga tacacctgct gtt 1860

<210> 86
 <211> 579
 <212> PRT
 <213> *Corynebacterium glutamicum*

<400> 86
 Met Ala His Ser Tyr Ala Glu Gln Leu Ile Asp Thr Leu Glu Ala Gln
 1 5 10 15

 Gly Val Lys Arg Ile Tyr Gly Leu Val Gly Asp Ser Leu Asn Pro Ile
 20 25 30

 Val Asp Ala Val Arg Gln Ser Asp Ile Glu Trp Val His Val Arg Asn
 35 40 45

 Glu Glu Ala Ala Ala Phe Ala Ala Gly Ala Glu Ser Leu Ile Thr Gly
 50 55 60

 Glu Leu Ala Val Cys Ala Ala Ser Cys Gly Pro Gly Asn Thr His Leu
 65 70 75 80

 Ile Gln Gly Leu Tyr Asp Ser His Arg Asn Gly Ala Lys Val Leu Ala
 85 90 95

 Ile Ala Ser His Ile Pro Ser Ala Gln Ile Gly Ser Thr Phe Phe Gln
 100 105 110

 Glu Thr His Pro Glu Ile Leu Phe Lys Glu Cys Ser Gly Tyr Cys Glu
 115 120 125

Met Val Asn Gly Gly Glu Gln Gly Glu Arg Ile Leu His His Ala Ile
 130 135 140
 Gln Ser Thr Met Ala Gly Lys Gly Val Ser Val Val Val Ile Pro Gly
 145 150 155 160
 Asp Ile Ala Lys Glu Asp Ala Gly Asp Gly Thr Tyr Ser Asn Ser Thr
 165 170 175
 Ile Ser Ser Gly Thr Pro Val Val Phe Pro Asp Pro Thr Glu Ala Ala
 180 185 190
 Ala Leu Val Glu Ala Ile Asn Asn Ala Lys Ser Val Thr Leu Phe Cys
 195 200 205
 Gly Ala Gly Val Lys Asn Ala Arg Ala Gln Val Leu Glu Leu Ala Glu
 210 215 220
 Lys Ile Lys Ser Pro Ile Gly His Ala Leu Gly Gly Lys Gln Tyr Ile
 225 230 235 240
 Gln His Glu Asn Pro Phe Glu Val Gly Met Ser Gly Leu Leu Gly Tyr
 245 250 255
 Gly Ala Cys Val Asp Ala Ser Asn Glu Ala Asp Leu Leu Ile Leu Leu
 260 265 270
 Gly Thr Asp Phe Pro Tyr Ser Asp Phe Leu Pro Lys Asp Asn Val Ala
 275 280 285
 Gln Val Asp Ile Asn Gly Ala His Ile Gly Arg Arg Thr Thr Val Lys
 290 295 300
 Tyr Pro Val Thr Gly Asp Val Ala Ala Thr Ile Glu Asn Ile Leu Pro
 305 310 315 320
 His Val Lys Glu Lys Thr Asp Arg Ser Phe Leu Asp Arg Met Leu Lys
 325 330 335
 Ala His Glu Arg Lys Leu Ser Ser Val Val Glu Thr Tyr Thr His Asn
 340 345 350
 Val Glu Lys His Val Pro Ile His Pro Glu Tyr Val Ala Ser Ile Leu
 355 360 365
 Asn Glu Leu Ala Asp Lys Asp Ala Val Phe Thr Val Asp Thr Gly Met
 370 375 380
 Cys Asn Val Trp His Ala Arg Tyr Ile Glu Asn Pro Glu Gly Thr Arg
 385 390 395 400
 Asp Phe Val Gly Ser Phe Arg His Gly Thr Met Ala Asn Ala Leu Pro
 405 410 415
 His Ala Ile Gly Ala Gln Ser Val Asp Arg Asn Arg Gln Val Ile Ala
 420 425 430
 Met Cys Gly Asp Gly Gly Leu Gly Met Leu Leu Gly Glu Leu Leu Thr
 435 440 445
 Val Lys Leu His Gln Leu Pro Leu Lys Ala Val Val Phe Asn Asn Ser

450	455	460
Ser Leu Gly Met Val Lys Leu Glu Met Leu Val Glu Gly Gln Pro Glu 465 470 475 480		
Phe Gly Thr Asp His Glu Glu Val Asn Phe Ala Glu Ile Ala Ala Ala 485 490 495		
Ala Gly Ile Lys Ser Val Arg Ile Thr Asp Pro Lys Lys Val Arg Glu 500 505 510		
Gln Leu Ala Glu Ala Leu Ala Tyr Pro Gly Pro Val Leu Ile Asp Ile 515 520 525		
Val Thr Asp Pro Asn Ala Leu Ser Ile Pro Pro Thr Ile Thr Trp Glu 530 535 540		
Gln Val Met Gly Phe Ser Lys Ala Ala Thr Arg Thr Val Phe Gly Gly 545 550 555 560		
Gly Val Gly Ala Met Ile Asp Leu Ala Arg Ser Asn Ile Arg Asn Ile 565 570 575		
Pro Thr Pro		

<210> 87
 <211> 552
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (88)..(552)
 <223> FRXA02807

<400> 87
 aaagcgtggc aacaactgga atttaagagc acaattgaag tcgcaccaag ttaggcaaca 60
 caatagccat aacgttgagg agttcagatg gca cac agc tac gca gaa caa tta 114
 Met Ala His Ser Tyr Ala Glu Gln Leu
 1 5
 att gac act ttg gaa gct caa ggt gtg aag cga att tat ggt ttg gtg 162
 Ile Asp Thr Leu Glu Ala Gln Gly Val Lys Arg Ile Tyr Gly Leu Val
 10 15 20 25
 ggt gac agc ctt aat ccg atc gtg gat gct gtc cgc caa tca gat att 210
 Gly Asp Ser Leu Asn Pro Ile Val Asp Ala Val Arg Gln Ser Asp Ile
 30 35 40
 gag tgg gtg cac gtt cga aat gag gaa gcg gcg gcg ttt gca gcc ggt 258
 Glu Trp Val His Val Arg Asn Glu Glu Ala Ala Ala Phe Ala Ala Gly
 45 50 55
 gcg gaa tcg ttg atc act ggg gag ctg gca gta tgt gct gct tct tgt 306
 Ala Glu Ser Leu Ile Thr Gly Glu Leu Ala Val Cys Ala Ala Ser Cys
 60 65 70
 ggt cct gga aac aca cac ctg att cag ggt ctt tat gat tcg cat cga 354

Gly	Pro	Gly	Asn	Thr	His	Leu	Ile	Gln	Gly	Leu	Tyr	Asp	Ser	His	Arg	
75						80					85					
aat	ggt	gcg	aag	gtg	ttg	gcc	atc	gct	agc	cat	att	ccg	agt	gcc	cag	402
Asn	Gly	Ala	Lys	Val	Leu	Ala	Ile	Ala	Ser	His	Ile	Pro	Ser	Ala	Gln	
90					95					100					105	
att	ggt	tcg	acg	ttc	ttc	cag	gaa	acg	cat	ccg	gag	att	ttg	ttt	aag	450
Ile	Gly	Ser	Thr	Phe	Phe	Gln	Glu	Thr	His	Pro	Glu	Ile	Leu	Phe	Lys	
				110					115					120		
gaa	tgc	tct	ggt	tac	tgc	gag	atg	gtg	aat	ggt	ggt	gag	cag	ggt	gaa	498
Glu	Cys	Ser	Gly	Tyr	Cys	Glu	Met	Val	Asn	Gly	Gly	Glu	Gln	Gly	Glu	
			125					130					135			
cgc	att	ttg	cat	cac	gcg	att	cag	tcc	acc	atg	gcg	ggt	aaa	ggt	gtg	546
Arg	Ile	Leu	His	His	Ala	Ile	Gln	Ser	Thr	Met	Ala	Gly	Lys	Gly	Val	
		140					145					150				
tcg	gtg															552
Ser	Val															
155																

<210> 88
 <211> 155
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 88
 Met Ala His Ser Tyr Ala Glu Gln Leu Ile Asp Thr Leu Glu Ala Gln
 1 5 10 15
 Gly Val Lys Arg Ile Tyr Gly Leu Val Gly Asp Ser Leu Asn Pro Ile
 20 25 30
 Val Asp Ala Val Arg Gln Ser Asp Ile Glu Trp Val His Val Arg Asn
 35 40 45
 Glu Glu Ala Ala Ala Phe Ala Ala Gly Ala Glu Ser Leu Ile Thr Gly
 50 55 60
 Glu Leu Ala Val Cys Ala Ala Ser Cys Gly Pro Gly Asn Thr His Leu
 65 70 75 80
 Ile Gln Gly Leu Tyr Asp Ser His Arg Asn Gly Ala Lys Val Leu Ala
 85 90 95
 Ile Ala Ser His Ile Pro Ser Ala Gln Ile Gly Ser Thr Phe Phe Gln
 100 105 110
 Glu Thr His Pro Glu Ile Leu Phe Lys Glu Cys Ser Gly Tyr Cys Glu
 115 120 125
 Met Val Asn Gly Gly Glu Gln Gly Glu Arg Ile Leu His His Ala Ile
 130 135 140
 Gln Ser Thr Met Ala Gly Lys Gly Val Ser Val
 145 150 155

<210> 89
 <211> 944
 <212> DNA
 <213> *Corynebacterium glutamicum*

<220>
 <221> CDS
 <222> (1)..(921)
 <223> FRXA00635

<400> 89
 ggt acg gat ttc cct tat tct gat ttc ctt cct aaa gac aac gtt gcc 48
 Gly Thr Asp Phe Pro Tyr Ser Asp Phe Leu Pro Lys Asp Asn Val Ala
 1 5 10 15

cag gtg gat atc aac ggt gcg cac att ggt cga cgt acc acg gtg aag 96
 Gln Val Asp Ile Asn Gly Ala His Ile Gly Arg Arg Thr Thr Val Lys
 20 25 30

tat ccg gtg acc ggt gat gtt gct gca aca atc gaa aat att ttg cct 144
 Tyr Pro Val Thr Gly Asp Val Ala Ala Thr Ile Glu Asn Ile Leu Pro
 35 40 45

cat gtg aag gaa aaa aca gat cgt tcc ttc ctt gat cgg atg ctc aag 192
 His Val Lys Glu Lys Thr Asp Arg Ser Phe Leu Asp Arg Met Leu Lys
 50 55 60

gca cac gag cgt aag ttg agc tcg gtg gta gag acg tac aca cat aac 240
 Ala His Glu Arg Lys Leu Ser Ser Val Val Glu Thr Tyr Thr His Asn
 65 70 75 80

gtc gag aag cat gtg cct att cac cct gaa tac gtt gcc tct att ttg 288
 Val Glu Lys His Val Pro Ile His Pro Glu Tyr Val Ala Ser Ile Leu
 85 90 95

aac gag ctg gcg gat aag gat gcg gtg ttt act gtg gat acc ggc atg 336
 Asn Glu Leu Ala Asp Lys Asp Ala Val Phe Thr Val Asp Thr Gly Met
 100 105 110

tgc aat gtg tgg cat gcg agg tac atc gag aat ccg gag gga acg cgc 384
 Cys Asn Val Trp His Ala Arg Tyr Ile Glu Asn Pro Glu Gly Thr Arg
 115 120 125

gac ttt gtg ggt tca ttc cgc cac ggc acg atg gct aat gcg ttg cct 432
 Asp Phe Val Gly Ser Phe Arg His Gly Thr Met Ala Asn Ala Leu Pro
 130 135 140

cat gcg att ggt gcg caa agt gtt gat cga aac cgc cag gtg atc gcg 480
 His Ala Ile Gly Ala Gln Ser Val Asp Arg Asn Arg Gln Val Ile Ala
 145 150 155 160

atg tgt ggc gat ggt ggt ttg ggc atg ctg ctg ggt gag ctt ctg acc 528
 Met Cys Gly Asp Gly Gly Leu Gly Met Leu Leu Gly Glu Leu Leu Thr
 165 170 175

gtt aag ctg cac caa ctt ccg ctg aag gct gtg gtg ttt aac aac agt 576
 Val Lys Leu His Gln Leu Pro Leu Lys Ala Val Val Phe Asn Asn Ser
 180 185 190

tct ttg ggc atg gtg aag ttg gag atg ctc gtg gag gga cag cca gaa 624
 Ser Leu Gly Met Val Lys Leu Glu Met Leu Val Glu Gly Gln Pro Glu

195	200	205	
ttt ggt act gac cat gag gaa gtg aat ttc gca gag att gcg gcg gct			672
Phe Gly Thr Asp His Glu Glu Val Asn Phe Ala Glu Ile Ala Ala Ala			
210	215	220	
gcg ggt atc aaa tcg gta cgc atc acc gat ccg aag aaa gtt cgc gag			720
Ala Gly Ile Lys Ser Val Arg Ile Thr Asp Pro Lys Lys Val Arg Glu			
225	230	235	240
cag cta gct gag gca ttg gca tat cct gga cct gta ctg atc gat atc			768
Gln Leu Ala Glu Ala Leu Ala Tyr Pro Gly Pro Val Leu Ile Asp Ile			
245	250	255	
gtc acg gat cct aat gcg ctg tcg atc cca cca acc atc acg tgg gaa			816
Val Thr Asp Pro Asn Ala Leu Ser Ile Pro Pro Thr Ile Thr Trp Glu			
260	265	270	
cag gtc atg gga ttc agc aag gcg gcc acc cga acc gtc ttt ggt gga			864
Gln Val Met Gly Phe Ser Lys Ala Ala Thr Arg Thr Val Phe Gly Gly			
275	280	285	
gga gta gga gcg atg atc gat ctg gcc cgt tcg aac ata agg aat att			912
Gly Val Gly Ala Met Ile Asp Leu Ala Arg Ser Asn Ile Arg Asn Ile			
290	295	300	
cct act cca tgatgattga tacacctgct gtt			944
Pro Thr Pro			
305			

<210> 90

<211> 307

<212> PRT

<213> Corynebacterium glutamicum

<400> 90

Gly Thr Asp Phe Pro Tyr Ser Asp Phe Leu Pro Lys Asp Asn Val Ala
1 5 10 15

Gln Val Asp Ile Asn Gly Ala His Ile Gly Arg Arg Thr Thr Val Lys
20 25 30

Tyr Pro Val Thr Gly Asp Val Ala Ala Thr Ile Glu Asn Ile Leu Pro
35 40 45

His Val Lys Glu Lys Thr Asp Arg Ser Phe Leu Asp Arg Met Leu Lys
50 55 60

Ala His Glu Arg Lys Leu Ser Ser Val Val Glu Thr Tyr Thr His Asn
65 70 75 80

Val Glu Lys His Val Pro Ile His Pro Glu Tyr Val Ala Ser Ile Leu
85 90 95

Asn Glu Leu Ala Asp Lys Asp Ala Val Phe Thr Val Asp Thr Gly Met
100 105 110

Cys Asn Val Trp His Ala Arg Tyr Ile Glu Asn Pro Glu Gly Thr Arg
115 120 125

Asp Phe Val Gly Ser Phe Arg His Gly Thr Met Ala Asn Ala Leu Pro
 130 135 140
 His Ala Ile Gly Ala Gln Ser Val Asp Arg Asn Arg Gln Val Ile Ala
 145 150 155 160
 Met Cys Gly Asp Gly Gly Leu Gly Met Leu Leu Gly Glu Leu Leu Thr
 165 170 175
 Val Lys Leu His Gln Leu Pro Leu Lys Ala Val Val Phe Asn Asn Ser
 180 185 190
 Ser Leu Gly Met Val Lys Leu Glu Met Leu Val Glu Gly Gln Pro Glu
 195 200 205
 Phe Gly Thr Asp His Glu Glu Val Asn Phe Ala Glu Ile Ala Ala Ala
 210 215 220
 Ala Gly Ile Lys Ser Val Arg Ile Thr Asp Pro Lys Lys Val Arg Glu
 225 230 235 240
 Gln Leu Ala Glu Ala Leu Ala Tyr Pro Gly Pro Val Leu Ile Asp Ile
 245 250 255
 Val Thr Asp Pro Asn Ala Leu Ser Ile Pro Pro Thr Ile Thr Trp Glu
 260 265 270
 Gln Val Met Gly Phe Ser Lys Ala Ala Thr Arg Thr Val Phe Gly Gly
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 Pro Thr Pro
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 Met Ala Arg Gly Phe
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 ctc ttg ggc gct acc gca ggt cgc acc acc ctg acc ggt gaa ggc ctc 163
 Leu Leu Gly Ala Thr Ala Gly Arg Thr Thr Leu Thr Gly Glu Gly Leu
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 cag cac atg gat gga cac tcc cct gtc ttg gct tcc acc aac gag ggt 211
 Gln His Met Asp Gly His Ser Pro Val Leu Ala Ser Thr Asn Glu Gly
 25 30 35

gtc gag acc tac gac cca tcc ttt gcg tac gag atc gca cac ctg gtt	259
Val Glu Thr Tyr Asp Pro Ser Phe Ala Tyr Glu Ile Ala His Leu Val	
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cac cgt ggc atc gac cgc atg tac ggc cca ggc aag ggt gaa gat gtt	307
His Arg Gly Ile Asp Arg Met Tyr Gly Pro Gly Lys Gly Glu Asp Val	
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atc tac tac atc acc atc tac aac gag cca acc cca cag cca gct gag	355
Ile Tyr Tyr Ile Thr Ile Tyr Asn Glu Pro Thr Pro Gln Pro Ala Glu	
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cca gaa gga ctg gac gta gaa ggc ctg cac aag ggc atc tac ctc tac	403
Pro Glu Gly Leu Asp Val Glu Gly Leu His Lys Gly Ile Tyr Leu Tyr	
90 95 100	
tcc cgc ggt gaa ggc acc ggc cat gag gca aac atc ttg gct tcc ggt	451
Ser Arg Gly Glu Gly Thr Gly His Glu Ala Asn Ile Leu Ala Ser Gly	
105 110 115	
gtt ggt atg cag tgg gct ctc aag gct gca tcc atc ctt gag gct gac	499
Val Gly Met Gln Trp Ala Leu Lys Ala Ala Ser Ile Leu Glu Ala Asp	
120 125 130	
tac gga gtt cgt gcc aac att tac tcc gct act tct tgg gtt aac ttg	547
Tyr Gly Val Arg Ala Asn Ile Tyr Ser Ala Thr Ser Trp Val Asn Leu	
135 140 145	
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Ala Arg Asp Gly Ala Ala Arg Asn Lys Ala Gln Leu Arg Asn Pro Gly	
150 155 160 165	
gca gat gct ggc gag gca ttc gta acc acc cag ctg aag cag acc tcc	643
Ala Asp Ala Gly Glu Ala Phe Val Thr Thr Gln Leu Lys Gln Thr Ser	
170 175 180	
ggc cca tac gtt gca gtg tct gac ttc tcc act gat ctg cca aac cag	691
Gly Pro Tyr Val Ala Val Ser Asp Phe Ser Thr Asp Leu Pro Asn Gln	
185 190 195	
atc cgt gaa tgg gtc cca ggc gac tac acc gtt ctc ggt gca gat ggc	739
Ile Arg Glu Trp Val Pro Gly Asp Tyr Thr Val Leu Gly Ala Asp Gly	
200 205 210	
ttc ggt ttc tct gat acc cgc cca gct gct cgt cgc ttc ttc aac atc	787
Phe Gly Phe Ser Asp Thr Arg Pro Ala Ala Arg Arg Phe Phe Asn Ile	
215 220 225	
gac gct gag tcc att gtt gtt gca gtg ctg aac tcc ctg gca cgc gaa	835
Asp Ala Glu Ser Ile Val Val Ala Val Leu Asn Ser Leu Ala Arg Glu	
230 235 240 245	
ggc aag atc gac gtc tcc gtt gct gct cag gct gct gag aag ttc aag	883
Gly Lys Ile Asp Val Ser Val Ala Ala Gln Ala Ala Glu Lys Phe Lys	
250 255 260	
ttg gat gat cct acg agt gtt tcc gta gat cca aac gct cct gag gaa	931
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<210> 92

<211> 277

<212> PRT

<213> Corynebacterium glutamicum

<400> 92

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Ser	Thr	Asn	Glu	Gly	Val	Glu	Thr	Tyr	Asp	Pro	Ser	Phe	Ala	Tyr	Glu
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Ile	Ala	His	Leu	Val	His	Arg	Gly	Ile	Asp	Arg	Met	Tyr	Gly	Pro	Gly
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Lys	Gly	Glu	Asp	Val	Ile	Tyr	Tyr	Ile	Thr	Ile	Tyr	Asn	Glu	Pro	Thr
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Pro	Gln	Pro	Ala	Glu	Pro	Glu	Gly	Leu	Asp	Val	Glu	Gly	Leu	His	Lys
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Gly	Ile	Tyr	Leu	Tyr	Ser	Arg	Gly	Glu	Gly	Thr	Gly	His	Glu	Ala	Asn
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Ile	Leu	Ala	Ser	Gly	Val	Gly	Met	Gln	Trp	Ala	Leu	Lys	Ala	Ala	Ser
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Ser	Trp	Val	Asn	Leu	Ala	Arg	Asp	Gly	Ala	Ala	Arg	Asn	Lys	Ala	Gln
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Leu	Arg	Asn	Pro	Gly	Ala	Asp	Ala	Gly	Glu	Ala	Phe	Val	Thr	Thr	Gln
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Leu	Lys	Gln	Thr	Ser	Gly	Pro	Tyr	Val	Ala	Val	Ser	Asp	Phe	Ser	Thr
		180						185					190		

Asp	Leu	Pro	Asn	Gln	Ile	Arg	Glu	Trp	Val	Pro	Gly	Asp	Tyr	Thr	Val
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Leu	Gly	Ala	Asp	Gly	Phe	Gly	Phe	Ser	Asp	Thr	Arg	Pro	Ala	Ala	Arg
	210					215					220				

Arg	Phe	Phe	Asn	Ile	Asp	Ala	Glu	Ser	Ile	Val	Val	Ala	Val	Leu	Asn
225					230					235					240

Ser	Leu	Ala	Arg	Glu	Gly	Lys	Ile	Asp	Val	Ser	Val	Ala	Ala	Gln	Ala
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 Trp Val Pro Gly Asp Tyr Thr Val Leu Gly Ala Asp Gly Phe Gly Phe
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 tct gat acc cgc cca gct gct cgt cgc ttc ttc aac atc gac gct gag 144
 Ser Asp Thr Arg Pro Ala Ala Arg Arg Phe Phe Asn Ile Asp Ala Glu
 35 40 45
 tcc att gtt gtt gca gtg ctg aac tcc ctg gca cgc gaa ggc aag atc 192
 Ser Ile Val Val Ala Val Leu Asn Ser Leu Ala Arg Glu Gly Lys Ile
 50 55 60
 gac gtc tcc gtt gct gct cag gct gct gag aag ttc aag ttg gat gat 240
 Asp Val Ser Val Ala Ala Gln Ala Ala Glu Lys Phe Lys Leu Asp Asp
 65 70 75 80
 cct acg agt gtt tcc gta gat cca aac gct cct gag gaa taaatcacct 289
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 <213> Corynebacterium glutamicum

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 35 40 45
 Ser Ile Val Val Ala Val Leu Asn Ser Leu Ala Arg Glu Gly Lys Ile
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Met Ala Arg Gly Phe
1 5
ttt ttg ggc gct acc gca ggt cgc acc acc ttg acc ggt gaa ggc ctc 163
Phe Leu Gly Ala Thr Ala Gly Arg Thr Leu Thr Gly Glu Gly Leu
10 15 20
cag cac atg gat gga cac tcc cct gtt ttg gct tcc acc aac gag ggt 211
Gln His Met Asp Gly His Ser Pro Val Leu Ala Ser Thr Asn Glu Gly
25 30 35
gtc gag acc tac gac cca tcc ttt gcg tac gag atc gca cac ctg gtt 259
Val Glu Thr Tyr Asp Pro Ser Phe Ala Tyr Glu Ile Ala His Leu Val
40 45 50
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His Arg Gly Ile Asp Arg Met Tyr Gly Pro Gly Lys Gly Glu Asp Val
55 60 65
atc tac tac atc acc atc tac aac gag cca acc cca cag cca gct gag 355
Ile Tyr Tyr Ile Thr Ile Tyr Asn Glu Pro Thr Pro Gln Pro Ala Glu
70 75 80 85
cca gaa gga ctg gac gta gaa ggc ctg cac aag ggc atc tac ctc tac 403
Pro Glu Gly Leu Asp Val Glu Gly Leu His Lys Gly Ile Tyr Leu Tyr
90 95 100
tcc cgc ggt gaa ggc acc ggc cat gag gca aac atc ttg gct tcc ggt 451
Ser Arg Gly Glu Gly Thr Gly His Glu Ala Asn Ile Leu Ala Ser Gly
105 110 115
gtt ggt atg cag tgg gct ctc aag gct gca tcc atc ctt gag gct gac 499
Val Gly Met Gln Trp Ala Leu Lys Ala Ala Ser Ile Leu Glu Ala Asp
120 125 130
tac gga gtt cgt gcc aac att tac tcc gct act tct tgg gtt aac ttg 547
Tyr Gly Val Arg Ala Asn Ile Tyr Ser Ala Thr Ser Trp Val Asn Leu
135 140 145
gct cgc gat ggc gct gct cgt aac aag gca cag ctg cgc aac cca ggt 595
Ala Arg Asp Gly Ala Ala Arg Asn Lys Ala Gln Leu Arg Asn Pro Gly
150 155 160 165

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 Ala Asp Ala Gly Glu Ala Phe Val Thr Thr Gln Leu Lys Gln Thr Ser
 170 175 180

ggc cca tac gtt gca gtg tct gac ttc tcc act gat ctg cca aac cag 691
 Gly Pro Tyr Val Ala Val Ser Asp Phe Ser Thr Asp Leu Pro Asn Gln
 185 190 195

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 Ile Arg Glu Trp Val Pro Gly Asp Tyr Thr Val Leu Gly Ala Asp Gly
 200 205 210

ttc ggt ttc tct gat acc cgc cca gct gct cgt cgc ttc ttc aac atc 787
 Phe Gly Phe Ser Asp Thr Arg Pro Ala Ala Arg Arg Phe Phe Asn Ile
 215 220 225

gac gct gag tcc att gtt gtt gca gtg ctg aac tcc ctg gca cgc gaa 835
 Asp Ala Glu Ser Ile Val Val Ala Val Leu Asn Ser Leu Ala Arg Glu
 230 235 240 245

ggc aag atc gac gtc tcc gtt gct gct cag gct gct gag aag ttc aag 883
 Gly Lys Ile Asp Val Ser Val Ala Ala Gln Ala Ala Glu Lys Phe Lys
 250 255 260

ttg gat gat cct acg agt gtt tcc gta gat cca aac gct cct gag gaa 931
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 <212> PRT
 <213> Corynebacterium glutamicum

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Ser Thr Asn Glu Gly Val Glu Thr Tyr Asp Pro Ser Phe Ala Tyr Glu
 35 40 45

Ile Ala His Leu Val His Arg Gly Ile Asp Arg Met Tyr Gly Pro Gly
 50 55 60

Lys Gly Glu Asp Val Ile Tyr Tyr Ile Thr Ile Tyr Asn Glu Pro Thr
 65 70 75 80

Pro Gln Pro Ala Glu Pro Glu Gly Leu Asp Val Glu Gly Leu His Lys
 85 90 95

Gly Ile Tyr Leu Tyr Ser Arg Gly Glu Gly Thr Gly His Glu Ala Asn
 100 105 110

Ile Leu Ala Ser Gly Val Gly Met Gln Trp Ala Leu Lys Ala Ala Ser
 115 120 125

Ile Leu Glu Ala Asp Tyr Gly Val Arg Ala Asn Ile Tyr Ser Ala Thr
 130 135 140
 Ser Trp Val Asn Leu Ala Arg Asp Gly Ala Ala Arg Asn Lys Ala Gln
 145 150 155 160
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 165 170 175
 Leu Lys Gln Thr Ser Gly Pro Tyr Val Ala Val Ser Asp Phe Ser Thr
 180 185 190
 Asp Leu Pro Asn Gln Ile Arg Glu Trp Val Pro Gly Asp Tyr Thr Val
 195 200 205
 Leu Gly Ala Asp Gly Phe Gly Phe Ser Asp Thr Arg Pro Ala Ala Arg
 210 215 220
 Arg Phe Phe Asn Ile Asp Ala Glu Ser Ile Val Val Ala Val Leu Asn
 225 230 235 240
 Ser Leu Ala Arg Glu Gly Lys Ile Asp Val Ser Val Ala Ala Gln Ala
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 Ala Glu Lys Phe Lys Leu Asp Asp Pro Thr Ser Val Ser Val Asp Pro
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 Asn Ala Pro Glu Glu
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 <212> DNA
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 Met Ala Asp Gln Ala
 1 5
 aaa ctt ggt ggc aag ccc tcg gat gac tct aac ttc gcg atg atc cgc 163
 Lys Leu Gly Gly Lys Pro Ser Asp Asp Ser Asn Phe Ala Met Ile Arg
 10 15 20
 gat ggc gtg gca tct tat ttg aac gac tca gat ccg gag gag acc aac 211
 Asp Gly Val Ala Ser Tyr Leu Asn Asp Ser Asp Pro Glu Glu Thr Asn
 25 30 35
 gag tgg atg gat tca ctc gac gga tta ctc cag gag tct tct cca gaa 259
 Glu Trp Met Asp Ser Leu Asp Gly Leu Leu Gln Glu Ser Ser Pro Glu
 40 45 50

cgt gct cgt tac ctc atg ctt cgt ttg ctt gag cgt gca tct gca aag 307
 Arg Ala Arg Tyr Leu Met Leu Arg Leu Leu Glu Arg Ala Ser Ala Lys
 55 60 65

cgc gta tct ctt ccc cca atg acg tca acc gac tac gtc aac acc att 355
 Arg Val Ser Leu Pro Pro Met Thr Ser Thr Asp Tyr Val Asn Thr Ile
 70 75 80 85

cca acc tct atg gaa cct gaa ttc cca ggc gat gag gaa atg gag aag 403
 Pro Thr Ser Met Glu Pro Glu Phe Pro Gly Asp Glu Glu Met Glu Lys
 90 95 100

cgt tac cgt cgt tgg att cgc tgg aac gca gcc atc atg gtt cac cgc 451
 Arg Tyr Arg Arg Trp Ile Arg Trp Asn Ala Ala Ile Met Val His Arg
 105 110 115

gct cag cga cca ggc atc ggc gtc ggc gga cac att tcc act tac gca 499
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 Gly Ala Ala
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<210> 98
 <211> 136
 <212> PRT
 <213> Corynebacterium glutamicum

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 20 25 30

Pro Glu Glu Thr Asn Glu Trp Met Asp Ser Leu Asp Gly Leu Leu Gln
 35 40 45

Glu Ser Ser Pro Glu Arg Ala Arg Tyr Leu Met Leu Arg Leu Leu Glu
 50 55 60

Arg Ala Ser Ala Lys Arg Val Ser Leu Pro Pro Met Thr Ser Thr Asp
 65 70 75 80

Tyr Val Asn Thr Ile Pro Thr Ser Met Glu Pro Glu Phe Pro Gly Asp
 85 90 95

Glu Glu Met Glu Lys Arg Tyr Arg Arg Trp Ile Arg Trp Asn Ala Ala
 100 105 110

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 115 120 125

Ile Ser Thr Tyr Ala Gly Ala Ala
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<210> 99
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<212> DNA

<213> *Corynebacterium glutamicum*

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<221> CDS

<222> (101)..(508)

<223> FRXA02887

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 Met Ala Asp Gln Ala
 1 5

aaa ctt ggt ggc aag ccc tcg gat gac tct aac ttc gcg atg atc cgc 163
 Lys Leu Gly Gly Lys Pro Ser Asp Asp Ser Asn Phe Ala Met Ile Arg
 10 15 20

gat ggc gtg gca tct tat ttg aac gac tca gat ccg gag gag acc aac 211
 Asp Gly Val Ala Ser Tyr Leu Asn Asp Ser Asp Pro Glu Glu Thr Asn
 25 30 35

gag tgg atg gat tca ctc gac gga tta ctc cag gag tct tct cca gaa 259
 Glu Trp Met Asp Ser Leu Asp Gly Leu Leu Gln Glu Ser Ser Pro Glu
 40 45 50

cgt gct cgt tac ctc atg ctt cgt ttg ctt gag cgt gca tct gca aag 307
 Arg Ala Arg Tyr Leu Met Leu Arg Leu Leu Glu Arg Ala Ser Ala Lys
 55 60 65

cgc gta tct ctt ccc cca atg acg tca acc gac tac gtc aac acc att 355
 Arg Val Ser Leu Pro Pro Met Thr Ser Thr Asp Tyr Val Asn Thr Ile
 70 75 80 85

cca acc tct atg gaa cct gaa ttc cca ggc gat gag gaa atg gag aag 403
 Pro Thr Ser Met Glu Pro Glu Phe Pro Gly Asp Glu Glu Met Glu Lys
 90 95 100

cgt tac cgt cgt tgg att cgc tgg aac gca gcc atc atg gtt cac cgc 451
 Arg Tyr Arg Arg Trp Ile Arg Trp Asn Ala Ala Ile Met Val His Arg
 105 110 115

gct cag cga cca ggc atc ggc gtc ggc gga cac att tcc act tac gca 499
 Ala Gln Arg Pro Gly Ile Gly Val Gly Gly His Ile Ser Thr Tyr Ala
 120 125 130

ggc gca gcc 508
 Gly Ala Ala
 135

<210> 100

<211> 136

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 100

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 20 25 30
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 35 40 45
 Glu Ser Ser Pro Glu Arg Ala Arg Tyr Leu Met Leu Arg Leu Leu Glu
 50 55 60
 Arg Ala Ser Ala Lys Arg Val Ser Leu Pro Pro Met Thr Ser Thr Asp
 65 70 75 80
 Tyr Val Asn Thr Ile Pro Thr Ser Met Glu Pro Glu Phe Pro Gly Asp
 85 90 95
 Glu Glu Met Glu Lys Arg Tyr Arg Arg Trp Ile Arg Trp Asn Ala Ala
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 <213> Corynebacterium glutamicum

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 <223> RXN03043

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 Pro Ser Tyr Pro His Pro His Gly Met Lys Asp Phe Trp Glu Phe Pro
 20 25 30
 act gtg tcc atg ggt ctt ggc cca atg gat gcc att tac cag gca cgt 144
 Thr Val Ser Met Gly Leu Gly Pro Met Asp Ala Ile Tyr Gln Ala Arg
 35 40 45
 ttc aac cgc tac ctc gaa aac cgt ggc atc aag gac acc tct gac cag 192
 Phe Asn Arg Tyr Leu Glu Asn Arg Gly Ile Lys Asp Thr Ser Asp Gln
 50 55 60
 cac gtc tgg gcc ttc ctt ggc gac ggc gaa atg gac gag cca gaa tca 240
 His Val Trp Ala Phe Leu Gly Asp Gly Glu Met Asp Glu Pro Glu Ser
 65 70 75 80
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 Arg Gly Leu Ile Gln Gln Ala Ala Leu Asn Asn Leu Asp Asn Leu Thr
 85 90 95
 ttc gtg gtt aac tgc aac ctg cag cgt ctc gac gga cct gtc cgc ggt 336

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Asn	Thr	Lys	Ile	Ile	Gln	Glu	Leu	Glu	Ser	Phe	Phe	Arg	Gly	Ala	Gly		
		115					120					125					
tgg	tct	gtg	atc	aag	gtt	gtt	tgg	ggg	cgc	gag	tgg	gat	gaa	ctt	ctg	432	
Trp	Ser	Val	Ile	Lys	Val	Val	Trp	Gly	Arg	Glu	Trp	Asp	Glu	Leu	Leu		
	130					135					140						
gag	aag	gac	cag	gat	ggg	gca	ctt	gtt	gag	atc	atg	aac	aac	acc	tcc	480	
Glu	Lys	Asp	Gln	Asp	Gly	Ala	Leu	Val	Glu	Ile	Met	Asn	Asn	Thr	Ser		
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Asp	Gly	Asp	Tyr	Gln	Thr	Phe	Lys	Ala	Asn	Asp	Gly	Ala	Tyr	Val	Arg		
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gag	cac	ttc	ttc	gga	cgt	gac	cca	cgc	acc	gca	aag	ctc	gtt	gag	aac	576	
Glu	His	Phe	Phe	Gly	Arg	Asp	Pro	Arg	Thr	Ala	Lys	Leu	Val	Glu	Asn		
			180					185					190				
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Met	Thr	Asp	Glu	Glu	Ile	Trp	Lys	Leu	Pro	Arg	Gly	Gly	His	Asp	Tyr		
		195					200					205					
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Arg	Lys	Val	Tyr	Ala	Ala	Tyr	Lys	Arg	Ala	Leu	Glu	Thr	Lys	Asp	Arg		
	210					215					220						
cca	acc	gtc	atc	ctt	gct	cac	acc	att	aag	ggc	tac	gga	ctc	ggc	cac	720	
Pro	Thr	Val	Ile	Leu	Ala	His	Thr	Ile	Lys	Gly	Tyr	Gly	Leu	Gly	His		
225					230					235					240		
aac	ttc	gaa	ggc	cgt	aac	gca	acc	cac	cag	atg	aag	aag	ctg	acg	ctt	768	
Asn	Phe	Glu	Gly	Arg	Asn	Ala	Thr	His	Gln	Met	Lys	Lys	Leu	Thr	Leu		
				245					250					255			
gat	gat	ctg	aag	ttg	ttc	cgc	gac	aag	cag	ggc	atc	cca	atc	acc	gat	816	
Asp	Asp	Leu	Lys	Leu	Phe	Arg	Asp	Lys	Gln	Gly	Ile	Pro	Ile	Thr	Asp		
			260					265					270				
gag	cag	ctg	gag	aag	gat	cct	tac	ctt	cct	cct	tac	tac	cac	cca	ggg	864	
Glu	Gln	Leu	Glu	Lys	Asp	Pro	Tyr	Leu	Pro	Pro	Tyr	Tyr	His	Pro	Gly		
		275					280					285					
gaa	gac	gct	cct	gaa	atc	aag	tac	atg	aag	gaa	cgt	cgc	gca	gcg	ctc	912	
Glu	Asp	Ala	Pro	Glu	Ile	Lys	Tyr	Met	Lys	Glu	Arg	Arg	Ala	Ala	Leu		
	290					295					300						
ggg	ggc	tac	ctg	cca	gag	cgt	cgt	gag	aac	tac	gat	cca	att	cag	gtt	960	
Gly	Gly	Tyr	Leu	Pro	Glu	Arg	Arg	Glu	Asn	Tyr	Asp	Pro	Ile	Gln	Val		
305					310				315						320		
cca	cca	ctg	gat	aag	ctt	cgc	tct	gtc	cgt	aag	ggc	tcc	ggc	aag	cag	1008	
Pro	Pro	Leu	Asp	Lys	Leu	Arg	Ser	Val	Arg	Lys	Gly	Ser	Gly	Lys	Gln		
				325					330					335			
cag	atc	gct	acc	acc	atg	gcg	act	gtt	cgt	acc	ttc	aag	gaa	ctg	atg	1056	
Gln	Ile	Ala	Thr	Thr	Met	Ala	Thr	Val	Arg	Thr	Phe	Lys	Glu	Leu	Met		

340	345	350	
cgc gat aag ggc ttg gct gat	cgc ctt gtc cca atc att	cct gat gag	1104
Arg Asp Lys Gly Leu Ala Asp	Arg Leu Val Pro Ile Ile	Pro Asp Glu	
355	360	365	
gca cgt acc ttc ggt ctt gac tct tgg ttc cca acc ttg aag atc tac			1152
Ala Arg Thr Phe Gly Leu Asp Ser Trp Phe Pro Thr Leu Lys Ile Tyr			
370	375	380	
aac ccg cac ggt cag aac tac gtg cct gtt gac cac gac ctg atg ctc			1200
Asn Pro His Gly Gln Asn Tyr Val Pro Val Asp His Asp Leu Met Leu			
385	390	395	400
tcc tac cgt gag gca cct gaa gga cag atc ctg cac gaa ggc atc aac			1248
Ser Tyr Arg Glu Ala Pro Glu Gly Gln Ile Leu His Glu Gly Ile Asn			
405	410	415	
gag gct ggt tcc gtg gca tcg ttc atc gct gcg ggt acc tcc tac gcc			1296
Glu Ala Gly Ser Val Ala Ser Phe Ile Ala Ala Gly Thr Ser Tyr Ala			
420	425	430	
acc cac ggc aag gcc atg att ccg ctg tac atc ttc tac tcg atg ttc			1344
Thr His Gly Lys Ala Met Ile Pro Leu Tyr Ile Phe Tyr Ser Met Phe			
435	440	445	
ggg att cca gcg cac cgg tgactccatc tgggcagcag ccg			1385
Gly Ile Pro Ala His Arg			
450			

<210> 102

<211> 454

<212> PRT

<213> Corynebacterium glutamicum

<400> 102

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Thr Val Ser Met Gly Leu Gly Pro Met Asp Ala Ile Tyr Gln Ala Arg	
35 40 45	
Phe Asn Arg Tyr Leu Glu Asn Arg Gly Ile Lys Asp Thr Ser Asp Gln	
50 55 60	
His Val Trp Ala Phe Leu Gly Asp Gly Glu Met Asp Glu Pro Glu Ser	
65 70 75 80	
Arg Gly Leu Ile Gln Gln Ala Ala Leu Asn Asn Leu Asp Asn Leu Thr	
85 90 95	
Phe Val Val Asn Cys Asn Leu Gln Arg Leu Asp Gly Pro Val Arg Gly	
100 105 110	
Asn Thr Lys Ile Ile Gln Glu Leu Glu Ser Phe Phe Arg Gly Ala Gly	
115 120 125	

Trp Ser Val Ile Lys Val Val Trp Gly Arg Glu Trp Asp Glu Leu Leu
 130 135 140
 Glu Lys Asp Gln Asp Gly Ala Leu Val Glu Ile Met Asn Asn Thr Ser
 145 150 155 160
 Asp Gly Asp Tyr Gln Thr Phe Lys Ala Asn Asp Gly Ala Tyr Val Arg
 165 170 175
 Glu His Phe Phe Gly Arg Asp Pro Arg Thr Ala Lys Leu Val Glu Asn
 180 185 190
 Met Thr Asp Glu Glu Ile Trp Lys Leu Pro Arg Gly Gly His Asp Tyr
 195 200 205
 Arg Lys Val Tyr Ala Ala Tyr Lys Arg Ala Leu Glu Thr Lys Asp Arg
 210 215 220
 Pro Thr Val Ile Leu Ala His Thr Ile Lys Gly Tyr Gly Leu Gly His
 225 230 235 240
 Asn Phe Glu Gly Arg Asn Ala Thr His Gln Met Lys Lys Leu Thr Leu
 245 250 255
 Asp Asp Leu Lys Leu Phe Arg Asp Lys Gln Gly Ile Pro Ile Thr Asp
 260 265 270
 Glu Gln Leu Glu Lys Asp Pro Tyr Leu Pro Pro Tyr Tyr His Pro Gly
 275 280 285
 Glu Asp Ala Pro Glu Ile Lys Tyr Met Lys Glu Arg Arg Ala Ala Leu
 290 295 300
 Gly Gly Tyr Leu Pro Glu Arg Arg Glu Asn Tyr Asp Pro Ile Gln Val
 305 310 315 320
 Pro Pro Leu Asp Lys Leu Arg Ser Val Arg Lys Gly Ser Gly Lys Gln
 325 330 335
 Gln Ile Ala Thr Thr Met Ala Thr Val Arg Thr Phe Lys Glu Leu Met
 340 345 350
 Arg Asp Lys Gly Leu Ala Asp Arg Leu Val Pro Ile Ile Pro Asp Glu
 355 360 365
 Ala Arg Thr Phe Gly Leu Asp Ser Trp Phe Pro Thr Leu Lys Ile Tyr
 370 375 380
 Asn Pro His Gly Gln Asn Tyr Val Pro Val Asp His Asp Leu Met Leu
 385 390 395 400
 Ser Tyr Arg Glu Ala Pro Glu Gly Gln Ile Leu His Glu Gly Ile Asn
 405 410 415
 Glu Ala Gly Ser Val Ala Ser Phe Ile Ala Ala Gly Thr Ser Tyr Ala
 420 425 430
 Thr His Gly Lys Ala Met Ile Pro Leu Tyr Ile Phe Tyr Ser Met Phe
 435 440 445
 Gly Ile Pro Ala His Arg

450

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 <211> 1287
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
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 <222> (1)..(1287)
 <223> FRXA02897

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ccg tcc tac cct cac cca cac ggt atg aag gac ttc tgg gag ttc cca 96
 Pro Ser Tyr Pro His Pro His Gly Met Lys Asp Phe Trp Glu Phe Pro
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act gtg tcc atg ggt ctt ggc cca atg gat gcc att tac cag gca cgt 144
 Thr Val Ser Met Gly Leu Gly Pro Met Asp Ala Ile Tyr Gln Ala Arg
 35 40 45

ttc aac cgc tac ctc gaa aac cgt ggc atc aag gac acc tct gac cag 192
 Phe Asn Arg Tyr Leu Glu Asn Arg Gly Ile Lys Asp Thr Ser Asp Gln
 50 55 60

cac gtc tgg gcc ttc ctt ggc gac ggc gaa atg gac gag cca gaa tca 240
 His Val Trp Ala Phe Leu Gly Asp Gly Glu Met Asp Glu Pro Glu Ser
 65 70 75 80

cgt ggt ctc atc cag cag gct gca ctg aac aac ctg gac aac ctg acc 288
 Arg Gly Leu Ile Gln Gln Ala Ala Leu Asn Asn Leu Asp Asn Leu Thr
 85 90 95

ttc gtg gtt aac tgc aac ctg cag cgt ctc gac gga cct gtc cgc ggt 336
 Phe Val Val Asn Cys Asn Leu Gln Arg Leu Asp Gly Pro Val Arg Gly
 100 105 110

aac acc aag atc atc cag gaa ctc gag tcc ttc ttc cgt ggc gca ggc 384
 Asn Thr Lys Ile Ile Gln Glu Leu Glu Ser Phe Phe Arg Gly Ala Gly
 115 120 125

tgg tct gtg atc aag gtt gtt tgg ggt cgc gag tgg gat gaa ctt ctg 432
 Trp Ser Val Ile Lys Val Val Trp Gly Arg Glu Trp Asp Glu Leu Leu
 130 135 140

gag aag gac cag gat ggt gca ctt gtt gag atc atg aac aac acc tcc 480
 Glu Lys Asp Gln Asp Gly Ala Leu Val Glu Ile Met Asn Asn Thr Ser
 145 150 155 160

gat ggt gac tac cag acc ttc aag gct aac gac ggc gca tat gtt cgt 528
 Asp Gly Asp Tyr Gln Thr Phe Lys Ala Asn Asp Gly Ala Tyr Val Arg
 165 170 175

gag cac ttc ttc gga cgt gac cca cgc acc gca aag ctc gtt gag aac 576
 Glu His Phe Phe Gly Arg Asp Pro Arg Thr Ala Lys Leu Val Glu Asn
 180 185 190

atg acc gac gaa gaa atc tgg aag ctt cca cgt ggc ggc cac gat tac	624
Met Thr Asp Glu Glu Ile Trp Lys Leu Pro Arg Gly Gly His Asp Tyr	
195 200 205	
cgc aag gtt tac gca gcc tac aag cga gct ctt gag acc aag gat cgc	672
Arg Lys Val Tyr Ala Ala Tyr Lys Arg Ala Leu Glu Thr Lys Asp Arg	
210 215 220	
cca acc gtc atc ctt gct cac acc att aag ggc tac gga ctc ggc cac	720
Pro Thr Val Ile Leu Ala His Thr Ile Lys Gly Tyr Gly Leu Gly His	
225 230 235 240	
aac ttc gaa ggc cgt aac gca acc cac cag atg aag aag ctg acg ctt	768
Asn Phe Glu Gly Arg Asn Ala Thr His Gln Met Lys Lys Leu Thr Leu	
245 250 255	
gat gat ctg aag ttg ttc cgc gac aag cag ggc atc cca atc acc gat	816
Asp Asp Leu Lys Leu Phe Arg Asp Lys Gln Gly Ile Pro Ile Thr Asp	
260 265 270	
gag cag ctg gag aag gat cct tac ctt cct cct tac tac cac cca ggt	864
Glu Gln Leu Glu Lys Asp Pro Tyr Leu Pro Pro Tyr Tyr His Pro Gly	
275 280 285	
gaa gac gct cct gaa atc aag tac atg aag gaa cgt cgc gca gcg ctc	912
Glu Asp Ala Pro Glu Ile Lys Tyr Met Lys Glu Arg Arg Ala Ala Leu	
290 295 300	
ggt ggc tac ctg cca gag cgt cgt gag aac tac gat cca att cag gtt	960
Gly Gly Tyr Leu Pro Glu Arg Arg Glu Asn Tyr Asp Pro Ile Gln Val	
305 310 315 320	
cca cca ctg gat aag ctt cgc tct gtc cgt aag ggc tcc ggc aag cag	1008
Pro Pro Leu Asp Lys Leu Arg Ser Val Arg Lys Gly Ser Gly Lys Gln	
325 330 335	
cag atc gct acc acc atg gcg act gtt cgt acc ttc aag gaa ctg atg	1056
Gln Ile Ala Thr Thr Met Ala Thr Val Arg Thr Phe Lys Glu Leu Met	
340 345 350	
cgc gat aag ggc ttg gct gat cgc ctt gtc cca atc att cct gat gag	1104
Arg Asp Lys Gly Leu Ala Asp Arg Leu Val Pro Ile Ile Pro Asp Glu	
355 360 365	
gca cgt acc ttc ggt ctt gac tct tgg ttc cca acc ttg aag atc tac	1152
Ala Arg Thr Phe Gly Leu Asp Ser Trp Phe Pro Thr Leu Lys Ile Tyr	
370 375 380	
aac ccg cac ggt cag aac tac gtg cct gtt gac cac gac ctg atg ctc	1200
Asn Pro His Gly Gln Asn Tyr Val Pro Val Asp His Asp Leu Met Leu	
385 390 395 400	
tcc tac cgt gag gca cct gaa gga cag atc ctg cac gaa ggc atc aac	1248
Ser Tyr Arg Glu Ala Pro Glu Gly Gln Ile Leu His Glu Gly Ile Asn	
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Glu Ala Gly Ser Val Ala Ser Phe Ile Ala Ala Gly Thr	
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<210> 104
 <211> 429
 <212> PRT
 <213> *Corynebacterium glutamicum*

<400> 104

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Thr Val Ser Met Gly Leu Gly Pro Met Asp Ala Ile Tyr Gln Ala Arg
      35           40           45

Phe Asn Arg Tyr Leu Glu Asn Arg Gly Ile Lys Asp Thr Ser Asp Gln
      50           55           60

His Val Trp Ala Phe Leu Gly Asp Gly Glu Met Asp Glu Pro Glu Ser
      65           70           75           80

Arg Gly Leu Ile Gln Gln Ala Ala Leu Asn Asn Leu Asp Asn Leu Thr
      85           90           95

Phe Val Val Asn Cys Asn Leu Gln Arg Leu Asp Gly Pro Val Arg Gly
      100          105          110

Asn Thr Lys Ile Ile Gln Glu Leu Glu Ser Phe Phe Arg Gly Ala Gly
      115          120          125

Trp Ser Val Ile Lys Val Val Trp Gly Arg Glu Trp Asp Glu Leu Leu
      130          135          140

Glu Lys Asp Gln Asp Gly Ala Leu Val Glu Ile Met Asn Asn Thr Ser
      145          150          155          160

Asp Gly Asp Tyr Gln Thr Phe Lys Ala Asn Asp Gly Ala Tyr Val Arg
      165          170          175

Glu His Phe Phe Gly Arg Asp Pro Arg Thr Ala Lys Leu Val Glu Asn
      180          185          190

Met Thr Asp Glu Glu Ile Trp Lys Leu Pro Arg Gly Gly His Asp Tyr
      195          200          205

Arg Lys Val Tyr Ala Ala Tyr Lys Arg Ala Leu Glu Thr Lys Asp Arg
      210          215          220

Pro Thr Val Ile Leu Ala His Thr Ile Lys Gly Tyr Gly Leu Gly His
      225          230          235          240

Asn Phe Glu Gly Arg Asn Ala Thr His Gln Met Lys Lys Leu Thr Leu
      245          250          255

Asp Asp Leu Lys Leu Phe Arg Asp Lys Gln Gly Ile Pro Ile Thr Asp
      260          265          270

Glu Gln Leu Glu Lys Asp Pro Tyr Leu Pro Pro Tyr Tyr His Pro Gly
      275          280          285
  
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Glu Asp Ala Pro Glu Ile Lys Tyr Met Lys Glu Arg Arg Ala Ala Leu
 290 295 300
 Gly Gly Tyr Leu Pro Glu Arg Arg Glu Asn Tyr Asp Pro Ile Gln Val
 305 310 315 320
 Pro Pro Leu Asp Lys Leu Arg Ser Val Arg Lys Gly Ser Gly Lys Gln
 325 330 335
 Gln Ile Ala Thr Thr Met Ala Thr Val Arg Thr Phe Lys Glu Leu Met
 340 345 350
 Arg Asp Lys Gly Leu Ala Asp Arg Leu Val Pro Ile Ile Pro Asp Glu
 355 360 365
 Ala Arg Thr Phe Gly Leu Asp Ser Trp Phe Pro Thr Leu Lys Ile Tyr
 370 375 380
 Asn Pro His Gly Gln Asn Tyr Val Pro Val Asp His Asp Leu Met Leu
 385 390 395 400
 Ser Tyr Arg Glu Ala Pro Glu Gly Gln Ile Leu His Glu Gly Ile Asn
 405 410 415
 Glu Ala Gly Ser Val Ala Ser Phe Ile Ala Ala Gly Thr
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<210> 105
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 <212> DNA
 <213> Corynebacterium glutamicum

<220>
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 <222> (88)..(1110)
 <223> RXN03083

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 Met Ala Lys Arg Ile Val Ile Ile Gly
 1 5
 ggt gga cct gca ggc tat gaa gcc gca ctc gca ggc gct aaa tac ggt 162
 Gly Gly Pro Ala Gly Tyr Glu Ala Ala Leu Ala Gly Ala Lys Tyr Gly
 10 15 20 25
 gca gaa gtt acc gtt att gaa gat gtc gga gtt ggc gga tcc gca gtc 210
 Ala Glu Val Thr Val Ile Glu Asp Val Gly Val Gly Gly Ser Ala Val
 30 35 40
 acc atg gac tgt gta cct tca aag tcc ttc atc gct ggt acc ggt atc 258
 Thr Met Asp Cys Val Pro Ser Lys Ser Phe Ile Ala Gly Thr Gly Ile
 45 50 55
 aaa acc gac ctc cga cgt gct gat gac atg gga ctt aac cgt ggg ctt 306
 Lys Thr Asp Leu Arg Arg Ala Asp Asp Met Gly Leu Asn Arg Gly Leu
 60 65 70

gga	aaa	gca	cac	cta	gaa	atc	gat	gca	ctg	aac	atc	cgt	gtg	aag	gac	354
Gly	Lys	Ala	His	Leu	Glu	Ile	Asp	Ala	Leu	Asn	Ile	Arg	Val	Lys	Asp	
	75					80					85					
ctt	gcg	aaa	gca	cag	tcc	gaa	gat	atc	ttg	ggc	cag	ctg	cag	cgc	tca	402
Leu	Ala	Lys	Ala	Gln	Ser	Glu	Asp	Ile	Leu	Gly	Gln	Leu	Gln	Arg	Ser	
90					95					100					105	
gat	gtc	cgc	atg	att	aac	ggt	gtg	ggc	cgc	ttt	gat	gat	tac	aac	acc	450
Asp	Val	Arg	Met	Ile	Asn	Gly	Val	Gly	Arg	Phe	Asp	Asp	Tyr	Asn	Thr	
				110					115					120		
aag	caa	acc	acc	cac	tac	att	aaa	gtc	acc	cac	agc	gat	ggc	tcc	gaa	498
Lys	Gln	Thr	Thr	His	Tyr	Ile	Lys	Val	Thr	His	Ser	Asp	Gly	Ser	Glu	
			125					130					135			
gaa	acc	gtt	gag	tgc	gat	ctg	gtg	ctg	gtt	gca	act	ggg	gca	acc	ccc	546
Glu	Thr	Val	Glu	Cys	Asp	Leu	Val	Leu	Val	Ala	Thr	Gly	Ala	Thr	Pro	
	140						145					150				
cgc	att	ctt	aaa	ggt	gca	gag	cca	gac	ggc	gag	cgc	atc	ttg	acc	tgg	594
Arg	Ile	Leu	Lys	Gly	Ala	Glu	Pro	Asp	Gly	Glu	Arg	Ile	Leu	Thr	Trp	
	155					160					165					
cgt	cag	gtc	tac	gac	att	gaa	gaa	ctc	ccc	acc	cac	ctt	atc	gtg	gtt	642
Arg	Gln	Val	Tyr	Asp	Ile	Glu	Glu	Leu	Pro	Thr	His	Leu	Ile	Val	Val	
170					175					180					185	
ggt	tcc	ggt	gtg	acc	ggt	gcg	gaa	ttt	gtc	tct	gcg	ttt	gct	gaa	ctc	690
Gly	Ser	Gly	Val	Thr	Gly	Ala	Glu	Phe	Val	Ser	Ala	Phe	Ala	Glu	Leu	
				190					195					200		
ggc	gtc	aaa	gtc	acc	atg	gtg	gca	tcc	cgt	gac	cgc	att	ttg	cct	cac	738
Gly	Val	Lys	Val	Thr	Met	Val	Ala	Ser	Arg	Asp	Arg	Ile	Leu	Pro	His	
			205					210					215			
gat	gac	gca	gat	gcc	gca	gac	gtg	ctg	gaa	acc	gtt	ctg	gct	gag	cgc	786
Asp	Asp	Ala	Asp	Ala	Ala	Asp	Val	Leu	Glu	Thr	Val	Leu	Ala	Glu	Arg	
		220					225					230				
gga	gta	tcc	ctg	gaa	aag	cat	gcc	cgc	gtg	gag	tct	gtc	acc	cgc	acc	834
Gly	Val	Ser	Leu	Glu	Lys	His	Ala	Arg	Val	Glu	Ser	Val	Thr	Arg	Thr	
	235					240					245					
gaa	gac	ggt	ggc	gtg	tgt	gtt	cgc	act	gct	gac	gga	cga	gaa	atc	tac	882
Glu	Asp	Gly	Gly	Val	Cys	Val	Arg	Thr	Ala	Asp	Gly	Arg	Glu	Ile	Tyr	
250					255					260					265	
ggt	tct	cac	gcg	ttg	atg	act	gtt	ggt	tcc	att	cca	aac	acg	gca	gat	930
Gly	Ser	His	Ala	Leu	Met	Thr	Val	Gly	Ser	Ile	Pro	Asn	Thr	Ala	Asp	
				270					275					280		
ctt	ggc	ctg	gag	aac	atc	ggt	gtt	gag	ctg	gca	cca	tcc	ggc	cat	atc	978
Leu	Gly	Leu	Glu	Asn	Ile	Gly	Val	Glu	Leu	Ala	Pro	Ser	Gly	His	Ile	
			285					290					295			
aag	gtt	gac	cgg	tct	ccc	gca	cca	aca	tcc	ccg	gtg	tgt	acg	cag	cag	1026
Lys	Val	Asp	Arg	Ser	Pro	Ala	Pro	Thr	Ser	Pro	Val	Cys	Thr	Gln	Gln	
		300					305					310				
gtg	act	gta	ctg	acc	tat	tcc	cac	tgg	cgt	ccg	ttg	cag	cga	tgc	agg	1074

Val Thr Val Leu Thr Tyr Ser His Trp Arg Pro Leu Gln Arg Cys Arg
 315 320 325

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<211> 341

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 106

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Asp Val Gly Val Gly Gly Ser Ala Val Thr Met Asp Cys Val Pro Ser
 35 40 45

Lys Ser Phe Ile Ala Gly Thr Gly Ile Lys Thr Asp Leu Arg Arg Ala
 50 55 60

Asp Asp Met Gly Leu Asn Arg Gly Leu Gly Lys Ala His Leu Glu Ile
 65 70 75 80

Asp Ala Leu Asn Ile Arg Val Lys Asp Leu Ala Lys Ala Gln Ser Glu
 85 90 95

Asp Ile Leu Gly Gln Leu Gln Arg Ser Asp Val Arg Met Ile Asn Gly
 100 105 110

Val Gly Arg Phe Asp Asp Tyr Asn Thr Lys Gln Thr Thr His Tyr Ile
 115 120 125

Lys Val Thr His Ser Asp Gly Ser Glu Glu Thr Val Glu Cys Asp Leu
 130 135 140

Val Leu Val Ala Thr Gly Ala Thr Pro Arg Ile Leu Lys Gly Ala Glu
 145 150 155 160

Pro Asp Gly Glu Arg Ile Leu Thr Trp Arg Gln Val Tyr Asp Ile Glu
 165 170 175

Glu Leu Pro Thr His Leu Ile Val Val Gly Ser Gly Val Thr Gly Ala
 180 185 190

Glu Phe Val Ser Ala Phe Ala Glu Leu Gly Val Lys Val Thr Met Val
 195 200 205

Ala Ser Arg Asp Arg Ile Leu Pro His Asp Asp Ala Asp Ala Ala Asp
 210 215 220

Val Leu Glu Thr Val Leu Ala Glu Arg Gly Val Ser Leu Glu Lys His
 225 230 235 240

Ala Arg Val Glu Ser Val Thr Arg Thr Glu Asp Gly Gly Val Cys Val
 245 250 255

Arg Thr Ala Asp Gly Arg Glu Ile Tyr Gly Ser His Ala Leu Met Thr
 260 265 270

Val Gly Ser Ile Pro Asn Thr Ala Asp Leu Gly Leu Glu Asn Ile Gly
 275 280 285

Val Glu Leu Ala Pro Ser Gly His Ile Lys Val Asp Arg Ser Pro Ala
 290 295 300

Pro Thr Ser Pro Val Cys Thr Gln Gln Val Thr Val Leu Thr Tyr Ser
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His Trp Arg Pro Leu Gln Arg Cys Arg Ala Val Ser Pro Cys Ile Thr
 325 330 335

His Ser Val Lys Ala
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<210> 107

<211> 1518

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (89)..(1495)

<223> FRXA02853

<400> 107

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 Met Ala Lys Arg Ile Val Ile Ile Gly
 1 5

ggt gga cct gca ggc tat gaa gcc gca ctc gca ggc gct aaa tac ggt 163
 Gly Gly Pro Ala Gly Tyr Glu Ala Ala Leu Ala Gly Ala Lys Tyr Gly
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gca gaa gtt acc gtt att gaa gat gtc gga gtt ggc gga tcc gca gtc 211
 Ala Glu Val Thr Val Ile Glu Asp Val Gly Val Gly Gly Ser Ala Val
 30 35 40

acc atg gac tgt gta cct tca aag tcc ttc atc gct ggt acc ggt atc 259
 Thr Met Asp Cys Val Pro Ser Lys Ser Phe Ile Ala Gly Thr Gly Ile
 45 50 55

aaa acc gac ctc cga cgt gct gat gac atg gga ctt aac cgt ggg ctt 307
 Lys Thr Asp Leu Arg Arg Ala Asp Asp Met Gly Leu Asn Arg Gly Leu
 60 65 70

gga aaa gca cac cta gaa atc gat gca ctg aac atc cgt gtg aag gac 355
 Gly Lys Ala His Leu Glu Ile Asp Ala Leu Asn Ile Arg Val Lys Asp
 75 80 85

ctt gcg aaa gca cag tcc gaa gat atc ttg ggc cag ctg cag cgc tca 403
 Leu Ala Lys Ala Gln Ser Glu Asp Ile Leu Gly Gln Leu Gln Arg Ser

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Asp Val Arg Met Ile Asn Gly Val Gly Arg Phe Asp Asp Tyr Asn Thr				
110 115 120				
aag caa acc acc cac tac att aaa gtc acc cac agc gat ggc tcc gaa	499			
Lys Gln Thr Thr His Tyr Ile Lys Val Thr His Ser Asp Gly Ser Glu				
125 130 135				
gaa acc gtt gag tgc gat ctg gtg ctg gtt gca act ggt gca acc ccc	547			
Glu Thr Val Glu Cys Asp Leu Val Leu Val Ala Thr Gly Ala Thr Pro				
140 145 150				
cgc att ctt aaa ggt gca gag cca gac ggc gag cgc atc ttg acc tgg	595			
Arg Ile Leu Lys Gly Ala Glu Pro Asp Gly Glu Arg Ile Leu Thr Trp				
155 160 165				
cgt cag gtc tac gac att gaa gaa ctc ccc acc cac ctt atc gtg gtt	643			
Arg Gln Val Tyr Asp Ile Glu Glu Leu Pro Thr His Leu Ile Val Val				
170 175 180 185				
ggt tcc ggt gtg acc ggt gcg gaa ttt gtc tct gcg ttt gct gaa ctc	691			
Gly Ser Gly Val Thr Gly Ala Glu Phe Val Ser Ala Phe Ala Glu Leu				
190 195 200				
ggc gtc aaa gtc acc atg gtg gca tcc cgt gac cgc att ttg cct cac	739			
Gly Val Lys Val Thr Met Val Ala Ser Arg Asp Arg Ile Leu Pro His				
205 210 215				
gat gac gca gat gcc gca gac gtg ctg gaa acc gtt ctg gct gag cgc	787			
Asp Asp Ala Asp Ala Ala Asp Val Leu Glu Thr Val Leu Ala Glu Arg				
220 225 230				
gga gta tcc ctg gaa aag cat gcc cgc gtg gag tct gtc acc cgc acc	835			
Gly Val Ser Leu Glu Lys His Ala Arg Val Glu Ser Val Thr Arg Thr				
235 240 245				
gaa gac ggt ggc gtg tgt gtt cgc act gct gac gga cga gaa atc tac	883			
Glu Asp Gly Gly Val Cys Val Arg Thr Ala Asp Gly Arg Glu Ile Tyr				
250 255 260 265				
ggt tct cac gcg ttg atg act gtt ggt tcc att cca aac acg gca gat	931			
Gly Ser His Ala Leu Met Thr Val Gly Ser Ile Pro Asn Thr Ala Asp				
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Gly Arg Ile Ala Met Tyr His Ala Leu Gly Glu Gly Val Ser Pro Ile				
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 Arg Leu Lys Thr Val Ala Thr Ala Val Phe Thr Arg Pro Glu Ile Ala
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 gct gat acc ttc gcg gtg tac cca tca ttg tca ggt tcg att act gaa 1459
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<213> *Corynebacterium glutamicum*

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Lys Ser Phe Ile Ala Gly Thr Gly Ile Lys Thr Asp Leu Arg Arg Ala
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Asp Asp Met Gly Leu Asn Arg Gly Leu Gly Lys Ala His Leu Glu Ile
 65 70 75 80

Asp Ala Leu Asn Ile Arg Val Lys Asp Leu Ala Lys Ala Gln Ser Glu
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Asp Ile Leu Gly Gln Leu Gln Arg Ser Asp Val Arg Met Ile Asn Gly

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Pro	Leu	Ala	Ser	Val	Ala	Ala	Met	Gln	Gly	Arg	Ile	Ala	Met	Tyr	His	
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Gln	Val	Asp	Ser	Gly	Glu	Val	Ser	Ala	Arg	Val	Ile	Val	Leu	Pro	Leu	
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Ala	Thr	Asn	Pro	Arg	Ala	Lys	Met	Arg	Ser	Leu	Arg	His	Gly	Phe	Val	
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Lys	Leu	Phe	Cys	Arg	Arg	Asn	Ser	Gly	Leu	Ile	Ile	Gly	Gly	Val	Val	
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Val	Ala	Pro	Thr	Ala	Ser	Glu	Leu	Ile	Leu	Pro	Ile	Ala	Val	Ala	Val	
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Thr Asn Arg Leu Thr Val Ala Asp Leu Ala Asp Thr Phe Ala Val Tyr
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His Asp Asp Leu Gly
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<213> Corynebacterium glutamicum

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<223> RXA02259

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 Val Phe Lys Val Val
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 Met Thr Asp Phe Leu Arg Asp Asp Ile Arg Phe Leu Gly Gln Ile Leu
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ggt gag gta att gcg gaa caa gaa ggc cag gag gtt tat gaa ctg gtc 211
 Gly Glu Val Ile Ala Glu Gln Glu Gly Gln Glu Val Tyr Glu Leu Val
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gaa caa gcg cgc ctg act tct ttt gat atc gcc aag ggc aac gcc gaa 259
 Glu Gln Ala Arg Leu Thr Ser Phe Asp Ile Ala Lys Gly Asn Ala Glu
 40 45 50

atg gat agc ctg gtt cag gtt ttc gac ggc att act cca gcc aag gca 307
 Met Asp Ser Leu Val Gln Val Phe Asp Gly Ile Thr Pro Ala Lys Ala
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aca ccg att gct cgc gca ttt tcc cac ttc gct ctg ctg gct aac ctg 355
 Thr Pro Ile Ala Arg Ala Phe Ser His Phe Ala Leu Leu Ala Asn Leu
 70 75 80 85

gcg gaa gac ctc tac gat gaa gag ctt cgt gaa cag gct ctc gat gca 403
 Ala Glu Asp Leu Tyr Asp Glu Glu Leu Arg Glu Gln Ala Leu Asp Ala
 90 95 100

ggc gac acc cct ccg gac agc act ctt gat gcc acc tgg ctg aaa ctc 451
 Gly Asp Thr Pro Pro Asp Ser Thr Leu Asp Ala Thr Trp Leu Lys Leu
 105 110 115

aat gag ggc aat gtt ggc gca gaa gct gtg gcc gat gtg ctg cgc aat 499
 Asn Glu Gly Asn Val Gly Ala Glu Ala Val Ala Asp Val Leu Arg Asn
 120 125 130

gct gag gtg gcg ccg gtt ctg act gcg cac cca act gag act cgc cgc 547

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Gln	Thr	Ala	Leu	Ile	Arg	Val	Ala	Arg	Pro	Arg	Ile	Glu	Asp	Glu	Ile		
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Glu	Val	Gly	Leu	Arg	Tyr	Tyr	Lys	Leu	Ser	Leu	Leu	Glu	Glu	Ile	Pro		
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ggt	gtt	cct	ttg	aag	ccc	gtg	gtc	aag	cca	ggt	tcc	tgg	att	ggt	gga	883	
Gly	Val	Pro	Leu	Lys	Pro	Val	Val	Lys	Pro	Gly	Ser	Trp	Ile	Gly	Gly		
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gac	cac	gac	ggt	aac	cct	tat	gtc	acc	gcg	gaa	aca	gtt	gag	tat	tcc	931	
Asp	His	Asp	Gly	Asn	Pro	Tyr	Val	Thr	Ala	Glu	Thr	Val	Glu	Tyr	Ser		
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Thr	His	Arg	Ala	Ala	Glu	Thr	Val	Leu	Lys	Tyr	Tyr	Ala	Arg	Gln	Leu		
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Ser	Arg	Val	Asp	Glu	Pro	Tyr	Arg	Arg	Ala	Val	His	Gly	Val	Arg	Gly		
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Gly	Val	Trp	Phe	Lys	Val	Phe	Thr	Pro	Tyr	Ala	Ser	Pro	Glu	Glu	Phe		
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tta	aac	gat	gcg	ttg	acc	att	gat	cat	tct	ctg	cgt	gaa	tcc	aag	gac	1267	
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agc tac gag gac gtc ctc acc gag ctt ttc gaa cgc gcc caa gtc acc Ser Tyr Glu Asp Val Leu Thr Glu Leu Phe Glu Arg Ala Gln Val Thr 425 430 435			1411
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Val Arg Ile Thr Glu Gln Gly Glu Ile Ile Ser Ala Lys Tyr Gly Asn	
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Pro Glu Thr Ala Arg Arg Asn Leu Glu Ala Leu Val Ser Ala Thr Leu	
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Glu Ala Ser Leu Leu Asp Val Ser Glu Leu Thr Asp His Gln Arg Ala	
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Tyr Asp Ile Met Ser Glu Ile Ser Glu Leu Ser Leu Lys Lys Tyr Ala	
695 700 705	
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Ser Leu Val His Glu Asp Gln Gly Phe Ile Asp Tyr Phe Thr Gln Ser	
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Thr Pro Leu Gln Glu Ile Gly Ser Leu Asn Ile Gly Ser Arg Pro Ser	
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Val Leu Ser Trp Ser Gln Ser Arg Val Met Leu Pro Gly Trp Phe Gly	
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Thr Ser Val Leu Asp Asn Met Ala Gln Val Met Ser Lys Ala Glu Leu	
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Arg Leu Ala Lys Leu Tyr Ala Asp Leu Ile Pro Asp Thr Glu Val Ala	
825 830 835	
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Glu Arg Val Tyr Ser Val Ile Arg Glu Glu Tyr Phe Leu Thr Lys Lys	
840 845 850	
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Met Phe Cys Val Ile Thr Gly Ser Asp Asp Leu Leu Asp Asp Asn Pro	
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 Asn Val Ile Gln Val Glu Met Met Arg Arg Tyr Arg Lys Gly Asp Gln
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<212> PRT

<213> *Corynebacterium glutamicum*

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Lys Gly Asn Ala Glu Met Asp Ser Leu Val Gln Val Phe Asp Gly Ile
 50 55 60

Thr Pro Ala Lys Ala Thr Pro Ile Ala Arg Ala Phe Ser His Phe Ala
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Gln Ala Leu Asp Ala Gly Asp Thr Pro Pro Asp Ser Thr Leu Asp Ala
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Thr Trp Leu Lys Leu Asn Glu Gly Asn Val Gly Ala Glu Ala Val Ala
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Asp Val Leu Arg Asn Ala Glu Val Ala Pro Val Leu Thr Ala His Pro
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Thr Glu Thr Arg Arg Arg Thr Val Phe Asp Ala Gln Lys Trp Ile Thr
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Thr His Met Arg Glu Arg His Ala Leu Gln Ser Ala Glu Pro Thr Ala
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Arg Thr Gln Ser Lys Leu Asp Glu Ile Glu Lys Asn Ile Arg Arg Arg
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Ile Thr Ile Leu Trp Gln Thr Ala Leu Ile Arg Val Ala Arg Pro Arg
 195 200 205

Ile Glu Asp Glu Ile Glu Val Gly Leu Arg Tyr Tyr Lys Leu Ser Leu
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 Leu Glu Glu Ile Pro Arg Ile Asn Arg Asp Val Ala Val Glu Leu Arg
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 Glu Arg Phe Gly Glu Gly Val Pro Leu Lys Pro Val Val Lys Pro Gly
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 Ser Trp Ile Gly Gly Asp His Asp Gly Asn Pro Tyr Val Thr Ala Glu
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 Thr Val Glu Tyr Ser Thr His Arg Ala Ala Glu Thr Val Leu Lys Tyr
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 Tyr Ala Arg Gln Leu His Ser Leu Glu His Glu Leu Ser Leu Ser Asp
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 Arg Met Asn Lys Val Thr Pro Gln Leu Leu Ala Leu Ala Asp Ala Gly
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 His Asn Asp Val Pro Ser Arg Val Asp Glu Pro Tyr Arg Arg Ala Val
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 His Gly Val Arg Gly Arg Ile Leu Ala Thr Thr Ala Glu Leu Ile Gly
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 Glu Asp Ala Val Glu Gly Val Trp Phe Lys Val Phe Thr Pro Tyr Ala
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 Ser Pro Glu Glu Phe Leu Asn Asp Ala Leu Thr Ile Asp His Ser Leu
 370 375 380
 Arg Glu Ser Lys Asp Val Leu Ile Ala Asp Asp Arg Leu Ser Val Leu
 385 390 395 400
 Ile Ser Ala Ile Glu Ser Phe Gly Phe Asn Leu Tyr Ala Leu Asp Leu
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 Arg Ala Gln Val Thr Ala Asn Tyr Arg Glu Leu Ser Glu Ala Glu Lys
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 Pro Met Val Leu Leu Lys Glu Phe Gly Leu Ile Ala Ala Asn Gly Asp
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 545 550 555 560
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 Leu Gly Tyr Ser Asp Ser Asn Lys Asp Gly Gly Tyr Phe Ser Ala Asn
 580 585 590
 Trp Ala Leu Tyr Asp Ala Glu Leu Gln Leu Val Glu Leu Cys Arg Ser
 595 600 605
 Ala Gly Val Lys Leu Arg Leu Phe His Gly Arg Gly Gly Thr Val Gly
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 Arg Gly Gly Gly Pro Ser Tyr Asp Ala Ile Leu Ala Gln Pro Arg Gly
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 645 650 655
 Ala Lys Tyr Gly Asn Pro Glu Thr Ala Arg Arg Asn Leu Glu Ala Leu
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 Val Ser Ala Thr Leu Glu Ala Ser Leu Leu Asp Val Ser Glu Leu Thr
 675 680 685
 Asp His Gln Arg Ala Tyr Asp Ile Met Ser Glu Ile Ser Glu Leu Ser
 690 695 700
 Leu Lys Lys Tyr Ala Ser Leu Val His Glu Asp Gln Gly Phe Ile Asp
 705 710 715 720
 Tyr Phe Thr Gln Ser Thr Pro Leu Gln Glu Ile Gly Ser Leu Asn Ile
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 Gly Ser Arg Pro Ser Ser Arg Lys Gln Thr Ser Ser Val Glu Asp Leu
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 Arg Ala Ile Pro Trp Val Leu Ser Trp Ser Gln Ser Arg Val Met Leu
 755 760 765
 Pro Gly Trp Phe Gly Val Gly Thr Ala Leu Glu Gln Trp Ile Gly Glu
 770 775 780
 Gly Glu Gln Ala Thr Gln Arg Ile Ala Glu Leu Gln Thr Leu Asn Glu
 785 790 795 800
 Ser Trp Pro Phe Phe Thr Ser Val Leu Asp Asn Met Ala Gln Val Met
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 820 825 830
 Asp Thr Glu Val Ala Glu Arg Val Tyr Ser Val Ile Arg Glu Glu Tyr
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 Phe Leu Thr Lys Lys Met Phe Cys Val Ile Thr Gly Ser Asp Asp Leu

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Arg	Lys	Gly	Asp 900	Gln	Ser	Glu	Gln	Val 905	Ser	Arg	Asn	Ile	Gln 910	Leu	Thr
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<212> DNA
<213> Corynebacterium glutamicum
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<222> (101) .. (916)  
<223> RXN02326
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				Met	Leu	Gly	Arg	Pro								
				1				5								
acc	aag	gtc	acc	cca	tcc	tcc	aag	gtt	gtt	ggc	gac	ctc	gca	ctc	cac	163
Thr	Lys	Val	Thr	Pro	Ser	Ser	Lys	Val	Val	Gly	Asp	Leu	Ala	Leu	His	
				10					15					20		
ctc	gtt	ggт	gcg	ggт	gtg	gat	cca	gca	gac	ttt	gct	gcc	gat	cca	caa	211
Leu	Val	Gly	Ala	Gly	Val	Asp	Pro	Ala	Asp	Phe	Ala	Ala	Asp	Pro	Gln	
			25					30					35			
aag	tac	gac	atc	cca	gac	tct	gtc	atc	gcg	ttc	ctg	cgc	ggc	gag	ctt	259
Lys	Tyr	Asp	Ile	Pro	Asp	Ser	Val	Ile	Ala	Phe	Leu	Arg	Gly	Glu	Leu	
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ggт	aac	cct	cca	ggт	ggc	tgg	cca	gag	cca	ctg	cgc	acc	cgc	gca	ctg	307
Gly	Asn	Pro	Pro	Gly	Gly	Trp	Pro	Glu	Pro	Leu	Arg	Thr	Arg	Ala	Leu	
	55					60					65					
gaa	ggc	cgc	tcc	gaa	ggc	aag	gca	cct	ctg	acg	gaa	gtt	cct	gag	gaa	355
Glu	Gly	Arg	Ser	Glu	Gly	Lys	Ala	Pro	Leu	Thr	Glu	Val	Pro	Glu	Glu	
70					75				80						85	
gag	cag	gcg	cac	ctc	gac	gct	gat	gat	tcc	aag	gaa	cgt	cgc	aat	agc	403
Glu	Gln	Ala	His	Leu	Asp	Ala	Asp	Asp	Ser	Lys	Glu	Arg	Arg	Asn	Ser	
				90				95						100		
ctc	aac	cgc	ctg	ctg	ttc	ccg	aag	cca	acc	gaa	gag	ttc	ctc	gag	cac	451
Leu	Asn	Arg	Leu	Leu	Phe	Pro	Lys	Pro	Thr	Glu	Glu	Phe	Leu	Glu	His	
			105					110					115			
cgt	cgc	cgc	ttc	ggc	aac	acc	tct	gcg	ctg	gat	gat	cgt	qaa	ttc	ttc	499

Arg Arg Arg Phe Gly Asn Thr Ser Ala Leu Asp Asp Arg Glu Phe Phe
 120 125 130
 tac ggc ctg gtc gaa ggc cgc gag act ttg atc cgc ctg cca gat gtg 547
 Tyr Gly Leu Val Glu Gly Arg Glu Thr Leu Ile Arg Leu Pro Asp Val
 135 140 145
 cgc acc cca ctg ctt gtt cgc ctg gat gcg atc tct gag cca gac gat 595
 Arg Thr Pro Leu Leu Val Arg Leu Asp Ala Ile Ser Glu Pro Asp Asp
 150 155 160 165
 aag ggt atg cgc aat gtt gtg gcc aac gtc aac ggc cag atc cgc cca 643
 Lys Gly Met Arg Asn Val Val Ala Asn Val Asn Gly Gln Ile Arg Pro
 170 175 180
 atg cgt gtg cgt gac cgc tcc gtt gag tct gtc acc gca acc gca gaa 691
 Met Arg Val Arg Asp Arg Ser Val Glu Ser Val Thr Ala Thr Ala Glu
 185 190 195
 aag gca gat tcc tcc aac aag ggc cat gtt gct gca cca ttc gct ggt 739
 Lys Ala Asp Ser Ser Asn Lys Gly His Val Ala Ala Pro Phe Ala Gly
 200 205 210
 gtt gtc acc gtg act gtt gct gaa ggt gat gag gtc aag gct gga gat 787
 Val Val Thr Val Thr Val Ala Glu Gly Asp Glu Val Lys Ala Gly Asp
 215 220 225
 gca gtc gca atc atc gag gct atg aag atg gaa gca aca atc act gct 835
 Ala Val Ala Ile Ile Glu Ala Met Lys Met Glu Ala Thr Ile Thr Ala
 230 235 240 245
 tct gtt gac ggc aaa atc gat cgc gtt gtg gtt cct gct gca acg aag 883
 Ser Val Asp Gly Lys Ile Asp Arg Val Val Val Pro Ala Ala Thr Lys
 250 255 260
 gtg gaa ggt ggc gac ttg atc gtc gtc gtt tcc taaacctttc tgtaaaaagc 936
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 265 270

ccc

939

<210> 112

<211> 272

<212> PRT

<213> Corynebacterium glutamicum

<400> 112

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Ala Ala Asp Pro Gln Lys Tyr Asp Ile Pro Asp Ser Val Ile Ala Phe
 35 40 45

Leu Arg Gly Glu Leu Gly Asn Pro Pro Gly Gly Trp Pro Glu Pro Leu
 50 55 60

Arg Thr Arg Ala Leu Glu Gly Arg Ser Glu Gly Lys Ala Pro Leu Thr

65	70	75	80
Glu Val Pro Glu Glu Glu Gln Ala His Leu Asp Ala Asp Asp Ser Lys	85	90	95
Glu Arg Arg Asn Ser Leu Asn Arg Leu Leu Phe Pro Lys Pro Thr Glu	100	105	110
Glu Phe Leu Glu His Arg Arg Arg Phe Gly Asn Thr Ser Ala Leu Asp	115	120	125
Asp Arg Glu Phe Phe Tyr Gly Leu Val Glu Gly Arg Glu Thr Leu Ile	130	135	140
Arg Leu Pro Asp Val Arg Thr Pro Leu Leu Val Arg Leu Asp Ala Ile	145	150	155
Ser Glu Pro Asp Asp Lys Gly Met Arg Asn Val Val Ala Asn Val Asn	165	170	175
Gly Gln Ile Arg Pro Met Arg Val Arg Asp Arg Ser Val Glu Ser Val	180	185	190
Thr Ala Thr Ala Glu Lys Ala Asp Ser Ser Asn Lys Gly His Val Ala	195	200	205
Ala Pro Phe Ala Gly Val Val Thr Val Thr Val Ala Glu Gly Asp Glu	210	215	220
Val Lys Ala Gly Asp Ala Val Ala Ile Ile Glu Ala Met Lys Met Glu	225	230	235
Ala Thr Ile Thr Ala Ser Val Asp Gly Lys Ile Asp Arg Val Val Val	245	250	255
Pro Ala Ala Thr Lys Val Glu Gly Gly Asp Leu Ile Val Val Val Ser	260	265	270

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 <213> Corynebacterium glutamicum

<220>
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 <222> (101)..(916)
 <223> FRXA02326

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 Met Leu Gly Arg Pro
 1 5
 acc aag gtc acc cca tcc tcc aag gtt gtt ggc gac ctc gca ctc cac 163
 Thr Lys Val Thr Pro Ser Ser Lys Val Val Gly Asp Leu Ala Leu His

10										15					20					
ctc	gtt	ggt	gcg	ggt	gtg	gat	cca	gca	gac	ttt	gct	gcc	gat	cca	caa					211
Leu	Val	Gly	Ala	Gly	Val	Asp	Pro	Ala	Asp	Phe	Ala	Ala	Asp	Pro	Gln					
			25						30					35						
aag	tac	gac	atc	cca	gac	tct	gtc	atc	gcg	ttc	ctg	cgc	ggc	gag	ctt					259
Lys	Tyr	Asp	Ile	Pro	Asp	Ser	Val	Ile	Ala	Phe	Leu	Arg	Gly	Glu	Leu					
		40					45					50								
ggt	aac	cct	cca	ggt	ggc	tgg	cca	gag	cca	ctg	cgc	acc	cgc	gca	ctg					307
Gly	Asn	Pro	Pro	Gly	Gly	Trp	Pro	Glu	Pro	Leu	Arg	Thr	Arg	Ala	Leu					
	55					60					65									
gaa	ggc	cgc	tcc	gaa	ggc	aag	gca	cct	ctg	acg	gaa	gtt	cct	gag	gaa					355
Glu	Gly	Arg	Ser	Glu	Gly	Lys	Ala	Pro	Leu	Thr	Glu	Val	Pro	Glu	Glu					
70					75				80						85					
gag	cag	gcg	cac	ctc	gac	gct	gat	gat	tcc	aag	gaa	cgt	cgc	aat	agc					403
Glu	Gln	Ala	His	Leu	Asp	Ala	Asp	Asp	Ser	Lys	Glu	Arg	Arg	Asn	Ser					
			90						95					100						
ctc	aac	cgc	ctg	ctg	ttc	ccg	aag	cca	acc	gaa	gag	ttc	ctc	gag	cac					451
Leu	Asn	Arg	Leu	Leu	Phe	Pro	Lys	Pro	Thr	Glu	Glu	Phe	Leu	Glu	His					
			105					110					115							
cgt	cgc	cgc	ttc	ggc	aac	acc	tct	gcg	ctg	gat	gat	cgt	gaa	ttc	ttc					499
Arg	Arg	Arg	Phe	Gly	Asn	Thr	Ser	Ala	Leu	Asp	Asp	Arg	Glu	Phe	Phe					
			120				125					130								
tac	ggc	ctg	gtc	gaa	ggc	cgc	gag	act	ttg	atc	cgc	ctg	cca	gat	gtg					547
Tyr	Gly	Leu	Val	Glu	Gly	Arg	Glu	Thr	Leu	Ile	Arg	Leu	Pro	Asp	Val					
	135					140				145										
cgc	acc	cca	ctg	ctt	gtt	cgc	ctg	gat	gcg	atc	tct	gag	cca	gac	gat					595
Arg	Thr	Pro	Leu	Leu	Val	Arg	Leu	Asp	Ala	Ile	Ser	Glu	Pro	Asp	Asp					
150					155					160					165					
aag	ggt	atg	cgc	aat	gtt	gtg	gcc	aac	gtc	aac	ggc	cag	atc	cgc	cca					643
Lys	Gly	Met	Arg	Asn	Val	Val	Ala	Asn	Val	Asn	Gly	Gln	Ile	Arg	Pro					
				170					175					180						
atg	cgt	gtg	cgt	gac	cgc	tcc	gtt	gag	tct	gtc	acc	gca	acc	gca	gaa					691
Met	Arg	Val	Arg	Asp	Arg	Ser	Val	Glu	Ser	Val	Thr	Ala	Thr	Ala	Glu					
			185					190					195							
aag	gca	gat	tcc	tcc	aac	aag	ggc	cat	gtt	gct	gca	cca	ttc	gct	ggt					739
Lys	Ala	Asp	Ser	Ser	Asn	Lys	Gly	His	Val	Ala	Ala	Pro	Phe	Ala	Gly					
		200					205					210								
gtt	gtc	acc	gtg	act	gtt	gct	gaa	ggt	gat	gag	gtc	aag	gct	gga	gat					787
Val	Val	Thr	Val	Thr	Val	Ala	Glu	Gly	Asp	Glu	Val	Lys	Ala	Gly	Asp					
	215					220					225									
gca	gtc	gca	atc	atc	gag	gct	atg	aag	atg	gaa	gca	aca	atc	act	gct					835
Ala	Val	Ala	Ile	Ile	Glu	Ala	Met	Lys	Met	Glu	Ala	Thr	Ile	Thr	Ala					
230					235					240					245					
tct	gtt	gac	ggc	aaa	atc	gat	cgc	gtt	gtg	gtt	cct	gct	gca	acg	aag					883
Ser	Val	Asp	Gly	Lys	Ile	Asp	Arg	Val	Val	Val	Pro	Ala	Ala	Thr	Lys					
				250					255						260					

gtg gaa ggt ggc gac ttg atc gtc gtc gtt tcc taaacctttc tgtaaaaagc 936
 Val Glu Gly Gly Asp Leu Ile Val Val Val Ser
 265 270

ccc

939

<210> 114

<211> 272

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 114

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 20 25 30

Ala Ala Asp Pro Gln Lys Tyr Asp Ile Pro Asp Ser Val Ile Ala Phe
 35 40 45

Leu Arg Gly Glu Leu Gly Asn Pro Pro Gly Gly Trp Pro Glu Pro Leu
 50 55 60

Arg Thr Arg Ala Leu Glu Gly Arg Ser Glu Gly Lys Ala Pro Leu Thr
 65 70 75 80

Glu Val Pro Glu Glu Glu Gln Ala His Leu Asp Ala Asp Asp Ser Lys
 85 90 95

Glu Arg Arg Asn Ser Leu Asn Arg Leu Leu Phe Pro Lys Pro Thr Glu
 100 105 110

Glu Phe Leu Glu His Arg Arg Arg Phe Gly Asn Thr Ser Ala Leu Asp
 115 120 125

Asp Arg Glu Phe Phe Tyr Gly Leu Val Glu Gly Arg Glu Thr Leu Ile
 130 135 140

Arg Leu Pro Asp Val Arg Thr Pro Leu Leu Val Arg Leu Asp Ala Ile
 145 150 155 160

Ser Glu Pro Asp Asp Lys Gly Met Arg Asn Val Val Ala Asn Val Asn
 165 170 175

Gly Gln Ile Arg Pro Met Arg Val Arg Asp Arg Ser Val Glu Ser Val
 180 185 190

Thr Ala Thr Ala Glu Lys Ala Asp Ser Ser Asn Lys Gly His Val Ala
 195 200 205

Ala Pro Phe Ala Gly Val Val Thr Val Thr Val Ala Glu Gly Asp Glu
 210 215 220

Val Lys Ala Gly Asp Ala Val Ala Ile Ile Glu Ala Met Lys Met Glu
 225 230 235 240

Ala Thr Ile Thr Ala Ser Val Asp Gly Lys Ile Asp Arg Val Val Val
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Pro Ala Ala Thr Lys Val Glu Gly Gly Asp Leu Ile Val Val Val Ser
 260 265 270

<210> 115
 <211> 1083
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
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 <222> (101)..(1060)
 <223> RXN02327

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 Leu Leu Ala Thr Arg
 1 5
 gtc cgc tca ttc gca ctg aag cct gcg gca gag gcc gtc gca aag ctg 163
 Val Arg Ser Phe Ala Leu Lys Pro Ala Ala Glu Ala Val Ala Lys Leu
 10 15 20
 act cct gag ctt ttg tcc gtg gag gcc tgg ggc ggc gcg acc tac gat 211
 Thr Pro Glu Leu Leu Ser Val Glu Ala Trp Gly Gly Ala Thr Tyr Asp
 25 30 35
 gtg gcg atg cgt ttc ctc ttt gag gat ccg tgg gac agg ctc gac gag 259
 Val Ala Met Arg Phe Leu Phe Glu Asp Pro Trp Asp Arg Leu Asp Glu
 40 45 50
 ctg cgc gag gcg atg ccg aat gta aac att cag atg ctg ctt cgc ggc 307
 Leu Arg Glu Ala Met Pro Asn Val Asn Ile Gln Met Leu Leu Arg Gly
 55 60 65
 cgc aac acc gtg gga tac acc ccg tac cca gac tcc gtc tgc cgc gcg 355
 Arg Asn Thr Val Gly Tyr Thr Pro Tyr Pro Asp Ser Val Cys Arg Ala
 70 75 80 85
 ttt gtt aag gaa gct gcc agc tcc ggc gtg gac atc ttc cgc atc ttc 403
 Phe Val Lys Glu Ala Ala Ser Ser Gly Val Asp Ile Phe Arg Ile Phe
 90 95 100
 gac gcg ctt aac gac gtc tcc cag atg cgt cca gca atc gac gca gtc 451
 Asp Ala Leu Asn Asp Val Ser Gln Met Arg Pro Ala Ile Asp Ala Val
 105 110 115
 ctg gag acc aac acc gcg gta gcc gag gtg gct atg gct tat tct ggt 499
 Leu Glu Thr Asn Thr Ala Val Ala Glu Val Ala Met Ala Tyr Ser Gly
 120 125 130
 gat ctc tct gat cca aat gaa aag ctc tac acc ctg gat tac tac cta 547
 Asp Leu Ser Asp Pro Asn Glu Lys Leu Tyr Thr Leu Asp Tyr Tyr Leu
 135 140 145

aag atg gca gag gag atc gtc aag tct ggc gct cac atc ttg gcc att 595
Lys Met Ala Glu Glu Ile Val Lys Ser Gly Ala His Ile Leu Ala Ile
150 155 160 165

aag gat atg gct ggt ctg ctt cgc cca gct gcg gta acc aag ctg gtc 643
Lys Asp Met Ala Gly Leu Leu Arg Pro Ala Ala Val Thr Lys Leu Val
170 175 180

acc gca ctg cgc cgt gaa ttc gat ctg cca gtg cac gtg cac acc cac 691
Thr Ala Leu Arg Arg Glu Phe Asp Leu Pro Val His Val His Thr His
185 190 195

gac act gcg ggt ggc cag ctg gca acc tac ttt gct gca gct caa gct 739
Asp Thr Ala Gly Gly Gln Leu Ala Thr Tyr Phe Ala Ala Ala Gln Ala
200 205 210

ggt gca gat gct gtt gac ggt gct tcc ggc acc act gtc tgg cac cac 787
Gly Ala Asp Ala Val Asp Gly Ala Ser Gly Thr Thr Val Trp His His
215 220 225

ctc cca agc cat ccc ttg tct gcc att gtt gct gca ttc gcg cac acc 835
Leu Pro Ser His Pro Leu Ser Ala Ile Val Ala Ala Phe Ala His Thr
230 235 240 245

cgt cgc gat acc ggt ttg agc ctc gag gct gtt tct gac ctc gag ccg 883
Arg Arg Asp Thr Gly Leu Ser Leu Glu Ala Val Ser Asp Leu Glu Pro
250 255 260

tac tgg gaa gca gtg cgc gga ctg tac ctg cca ttt gag tct gga acc 931
Tyr Trp Glu Ala Val Arg Gly Leu Tyr Leu Pro Phe Glu Ser Gly Thr
265 270 275

cca ggc cca acc ggt cgc gtc tac cgc cac gaa atc cca ggc gga cag 979
Pro Gly Pro Thr Gly Arg Val Tyr Arg His Glu Ile Pro Gly Gly Gln
280 285 290

ttg tcc aac ctg cgt gca cag gcc acc gca ctg ggc ctt gcg gat cgt 1027
Leu Ser Asn Leu Arg Ala Gln Ala Thr Ala Leu Gly Leu Ala Asp Arg
295 300 305

ttc gaa ctc atc gaa gac aac tac gca agc cgt taatgagatg ctgggacgcc 1080
Phe Glu Leu Ile Glu Asp Asn Tyr Ala Ser Arg
310 315 320

caa 1083

<210> 116

<211> 320

<212> PRT

<213> Corynebacterium glutamicum

<400> 116

Leu Leu Ala Thr Arg Val Arg Ser Phe Ala Leu Lys Pro Ala Ala Glu
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Ala Val Ala Lys Leu Thr Pro Glu Leu Leu Ser Val Glu Ala Trp Gly
20 25 30

Gly Ala Thr Tyr Asp Val Ala Met Arg Phe Leu Phe Glu Asp Pro Trp
35 40 45

Asp Arg Leu Asp Glu Leu Arg Glu Ala Met Pro Asn Val Asn Ile Gln
 50 55 60
 Met Leu Leu Arg Gly Arg Asn Thr Val Gly Tyr Thr Pro Tyr Pro Asp
 65 70 75 80
 Ser Val Cys Arg Ala Phe Val Lys Glu Ala Ala Ser Ser Gly Val Asp
 85 90 95
 Ile Phe Arg Ile Phe Asp Ala Leu Asn Asp Val Ser Gln Met Arg Pro
 100 105 110
 Ala Ile Asp Ala Val Leu Glu Thr Asn Thr Ala Val Ala Glu Val Ala
 115 120 125
 Met Ala Tyr Ser Gly Asp Leu Ser Asp Pro Asn Glu Lys Leu Tyr Thr
 130 135 140
 Leu Asp Tyr Tyr Leu Lys Met Ala Glu Glu Ile Val Lys Ser Gly Ala
 145 150 155 160
 His Ile Leu Ala Ile Lys Asp Met Ala Gly Leu Leu Arg Pro Ala Ala
 165 170 175
 Val Thr Lys Leu Val Thr Ala Leu Arg Arg Glu Phe Asp Leu Pro Val
 180 185 190
 His Val His Thr His Asp Thr Ala Gly Gly Gln Leu Ala Thr Tyr Phe
 195 200 205
 Ala Ala Ala Gln Ala Gly Ala Asp Ala Val Asp Gly Ala Ser Gly Thr
 210 215 220
 Thr Val Trp His His Leu Pro Ser His Pro Leu Ser Ala Ile Val Ala
 225 230 235 240
 Ala Phe Ala His Thr Arg Arg Asp Thr Gly Leu Ser Leu Glu Ala Val
 245 250 255
 Ser Asp Leu Glu Pro Tyr Trp Glu Ala Val Arg Gly Leu Tyr Leu Pro
 260 265 270
 Phe Glu Ser Gly Thr Pro Gly Pro Thr Gly Arg Val Tyr Arg His Glu
 275 280 285
 Ile Pro Gly Gly Gln Leu Ser Asn Leu Arg Ala Gln Ala Thr Ala Leu
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 Gly Leu Ala Asp Arg Phe Glu Leu Ile Glu Asp Asn Tyr Ala Ser Arg
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<211> 1083

<212> DNA

<213> Corynebacterium glutamicum

<220>

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<222> (101)..(1060)

<223> FRXA02327

<400> 117

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                Leu Leu Ala Thr Arg
                1                    5

gtc cgc tca ttc gca ctg aag cct gcg gca gag gcc gtc gca aag ctg 163
Val Arg Ser Phe Ala Leu Lys Pro Ala Ala Glu Ala Val Ala Lys Leu
                10                    15                    20

act cct gag ctt ttg tcc gtg gag gcc tgg ggc ggc gcg acc tac gat 211
Thr Pro Glu Leu Leu Ser Val Glu Ala Trp Gly Gly Ala Thr Tyr Asp
                25                    30                    35

gtg gcg atg cgt ttc ctc ttt gag gat ccg tgg gac agg ctc gac gag 259
Val Ala Met Arg Phe Leu Phe Glu Asp Pro Trp Asp Arg Leu Asp Glu
                40                    45                    50

ctg cgc gag gcg atg ccg aat gta aac att cag atg ctg ctt cgc gcc 307
Leu Arg Glu Ala Met Pro Asn Val Asn Ile Gln Met Leu Leu Arg Gly
                55                    60                    65

cgc aac acc gtg gga tac acc ccg tac cca gac tcc gtc tgc cgc gcg 355
Arg Asn Thr Val Gly Tyr Thr Pro Tyr Pro Asp Ser Val Cys Arg Ala
                70                    75                    80                    85

ttt gtt aag gaa gct gcc agc tcc ggc gtg gac atc ttc cgc atc ttc 403
Phe Val Lys Glu Ala Ala Ser Ser Gly Val Asp Ile Phe Arg Ile Phe
                90                    95                    100

gac gcg ctt aac gac gtc tcc cag atg cgt cca gca atc gac gca gtc 451
Asp Ala Leu Asn Asp Val Ser Gln Met Arg Pro Ala Ile Asp Ala Val
                105                    110                    115

ctg gag acc aac acc gcg gta gcc gag gtg gct atg gct tat tct ggt 499
Leu Glu Thr Asn Thr Ala Val Ala Glu Val Ala Met Ala Tyr Ser Gly
                120                    125                    130

gat ctc tct gat cca aat gaa aag ctc tac acc ctg gat tac tac cta 547
Asp Leu Ser Asp Pro Asn Glu Lys Leu Tyr Thr Leu Asp Tyr Tyr Leu
                135                    140                    145

aag atg gca gag gag atc gtc aag tct ggc gct cac atc ttg gcc att 595
Lys Met Ala Glu Glu Ile Val Lys Ser Gly Ala His Ile Leu Ala Ile
                150                    155                    160                    165

aag gat atg gct ggt ctg ctt cgc cca gct gcg gta acc aag ctg gtc 643
Lys Asp Met Ala Gly Leu Leu Arg Pro Ala Ala Val Thr Lys Leu Val
                170                    175                    180

acc gca ctg cgc cgt gaa ttc gat ctg cca gtg cac gtg cac acc cac 691
Thr Ala Leu Arg Arg Glu Phe Asp Leu Pro Val His Val His Thr His
                185                    190                    195

gac act gcg ggt ggc cag ctg gca acc tac ttt gct gca gct caa gct 739

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Asp Thr Ala Gly Gly Gln Leu Ala Thr Tyr Phe Ala Ala Ala Gln Ala
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 ggt gca gat gct gtt gac ggt gct tcc ggc acc act gtc tgg cac cac 787
 Gly Ala Asp Ala Val Asp Gly Ala Ser Gly Thr Thr Val Trp His His
 215 220 225
 ctc cca agc cat ccc ttg tct gcc att gtt gct gca ttc gcg cac acc 835
 Leu Pro Ser His Pro Leu Ser Ala Ile Val Ala Ala Phe Ala His Thr
 230 235 240 245
 cgt cgc gat acc ggt ttg agc ctc gag gct gtt tct gac ctc gag ccg 883
 Arg Arg Asp Thr Gly Leu Ser Leu Glu Ala Val Ser Asp Leu Glu Pro
 250 255 260
 tac tgg gaa gca gtg cgc gga ctg tac ctg cca ttt gag tct gga acc 931
 Tyr Trp Glu Ala Val Arg Gly Leu Tyr Leu Pro Phe Glu Ser Gly Thr
 265 270 275
 cca ggc cca acc ggt cgc gtc tac cgc cac gaa atc cca ggc gga cag 979
 Pro Gly Pro Thr Gly Arg Val Tyr Arg His Glu Ile Pro Gly Gly Gln
 280 285 290
 ttg tcc aac ctg cgt gca cag gcc acc gca ctg ggc ctt gcg gat cgt 1027
 Leu Ser Asn Leu Arg Ala Gln Ala Thr Ala Leu Gly Leu Ala Asp Arg
 295 300 305
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 310 315 320
 caa 1083
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 <213> Corynebacterium glutamicum
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 Gly Ala Thr Tyr Asp Val Ala Met Arg Phe Leu Phe Glu Asp Pro Trp
 35 40 45
 Asp Arg Leu Asp Glu Leu Arg Glu Ala Met Pro Asn Val Asn Ile Gln
 50 55 60
 Met Leu Leu Arg Gly Arg Asn Thr Val Gly Tyr Thr Pro Tyr Pro Asp
 65 70 75 80
 Ser Val Cys Arg Ala Phe Val Lys Glu Ala Ala Ser Ser Gly Val Asp
 85 90 95
 Ile Phe Arg Ile Phe Asp Ala Leu Asn Asp Val Ser Gln Met Arg Pro
 100 105 110

Ala Ile Asp Ala Val Leu Glu Thr Asn Thr Ala Val Ala Glu Val Ala
 115 120 125

Met Ala Tyr Ser Gly Asp Leu Ser Asp Pro Asn Glu Lys Leu Tyr Thr
 130 135 140

Leu Asp Tyr Tyr Leu Lys Met Ala Glu Glu Ile Val Lys Ser Gly Ala
 145 150 155 160

His Ile Leu Ala Ile Lys Asp Met Ala Gly Leu Leu Arg Pro Ala Ala
 165 170 175

Val Thr Lys Leu Val Thr Ala Leu Arg Arg Glu Phe Asp Leu Pro Val
 180 185 190

His Val His Thr His Asp Thr Ala Gly Gly Gln Leu Ala Thr Tyr Phe
 195 200 205

Ala Ala Ala Gln Ala Gly Ala Asp Ala Val Asp Gly Ala Ser Gly Thr
 210 215 220

Thr Val Trp His His Leu Pro Ser His Pro Leu Ser Ala Ile Val Ala
 225 230 235 240

Ala Phe Ala His Thr Arg Arg Asp Thr Gly Leu Ser Leu Glu Ala Val
 245 250 255

Ser Asp Leu Glu Pro Tyr Trp Glu Ala Val Arg Gly Leu Tyr Leu Pro
 260 265 270

Phe Glu Ser Gly Thr Pro Gly Pro Thr Gly Arg Val Tyr Arg His Glu
 275 280 285

Ile Pro Gly Gly Gln Leu Ser Asn Leu Arg Ala Gln Ala Thr Ala Leu
 290 295 300

Gly Leu Ala Asp Arg Phe Glu Leu Ile Glu Asp Asn Tyr Ala Ser Arg
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<210> 119
 <211> 1719
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
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 <222> (101)..(1696)
 <223> RXN02328

<400> 119
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 gtttgattgg gggaaatcggg ggttacgata ctaggacgca gtg act gct atc acc 115
 Val Thr Ala Ile Thr 5
 1
 ctt ggc ggt ctc ttg ttg aaa gga ata att act cta gtg tcg act cac 163

Leu	Gly	Gly	Leu	Leu	Leu	Lys	Gly	Ile	Ile	Thr	Leu	Val	Ser	Thr	His	
				10					15					20		
aca	tct	tca	acg	ctt	cca	gca	ttc	aaa	aag	atc	ttg	gta	gca	aac	cgc	211
Thr	Ser	Ser	Thr	Leu	Pro	Ala	Phe	Lys	Lys	Ile	Leu	Val	Ala	Asn	Arg	
			25					30					35			
ggc	gaa	atc	gcg	gtc	cgt	gct	ttc	cgt	gca	gca	ctc	gaa	acc	ggg	gca	259
Gly	Glu	Ile	Ala	Val	Arg	Ala	Phe	Arg	Ala	Ala	Leu	Glu	Thr	Gly	Ala	
		40					45					50				
gcc	acg	gta	gct	att	tac	ccc	cgt	gaa	gat	cgg	gga	tca	ttc	cac	cgc	307
Ala	Thr	Val	Ala	Ile	Tyr	Pro	Arg	Glu	Asp	Arg	Gly	Ser	Phe	His	Arg	
	55					60					65					
tct	ttt	gct	tct	gaa	gct	gtc	cgc	att	ggg	acc	gaa	ggc	tca	cca	gtc	355
Ser	Phe	Ala	Ser	Glu	Ala	Val	Arg	Ile	Gly	Thr	Glu	Gly	Ser	Pro	Val	
70					75					80					85	
aag	gcg	tac	ctg	gac	atc	gat	gaa	att	atc	ggg	gca	gct	aaa	aaa	gtt	403
Lys	Ala	Tyr	Leu	Asp	Ile	Asp	Glu	Ile	Ile	Gly	Ala	Ala	Lys	Lys	Val	
				90				95						100		
aaa	gca	gat	gcc	att	tac	ccg	gga	tac	ggc	ttc	ctg	tct	gaa	aat	gcc	451
Lys	Ala	Asp	Ala	Ile	Tyr	Pro	Gly	Tyr	Gly	Phe	Leu	Ser	Glu	Asn	Ala	
			105					110						115		
cag	ctt	gcc	cgc	gag	tgt	gcg	gaa	aac	ggc	att	act	ttt	att	ggc	cca	499
Gln	Leu	Ala	Arg	Glu	Cys	Ala	Glu	Asn	Gly	Ile	Thr	Phe	Ile	Gly	Pro	
		120					125					130				
acc	cca	gag	gtt	ctt	gat	ctc	acc	ggg	gat	aag	tct	cgc	gcg	gta	acc	547
Thr	Pro	Glu	Val	Leu	Asp	Leu	Thr	Gly	Asp	Lys	Ser	Arg	Ala	Val	Thr	
	135					140					145					
gcc	gcg	aag	aag	gct	ggg	ctg	cca	gtt	ttg	gcg	gaa	tcc	acc	ccg	agc	595
Ala	Ala	Lys	Lys	Ala	Gly	Leu	Pro	Val	Leu	Ala	Glu	Ser	Thr	Pro	Ser	
150				155					160						165	
aaa	aac	atc	gat	gag	atc	gtt	aaa	agc	gct	gaa	ggc	cag	act	tac	ccc	643
Lys	Asn	Ile	Asp	Glu	Ile	Val	Lys	Ser	Ala	Glu	Gly	Gln	Thr	Tyr	Pro	
				170				175						180		
atc	ttt	gtg	aag	gca	gtt	gcc	ggg	ggg	ggc	gga	cgc	ggg	atg	cgt	ttt	691
Ile	Phe	Val	Lys	Ala	Val	Ala	Gly	Gly	Gly	Gly	Arg	Gly	Met	Arg	Phe	
		185					190						195			
gtt	gct	tca	cct	gat	gag	ctt	cgc	aaa	tta	gca	aca	gaa	gca	tct	cgt	739
Val	Ala	Ser	Pro	Asp	Glu	Leu	Arg	Lys	Leu	Ala	Thr	Glu	Ala	Ser	Arg	
		200					205					210				
gaa	gct	gaa	gcg	gct	ttc	ggc	gat	ggc	gcg	gta	tat	gtc	gaa	cgt	gct	787
Glu	Ala	Glu	Ala	Ala	Phe	Gly	Asp	Gly	Ala	Val	Tyr	Val	Glu	Arg	Ala	
	215					220					225					
gtg	att	aac	cct	cag	cat	att	gaa	gtg	cag	atc	ctt	ggc	gat	cac	act	835
Val	Ile	Asn	Pro	Gln	His	Ile	Glu	Val	Gln	Ile	Leu	Gly	Asp	His	Thr	
230				235					240						245	
gga	gaa	gtt	gta	cac	ctt	tat	gaa	cgt	gac	tgc	tca	ctg	cag	cgt	cgt	883
Gly	Glu	Val	Val	His	Leu	Tyr	Glu	Arg	Asp	Cys	Ser	Leu	Gln	Arg	Arg	

250								255				260				
cac	caa	aaa	gtt	gtc	gaa	att	gcg	cca	gca	cag	cat	ttg	gat	cca	gaa	931
His	Gln	Lys	Val	Val	Glu	Ile	Ala	Pro	Ala	Gln	His	Leu	Asp	Pro	Glu	
			265					270					275			
ctg	cgt	gat	cgc	att	tgt	gcg	gat	gca	gta	aag	ttc	tgc	cgc	tcc	att	979
Leu	Arg	Asp	Arg	Ile	Cys	Ala	Asp	Ala	Val	Lys	Phe	Cys	Arg	Ser	Ile	
		280					285					290				
ggt	tac	cag	ggc	gcg	gga	acc	gtg	gaa	ttc	ttg	gtc	gat	gaa	aag	ggc	1027
Gly	Tyr	Gln	Gly	Ala	Gly	Thr	Val	Glu	Phe	Leu	Val	Asp	Glu	Lys	Gly	
	295					300					305					
aac	cac	gtc	ttc	atc	gaa	atg	aac	cca	cgt	atc	cag	gtt	gag	cac	acc	1075
Asn	His	Val	Phe	Ile	Glu	Met	Asn	Pro	Arg	Ile	Gln	Val	Glu	His	Thr	
310					315					320					325	
gtg	act	gaa	gaa	gtc	acc	gag	gtg	gac	ctg	gtg	aag	gcg	cag	atg	cgc	1123
Val	Thr	Glu	Glu	Val	Thr	Glu	Val	Asp	Leu	Val	Lys	Ala	Gln	Met	Arg	
				330				335						340		
ttg	gct	gct	ggt	gca	acc	ttg	aag	gaa	ttg	ggt	ctg	acc	caa	gat	aag	1171
Leu	Ala	Ala	Gly	Ala	Thr	Leu	Lys	Glu	Leu	Gly	Leu	Thr	Gln	Asp	Lys	
			345					350					355			
atc	aag	acc	cac	ggt	gca	gca	ctg	cag	tgc	cgc	atc	acc	acg	gaa	gat	1219
Ile	Lys	Thr	His	Gly	Ala	Ala	Leu	Gln	Cys	Arg	Ile	Thr	Thr	Glu	Asp	
		360					365					370				
cca	aac	aac	ggc	ttc	cgc	cca	gat	acc	gga	act	atc	acc	gcg	tac	cgc	1267
Pro	Asn	Asn	Gly	Phe	Arg	Pro	Asp	Thr	Gly	Thr	Ile	Thr	Ala	Tyr	Arg	
	375					380					385					
tca	cca	ggc	gga	gct	ggc	gtt	cgt	ctt	gac	ggt	gca	gct	cag	ctc	ggt	1315
Ser	Pro	Gly	Gly	Ala	Gly	Val	Arg	Leu	Asp	Gly	Ala	Ala	Gln	Leu	Gly	
390					395					400					405	
ggc	gaa	atc	acc	gca	cac	ttt	gac	tcc	atg	ctg	gtg	aaa	atg	acc	tgc	1363
Gly	Glu	Ile	Thr	Ala	His	Phe	Asp	Ser	Met	Leu	Val	Lys	Met	Thr	Cys	
			410					415					420			
cgt	ggt	tcc	gac	ttt	gaa	act	gct	gtt	gct	cgt	gca	cag	cgc	gcg	ttg	1411
Arg	Gly	Ser	Asp	Phe	Glu	Thr	Ala	Val	Ala	Arg	Ala	Gln	Arg	Ala	Leu	
			425					430					435			
gct	gag	ttc	acc	gtg	tct	ggt	gtt	gca	acc	aac	att	ggt	ttc	ttg	cgt	1459
Ala	Glu	Phe	Thr	Val	Ser	Gly	Val	Ala	Thr	Asn	Ile	Gly	Phe	Leu	Arg	
			440				445					450				
gcg	ttg	ctg	cgg	gaa	gag	gac	ttc	act	tcc	aag	cgc	atc	gcc	acc	gga	1507
Ala	Leu	Leu	Arg	Glu	Glu	Asp	Phe	Thr	Ser	Lys	Arg	Ile	Ala	Thr	Gly	
	455					460					465					
ttc	att	gcc	gat	cac	ccg	cac	ctc	ctt	cag	gct	cca	cct	gct	gat	gat	1555
Phe	Ile	Ala	Asp	His	Pro	His	Leu	Leu	Gln	Ala	Pro	Pro	Ala	Asp	Asp	
470					475					480					485	
gag	cag	gga	cgc	atc	ctg	gat	tac	ttg	gca	gat	gtc	acc	gtg	aac	aag	1603
Glu	Gln	Gly	Arg	Ile	Leu	Asp	Tyr	Leu	Ala	Asp	Val	Thr	Val	Asn	Lys	
				490					495					500		

cct cat ggt gtg cgt cca aag gat gtt gca gct cct atc gat aag ctg 1651
 Pro His Gly Val Arg Pro Lys Asp Val Ala Ala Pro Ile Asp Lys Leu
 505 510 515

cct aac atc aag gat ctg cca ctg cca cgc ggt tcc cgt gac cgc 1696
 Pro Asn Ile Lys Asp Leu Pro Leu Pro Arg Gly Ser Arg Asp Arg
 520 525 530

tgaagcagct tggcccagcc gcg 1719

<210> 120

<211> 532

<212> PRT

<213> Corynebacterium glutamicum

<400> 120

Val Thr Ala Ile Thr Leu Gly Gly Leu Leu Leu Lys Gly Ile Ile Thr
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Leu Val Ser Thr His Thr Ser Ser Thr Leu Pro Ala Phe Lys Lys Ile
 20 25 30

Leu Val Ala Asn Arg Gly Glu Ile Ala Val Arg Ala Phe Arg Ala Ala
 35 40 45

Leu Glu Thr Gly Ala Ala Thr Val Ala Ile Tyr Pro Arg Glu Asp Arg
 50 55 60

Gly Ser Phe His Arg Ser Phe Ala Ser Glu Ala Val Arg Ile Gly Thr
 65 70 75 80

Glu Gly Ser Pro Val Lys Ala Tyr Leu Asp Ile Asp Glu Ile Ile Gly
 85 90 95

Ala Ala Lys Lys Val Lys Ala Asp Ala Ile Tyr Pro Gly Tyr Gly Phe
 100 105 110

Leu Ser Glu Asn Ala Gln Leu Ala Arg Glu Cys Ala Glu Asn Gly Ile
 115 120 125

Thr Phe Ile Gly Pro Thr Pro Glu Val Leu Asp Leu Thr Gly Asp Lys
 130 135 140

Ser Arg Ala Val Thr Ala Ala Lys Lys Ala Gly Leu Pro Val Leu Ala
 145 150 155 160

Glu Ser Thr Pro Ser Lys Asn Ile Asp Glu Ile Val Lys Ser Ala Glu
 165 170 175

Gly Gln Thr Tyr Pro Ile Phe Val Lys Ala Val Ala Gly Gly Gly Gly
 180 185 190

Arg Gly Met Arg Phe Val Ala Ser Pro Asp Glu Leu Arg Lys Leu Ala
 195 200 205

Thr Glu Ala Ser Arg Glu Ala Glu Ala Ala Phe Gly Asp Gly Ala Val
 210 215 220

Tyr Val Glu Arg Ala Val Ile Asn Pro Gln His Ile Glu Val Gln Ile

225		230		235		240
Leu Gly Asp His Thr Gly Glu Val Val His Leu Tyr Glu Arg Asp Cys						
		245		250		255
Ser Leu Gln Arg Arg His Gln Lys Val Val Glu Ile Ala Pro Ala Gln						
		260		265		270
His Leu Asp Pro Glu Leu Arg Asp Arg Ile Cys Ala Asp Ala Val Lys						
		275		280		285
Phe Cys Arg Ser Ile Gly Tyr Gln Gly Ala Gly Thr Val Glu Phe Leu						
		290		295		300
Val Asp Glu Lys Gly Asn His Val Phe Ile Glu Met Asn Pro Arg Ile						
		305		310		315
Gln Val Glu His Thr Val Thr Glu Glu Val Thr Glu Val Asp Leu Val						
		325		330		335
Lys Ala Gln Met Arg Leu Ala Ala Gly Ala Thr Leu Lys Glu Leu Gly						
		340		345		350
Leu Thr Gln Asp Lys Ile Lys Thr His Gly Ala Ala Leu Gln Cys Arg						
		355		360		365
Ile Thr Thr Glu Asp Pro Asn Asn Gly Phe Arg Pro Asp Thr Gly Thr						
		370		375		380
Ile Thr Ala Tyr Arg Ser Pro Gly Gly Ala Gly Val Arg Leu Asp Gly						
		385		390		395
Ala Ala Gln Leu Gly Gly Glu Ile Thr Ala His Phe Asp Ser Met Leu						
		405		410		415
Val Lys Met Thr Cys Arg Gly Ser Asp Phe Glu Thr Ala Val Ala Arg						
		420		425		430
Ala Gln Arg Ala Leu Ala Glu Phe Thr Val Ser Gly Val Ala Thr Asn						
		435		440		445
Ile Gly Phe Leu Arg Ala Leu Leu Arg Glu Glu Asp Phe Thr Ser Lys						
		450		455		460
Arg Ile Ala Thr Gly Phe Ile Ala Asp His Pro His Leu Leu Gln Ala						
		465		470		475
Pro Pro Ala Asp Asp Glu Gln Gly Arg Ile Leu Asp Tyr Leu Ala Asp						
		485		490		495
Val Thr Val Asn Lys Pro His Gly Val Arg Pro Lys Asp Val Ala Ala						
		500		505		510
Pro Ile Asp Lys Leu Pro Asn Ile Lys Asp Leu Pro Leu Pro Arg Gly						
		515		520		525
Ser Arg Asp Arg						
		530				

<210> 121

<211> 1406

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (1)..(1383)

<223> FRXA02328

<400> 121

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Ala Ser Glu Ala Val Arg Ile Gly Thr Glu Gly Ser Pro Val Lys Ala	
1 5 10 15	
tac ctg gac atc gat gaa att atc ggt gca gct aaa aaa gtt aaa gca	96
Tyr Leu Asp Ile Asp Glu Ile Ile Gly Ala Ala Lys Lys Val Lys Ala	
20 25 30	
gat gcc att tac ccg gga tac ggc ttc ctg tct gaa aat gcc cag ctt	144
Asp Ala Ile Tyr Pro Gly Tyr Gly Phe Leu Ser Glu Asn Ala Gln Leu	
35 40 45	
gcc cgc gag tgt gcg gaa aac ggc att act ttt att ggc cca acc cca	192
Ala Arg Glu Cys Ala Glu Asn Gly Ile Thr Phe Ile Gly Pro Thr Pro	
50 55 60	
gag gtt ctt gat ctc acc ggt gat aag tct cgc gcg gta acc gcc gcg	240
Glu Val Leu Asp Leu Thr Gly Asp Lys Ser Arg Ala Val Thr Ala Ala	
65 70 75 80	
aag aag gct ggt ctg cca gtt ttg gcg gaa tcc acc ccg agc aaa aac	288
Lys Lys Ala Gly Leu Pro Val Leu Ala Glu Ser Thr Pro Ser Lys Asn	
85 90 95	
atc gat gag atc gtt aaa agc gct gaa ggc cag act tac ccc atc ttt	336
Ile Asp Glu Ile Val Lys Ser Ala Glu Gly Gln Thr Tyr Pro Ile Phe	
100 105 110	
gtg aag gca gtt gcc ggt ggt ggc gga cgc ggt atg cgt ttt gtt gct	384
Val Lys Ala Val Ala Gly Gly Gly Gly Arg Gly Met Arg Phe Val Ala	
115 120 125	
tca cct gat gag ctt cgc aaa tta gca aca gaa gca tct cgt gaa gct	432
Ser Pro Asp Glu Leu Arg Lys Leu Ala Thr Glu Ala Ser Arg Glu Ala	
130 135 140	
gaa gcg gct ttc ggc gat ggc gcg gta tat gtc gaa cgt gct gtg att	480
Glu Ala Ala Phe Gly Asp Gly Ala Val Tyr Val Glu Arg Ala Val Ile	
145 150 155 160	
aac cct cag cat att gaa gtg cag atc ctt ggc gat cac act gga gaa	528
Asn Pro Gln His Ile Glu Val Gln Ile Leu Gly Asp His Thr Gly Glu	
165 170 175	
gtt gta cac ctt tat gaa cgt gac tgc tca ctg cag cgt cgt cac caa	576
Val Val His Leu Tyr Glu Arg Asp Cys Ser Leu Gln Arg Arg His Gln	
180 185 190	
aaa gtt gtc gaa att gcg cca gca cag cat ttg gat cca gaa ctg cgt	624
Lys Val Val Glu Ile Ala Pro Ala Gln His Leu Asp Pro Glu Leu Arg	
195 200 205	

gat cgc att tgt gcg gat gca gta aag ttc tgc cgc tcc att ggt tac	672
Asp Arg Ile Cys Ala Asp Ala Val Lys Phe Cys Arg Ser Ile Gly Tyr	
210 215 220	
cag ggc gcg gga acc gtg gaa ttc ttg gtc gat gaa aag ggc aac cac	720
Gln Gly Ala Gly Thr Val Glu Phe Leu Val Asp Glu Lys Gly Asn His	
225 230 235 240	
gtc ttc atc gaa atg aac cca cgt atc cag gtt gag cac acc gtg act	768
Val Phe Ile Glu Met Asn Pro Arg Ile Gln Val Glu His Thr Val Thr	
245 250 255	
gaa gaa gtc acc gag gtg gac ctg gtg aag gcg cag atg cgc ttg gct	816
Glu Glu Val Thr Glu Val Asp Leu Val Lys Ala Gln Met Arg Leu Ala	
260 265 270	
gct ggt gca acc ttg aag gaa ttg ggt ctg acc caa gat aag atc aag	864
Ala Gly Ala Thr Leu Lys Glu Leu Gly Leu Thr Gln Asp Lys Ile Lys	
275 280 285	
acc cac ggt gca gca ctg cag tgc cgc atc acc acg gaa gat cca aac	912
Thr His Gly Ala Ala Leu Gln Cys Arg Ile Thr Thr Glu Asp Pro Asn	
290 295 300	
aac ggc ttc cgc cca gat acc gga act atc acc gcg tac cgc tca cca	960
Asn Gly Phe Arg Pro Asp Thr Gly Thr Ile Thr Ala Tyr Arg Ser Pro	
305 310 315 320	
ggc gga gct ggc gtt cgt ctt gac ggt gca gct cag ctc ggt ggc gaa	1008
Gly Gly Ala Gly Val Arg Leu Asp Gly Ala Ala Gln Leu Gly Gly Glu	
325 330 335	
atc acc gca cac ttt gac tcc atg ctg gtg aaa atg acc tgc cgt ggt	1056
Ile Thr Ala His Phe Asp Ser Met Leu Val Lys Met Thr Cys Arg Gly	
340 345 350	
tcc gac ttt gaa act gct gtt gct cgt gca cag cgc gcg ttg gct gag	1104
Ser Asp Phe Glu Thr Ala Val Ala Arg Ala Gln Arg Ala Leu Ala Glu	
355 360 365	
ttc acc gtg tct ggt gtt gca acc aac att ggt ttc ttg cgt gcg ttg	1152
Phe Thr Val Ser Gly Val Ala Thr Asn Ile Gly Phe Leu Arg Ala Leu	
370 375 380	
ctg cgg gaa gag gac ttc act tcc aag cgc atc gcc acc gga ttc att	1200
Leu Arg Glu Glu Asp Phe Thr Ser Lys Arg Ile Ala Thr Gly Phe Ile	
385 390 395 400	
gcc gat cac ccg cac ctc ctt cag gct cca cct gct gat gat gag cag	1248
Ala Asp His Pro His Leu Leu Gln Ala Pro Pro Ala Asp Asp Glu Gln	
405 410 415	
gga cgc atc ctg gat tac ttg gca gat gtc acc gtg aac aag cct cat	1296
Gly Arg Ile Leu Asp Tyr Leu Ala Asp Val Thr Val Asn Lys Pro His	
420 425 430	
ggt gtg cgt cca aag gat gtt gca gct cct atc gat aag ctg cct aac	1344
Gly Val Arg Pro Lys Asp Val Ala Ala Pro Ile Asp Lys Leu Pro Asn	
435 440 445	

atc aag gat ctg cca ctg cca cgc ggt tcc cgt gac cgc tgaagcagct 1393
 Ile Lys Asp Leu Pro Leu Pro Arg Gly Ser Arg Asp Arg
 450 455 460

tggcccagcc gcg 1406

<210> 122

<211> 461

<212> PRT

<213> Corynebacterium glutamicum

<400> 122

Ala Ser Glu Ala Val Arg Ile Gly Thr Glu Gly Ser Pro Val Lys Ala
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Tyr Leu Asp Ile Asp Glu Ile Ile Gly Ala Ala Lys Lys Val Lys Ala
 20 25 30

Asp Ala Ile Tyr Pro Gly Tyr Gly Phe Leu Ser Glu Asn Ala Gln Leu
 35 40 45

Ala Arg Glu Cys Ala Glu Asn Gly Ile Thr Phe Ile Gly Pro Thr Pro
 50 55 60

Glu Val Leu Asp Leu Thr Gly Asp Lys Ser Arg Ala Val Thr Ala Ala
 65 70 75 80

Lys Lys Ala Gly Leu Pro Val Leu Ala Glu Ser Thr Pro Ser Lys Asn
 85 90 95

Ile Asp Glu Ile Val Lys Ser Ala Glu Gly Gln Thr Tyr Pro Ile Phe
 100 105 110

Val Lys Ala Val Ala Gly Gly Gly Gly Arg Gly Met Arg Phe Val Ala
 115 120 125

Ser Pro Asp Glu Leu Arg Lys Leu Ala Thr Glu Ala Ser Arg Glu Ala
 130 135 140

Glu Ala Ala Phe Gly Asp Gly Ala Val Tyr Val Glu Arg Ala Val Ile
 145 150 155 160

Asn Pro Gln His Ile Glu Val Gln Ile Leu Gly Asp His Thr Gly Glu
 165 170 175

Val Val His Leu Tyr Glu Arg Asp Cys Ser Leu Gln Arg Arg His Gln
 180 185 190

Lys Val Val Glu Ile Ala Pro Ala Gln His Leu Asp Pro Glu Leu Arg
 195 200 205

Asp Arg Ile Cys Ala Asp Ala Val Lys Phe Cys Arg Ser Ile Gly Tyr
 210 215 220

Gln Gly Ala Gly Thr Val Glu Phe Leu Val Asp Glu Lys Gly Asn His
 225 230 235 240

Val Phe Ile Glu Met Asn Pro Arg Ile Gln Val Glu His Thr Val Thr
 245 250 255

Glu Glu Val Thr Glu Val Asp Leu Val Lys Ala Gln Met Arg Leu Ala
 260 265 270
 Ala Gly Ala Thr Leu Lys Glu Leu Gly Leu Thr Gln Asp Lys Ile Lys
 275 280 285
 Thr His Gly Ala Ala Leu Gln Cys Arg Ile Thr Thr Glu Asp Pro Asn
 290 295 300
 Asn Gly Phe Arg Pro Asp Thr Gly Thr Ile Thr Ala Tyr Arg Ser Pro
 305 310 315 320
 Gly Gly Ala Gly Val Arg Leu Asp Gly Ala Ala Gln Leu Gly Gly Glu
 325 330 335
 Ile Thr Ala His Phe Asp Ser Met Leu Val Lys Met Thr Cys Arg Gly
 340 345 350
 Ser Asp Phe Glu Thr Ala Val Ala Arg Ala Gln Arg Ala Leu Ala Glu
 355 360 365
 Phe Thr Val Ser Gly Val Ala Thr Asn Ile Gly Phe Leu Arg Ala Leu
 370 375 380
 Leu Arg Glu Glu Asp Phe Thr Ser Lys Arg Ile Ala Thr Gly Phe Ile
 385 390 395 400
 Ala Asp His Pro His Leu Leu Gln Ala Pro Pro Ala Asp Asp Glu Gln
 405 410 415
 Gly Arg Ile Leu Asp Tyr Leu Ala Asp Val Thr Val Asn Lys Pro His
 420 425 430
 Gly Val Arg Pro Lys Asp Val Ala Ala Pro Ile Asp Lys Leu Pro Asn
 435 440 445
 Ile Lys Asp Leu Pro Leu Pro Arg Gly Ser Arg Asp Arg
 450 455 460

<210> 123

<211> 1347

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(1324)

<223> RXN01048

<400> 123

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gagcttcccg caaaaacacc gattaacaag gctaaatgat atg acc atc gac ctg 115
 Met Thr Ile Asp Leu
 1 5

cag cgt tcc acc caa aac ctc acc cat gag gaa atc ttc gag gca cac 163
 Gln Arg Ser Thr Gln Asn Leu Thr His Glu Glu Ile Phe Glu Ala His
 10 15 20

gag ggc gga aag ctc tcc att agt tcc act cgt ccg ctc cgc gac atg	211
Glu Gly Gly Lys Leu Ser Ile Ser Ser Thr Arg Pro Leu Arg Asp Met	
25 30 35	
cgc gat ctt tcc ctt gct tac acc cct ggt gtt gct cag gtt tgt gaa	259
Arg Asp Leu Ser Leu Ala Tyr Thr Pro Gly Val Ala Gln Val Cys Glu	
40 45 50	
gca atc aag gaa gat cca gag gtt gcg cgc acc cac acg ggc att gga	307
Ala Ile Lys Glu Asp Pro Glu Val Ala Arg Thr His Thr Gly Ile Gly	
55 60 65	
aac acc gtc gcg gtt att tcc gac ggc acc gct gtt ctt ggc ctt ggc	355
Asn Thr Val Ala Val Ile Ser Asp Gly Thr Ala Val Leu Gly Leu Gly	
70 75 80 85	
gat atc gga cct cag gcc tcc ctt ccc gtc atg gag ggc aag gct cag	403
Asp Ile Gly Pro Gln Ala Ser Leu Pro Val Met Glu Gly Lys Ala Gln	
90 95 100	
ctg ttt agc tct ttc gct ggc ctg aag gct atc cct atc gtt ttg gac	451
Leu Phe Ser Ser Phe Ala Gly Leu Lys Ala Ile Pro Ile Val Leu Asp	
105 110 115	
gtt cac gat gtt gac gct ttg gtt gag acc atc gca gcc atc gcg cct	499
Val His Asp Val Asp Ala Leu Val Glu Thr Ile Ala Ala Ile Ala Pro	
120 125 130	
tct ttc ggt gct atc aac ttg gag gac atc tcc gct cct cgt tgc ttc	547
Ser Phe Gly Ala Ile Asn Leu Glu Asp Ile Ser Ala Pro Arg Cys Phe	
135 140 145	
gag gtg gag cgc cgc ctc atc gag cgt ctc gat att cca gtt atg cac	595
Glu Val Glu Arg Arg Leu Ile Glu Arg Leu Asp Ile Pro Val Met His	
150 155 160 165	
gat gac cag cac ggc acc gct gtg gtt atc ctc gct gcg ctg cgc aac	643
Asp Asp Gln His Gly Thr Ala Val Val Ile Leu Ala Ala Leu Arg Asn	
170 175 180	
tcc ctg aag ctg ctg gat cgc aag atc gaa gac ctc aag att gtt att	691
Ser Leu Lys Leu Leu Asp Arg Lys Ile Glu Asp Leu Lys Ile Val Ile	
185 190 195	
tcc ggc gca ggc gca gcg ggc gtt gca gct gta gat atg ctg acc aac	739
Ser Gly Ala Gly Ala Ala Gly Val Ala Ala Val Asp Met Leu Thr Asn	
200 205 210	
gct gga gca acc gac atc gtg gtt ctt gat tcc cga ggc atc atc cac	787
Ala Gly Ala Thr Asp Ile Val Val Leu Asp Ser Arg Gly Ile Ile His	
215 220 225	
gac agc cgt gag gat ctt tcc cca gtt aag gct gct ctt gca gag aag	835
Asp Ser Arg Glu Asp Leu Ser Pro Val Lys Ala Ala Leu Ala Glu Lys	
230 235 240 245	
acc aac cct cgt ggc atc agc ggt ggc atc aat gag gct ttc acc ggc	883
Thr Asn Pro Arg Gly Ile Ser Gly Gly Ile Asn Glu Ala Phe Thr Gly	
250 255 260	
gcg gac ctg ttc att ggc gtg tcc ggc ggc aac atc ggc gag gac gct	931

Ala Asp Leu Phe Ile Gly Val Ser Gly Gly Asn Ile Gly Glu Asp Ala
 265 270 275

ctc aaa ctc atg gcc ccg gag cca atc ctg ttc acc ctg gcg aac cca 979
 Leu Lys Leu Met Ala Pro Glu Pro Ile Leu Phe Thr Leu Ala Asn Pro
 280 285 290

acc cca gag atc gat cct gag ctg tct cag aag tac ggc gcc atc gtc 1027
 Thr Pro Glu Ile Asp Pro Glu Leu Ser Gln Lys Tyr Gly Ala Ile Val
 295 300 305

gcg acc ggg cgc tct gac ctg cct aac cag atc aac aac gtg ctg gcg 1075
 Ala Thr Gly Arg Ser Asp Leu Pro Asn Gln Ile Asn Asn Val Leu Ala
 310 315 320 325

ttc cca gga att ttc gcc ggc gct ctc gca gcc aag gct aag aag atc 1123
 Phe Pro Gly Ile Phe Ala Gly Ala Leu Ala Ala Lys Ala Lys Lys Ile
 330 335 340

acc ccc gag atg aag ctc gcc gct cag agg caa tcg cag aca tcg cag 1171
 Thr Pro Glu Met Lys Leu Ala Ala Gln Arg Gln Ser Gln Thr Ser Gln
 345 350 355

ctg agg acc tcg agg tcg gcc gca tcg tgc cta ccg ccc tgg atc ccc 1219
 Leu Arg Thr Ser Arg Ser Ala Ala Ser Cys Leu Pro Pro Trp Ile Pro
 360 365 370

gcg ttg ccc caa cag tca agg cag ctg tcc agg ccg tcg cca aag cgc 1267
 Ala Leu Pro Gln Gln Ser Arg Gln Leu Ser Arg Pro Ser Pro Lys Arg
 375 380 385

aaa acg ctt aaa aat ttg ctt atc gac gcc tcc ctc ccc gtc gag gcg 1315
 Lys Thr Leu Lys Asn Leu Leu Ile Asp Ala Ser Leu Pro Val Glu Ala
 390 395 400 405

cca ata ttt taagagcaaa cttgaggccc aca 1347
 Pro Ile Phe

<210> 124

<211> 408

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 124

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Ile Phe Glu Ala His Glu Gly Gly Lys Leu Ser Ile Ser Ser Thr Arg
 20 25 30

Pro Leu Arg Asp Met Arg Asp Leu Ser Leu Ala Tyr Thr Pro Gly Val
 35 40 45

Ala Gln Val Cys Glu Ala Ile Lys Glu Asp Pro Glu Val Ala Arg Thr
 50 55 60

His Thr Gly Ile Gly Asn Thr Val Ala Val Ile Ser Asp Gly Thr Ala
 65 70 75 80

Val Leu Gly Leu Gly Asp Ile Gly Pro Gln Ala Ser Leu Pro Val Met
 85 90 95
 Glu Gly Lys Ala Gln Leu Phe Ser Ser Phe Ala Gly Leu Lys Ala Ile
 100 105 110
 Pro Ile Val Leu Asp Val His Asp Val Asp Ala Leu Val Glu Thr Ile
 115 120 125
 Ala Ala Ile Ala Pro Ser Phe Gly Ala Ile Asn Leu Glu Asp Ile Ser
 130 135 140
 Ala Pro Arg Cys Phe Glu Val Glu Arg Arg Leu Ile Glu Arg Leu Asp
 145 150 155 160
 Ile Pro Val Met His Asp Asp Gln His Gly Thr Ala Val Val Ile Leu
 165 170 175
 Ala Ala Leu Arg Asn Ser Leu Lys Leu Leu Asp Arg Lys Ile Glu Asp
 180 185 190
 Leu Lys Ile Val Ile Ser Gly Ala Gly Ala Ala Gly Val Ala Ala Val
 195 200 205
 Asp Met Leu Thr Asn Ala Gly Ala Thr Asp Ile Val Val Leu Asp Ser
 210 215 220
 Arg Gly Ile Ile His Asp Ser Arg Glu Asp Leu Ser Pro Val Lys Ala
 225 230 235 240
 Ala Leu Ala Glu Lys Thr Asn Pro Arg Gly Ile Ser Gly Gly Ile Asn
 245 250 255
 Glu Ala Phe Thr Gly Ala Asp Leu Phe Ile Gly Val Ser Gly Gly Asn
 260 265 270
 Ile Gly Glu Asp Ala Leu Lys Leu Met Ala Pro Glu Pro Ile Leu Phe
 275 280 285
 Thr Leu Ala Asn Pro Thr Pro Glu Ile Asp Pro Glu Leu Ser Gln Lys
 290 295 300
 Tyr Gly Ala Ile Val Ala Thr Gly Arg Ser Asp Leu Pro Asn Gln Ile
 305 310 315 320
 Asn Asn Val Leu Ala Phe Pro Gly Ile Phe Ala Gly Ala Leu Ala Ala
 325 330 335
 Lys Ala Lys Lys Ile Thr Pro Glu Met Lys Leu Ala Ala Gln Arg Gln
 340 345 350
 Ser Gln Thr Ser Gln Leu Arg Thr Ser Arg Ser Ala Ala Ser Cys Leu
 355 360 365
 Pro Pro Trp Ile Pro Ala Leu Pro Gln Gln Ser Arg Gln Leu Ser Arg
 370 375 380
 Pro Ser Pro Lys Arg Lys Thr Leu Lys Asn Leu Leu Ile Asp Ala Ser
 385 390 395 400
 Leu Pro Val Glu Ala Pro Ile Phe

405

<210> 125
 <211> 311
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (1)..(288)
 <223> FRXA01048

<400> 125
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 Arg Ser Asp Leu Pro Asn Gln Ile Asn Asn Val Leu Ala Phe Pro Gly
 1 5 10 15
 att ttc gcc ggc gct ctc gca gcc aag gct aag aag atc acc ccc gag 96
 Ile Phe Ala Gly Ala Leu Ala Ala Lys Ala Lys Lys Ile Thr Pro Glu
 20 25 30
 atg aag ctc gcc gct cag agg caa tcg cag aca tcg cag ctg agg acc 144
 Met Lys Leu Ala Ala Gln Arg Gln Ser Gln Thr Ser Gln Leu Arg Thr
 35 40 45
 tcg agg tcg gcc gca tcg tgc cta ccg ccc tgg atc ccc gcg ttg ccc 192
 Ser Arg Ser Ala Ala Ser Cys Leu Pro Pro Trp Ile Pro Ala Leu Pro
 50 55 60
 caa cag tca agg cag ctg tcc agg ccg tcg cca aag cgc aaa acg ctt 240
 Gln Gln Ser Arg Gln Leu Ser Arg Pro Ser Pro Lys Arg Lys Thr Leu
 65 70 75 80
 aaa aat ttg ctt atc gac gcc tcc ctc ccc gtc gag gcg cca ata ttt 288
 Lys Asn Leu Leu Ile Asp Ala Ser Leu Pro Val Glu Ala Pro Ile Phe
 85 90 95
 taagagcaaa cttgaggccc aca 311

<210> 126
 <211> 96
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 126
 Arg Ser Asp Leu Pro Asn Gln Ile Asn Asn Val Leu Ala Phe Pro Gly
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 Ile Phe Ala Gly Ala Leu Ala Ala Lys Ala Lys Lys Ile Thr Pro Glu
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 Met Lys Leu Ala Ala Gln Arg Gln Ser Gln Thr Ser Gln Leu Arg Thr
 35 40 45
 Ser Arg Ser Ala Ala Ser Cys Leu Pro Pro Trp Ile Pro Ala Leu Pro
 50 55 60
 Gln Gln Ser Arg Gln Leu Ser Arg Pro Ser Pro Lys Arg Lys Thr Leu
 65 70 75 80

Lys Asn Leu Leu Ile Asp Ala Ser Leu Pro Val Glu Ala Pro Ile Phe
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<210> 127
<211> 1063
<212> DNA
<213> Corynebacterium glutamicum
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<222> (101)..(1063)  
<223> FRXA00290
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Met Thr Ile Asp Leu															
1 5															
cag cgt tcc acc caa aac ctc acc cat gag gaa atc ttc gag gca cac															163
Gln Arg Ser Thr Gln Asn Leu Thr His Glu Glu Ile Phe Glu Ala His															
10 15 20															
gag ggc gga aag ctc tcc att agt tcc act cgt ccg ctc cgc gac atg															211
Glu Gly Gly Lys Leu Ser Ile Ser Ser Thr Arg Pro Leu Arg Asp Met															
25 30 35															
cgc gat ctt tcc ctt gct tac acc cct ggt gtt gct cag gtt tgt gaa															259
Arg Asp Leu Ser Leu Ala Tyr Thr Pro Gly Val Ala Gln Val Cys Glu															
40 45 50															
gca atc aag gaa gat cca gag gtt gcg cgc acc cac acg ggc att gga															307
Ala Ile Lys Glu Asp Pro Glu Val Ala Arg Thr His Thr Gly Ile Gly															
55 60 65															
aac acc gtc gcg gtt att tcc gac ggc acc gct gtt ctt ggc ctt ggc															355
Asn Thr Val Ala Val Ile Ser Asp Gly Thr Ala Val Leu Gly Leu Gly															
70 75 80 85															
gat atc gga cct cag gcc tcc ctt ccc gtc atg gag ggc aag gct cag															403
Asp Ile Gly Pro Gln Ala Ser Leu Pro Val Met Glu Gly Lys Ala Gln															
90 95 100															
ctg ttt agc tct ttc gct ggc ctg aag gct atc cct atc gtt ttg gac															451
Leu Phe Ser Ser Phe Ala Gly Leu Lys Ala Ile Pro Ile Val Leu Asp															
105 110 115															
gtt cac gat gtt gac gct ttg gtt gag acc atc gca gcc atc gcg cct															499
Val His Asp Val Asp Ala Leu Val Glu Thr Ile Ala Ala Ile Ala Pro															
120 125 130															
tct ttc ggt gct atc aac ttg gag gac atc tcc gct cct cgt tgc ttc															547
Ser Phe Gly Ala Ile Asn Leu Glu Asp Ile Ser Ala Pro Arg Cys Phe															
135 140 145															

gag gtg gag cgc cgc ctc atc gag cgt ctc gat att cca gtt atg cac 595
 Glu Val Glu Arg Arg Leu Ile Glu Arg Leu Asp Ile Pro Val Met His
 150 155 160 165

 gat gac cag cac ggc acc gct gtg gtt atc ctc gct gcg ctg cgc aac 643
 Asp Asp Gln His Gly Thr Ala Val Val Ile Leu Ala Ala Leu Arg Asn
 170 175 180

 tcc ctg aag ctg ctg gat cgc aag atc gaa gac ctc aag att gtt att 691
 Ser Leu Lys Leu Leu Asp Arg Lys Ile Glu Asp Leu Lys Ile Val Ile
 185 190 195

 tcc ggc gca ggc gca gcg ggc gtt gca gct gta gat atg ctg acc aac 739
 Ser Gly Ala Gly Ala Ala Gly Val Ala Ala Val Asp Met Leu Thr Asn
 200 205 210

 gct gga gca acc gac atc gtg gtt ctt gat tcc cga ggc atc atc cac 787
 Ala Gly Ala Thr Asp Ile Val Val Leu Asp Ser Arg Gly Ile Ile His
 215 220 225

 gac agc cgt gag gat ctt tcc cca gtt aag gct gct ctt gca gag aag 835
 Asp Ser Arg Glu Asp Leu Ser Pro Val Lys Ala Ala Leu Ala Glu Lys
 230 235 240 245

 acc aac cct cgt ggc atc agc ggt ggc atc aat gag gct ttc acc ggc 883
 Thr Asn Pro Arg Gly Ile Ser Gly Gly Ile Asn Glu Ala Phe Thr Gly
 250 255 260

 gcg gac ctg ttc att ggc gtg tcc ggc ggc aac atc ggc gag gac gct 931
 Ala Asp Leu Phe Ile Gly Val Ser Gly Gly Asn Ile Gly Glu Asp Ala
 265 270 275

 ctc aaa ctc atg gcc ccg gag cca atc ctg ttc acc ctg gcg aac cca 979
 Leu Lys Leu Met Ala Pro Glu Pro Ile Leu Phe Thr Leu Ala Asn Pro
 280 285 290

 acc cca gag atc gat cct gag ctg tct cag aag tac ggc gcc atc gtc 1027
 Thr Pro Glu Ile Asp Pro Glu Leu Ser Gln Lys Tyr Gly Ala Ile Val
 295 300 305

 gcg acc ggg ccg gtc ttg acc tgc cta acc aga tca 1063
 Ala Thr Gly Pro Val Leu Thr Cys Leu Thr Arg Ser
 310 315 320

<210> 128

<211> 321

<212> PRT

<213> Corynebacterium glutamicum

<400> 128

Met Thr Ile Asp Leu Gln Arg Ser Thr Gln Asn Leu Thr His Glu Glu
 1 5 10 15

Ile Phe Glu Ala His Glu Gly Gly Lys Leu Ser Ile Ser Ser Thr Arg
 20 25 30

Pro Leu Arg Asp Met Arg Asp Leu Ser Leu Ala Tyr Thr Pro Gly Val
 35 40 45

Ala Gln Val Cys Glu Ala Ile Lys Glu Asp Pro Glu Val Ala Arg Thr

50	55	60
His Thr Gly Ile Gly Asn Thr Val Ala Val Ile Ser Asp Gly Thr Ala 65 70 75 80		
Val Leu Gly Leu Gly Asp Ile Gly Pro Gln Ala Ser Leu Pro Val Met 85 90 95		
Glu Gly Lys Ala Gln Leu Phe Ser Ser Phe Ala Gly Leu Lys Ala Ile 100 105 110		
Pro Ile Val Leu Asp Val His Asp Val Asp Ala Leu Val Glu Thr Ile 115 120 125		
Ala Ala Ile Ala Pro Ser Phe Gly Ala Ile Asn Leu Glu Asp Ile Ser 130 135 140		
Ala Pro Arg Cys Phe Glu Val Glu Arg Arg Leu Ile Glu Arg Leu Asp 145 150 155 160		
Ile Pro Val Met His Asp Asp Gln His Gly Thr Ala Val Val Ile Leu 165 170 175		
Ala Ala Leu Arg Asn Ser Leu Lys Leu Leu Asp Arg Lys Ile Glu Asp 180 185 190		
Leu Lys Ile Val Ile Ser Gly Ala Gly Ala Ala Gly Val Ala Ala Val 195 200 205		
Asp Met Leu Thr Asn Ala Gly Ala Thr Asp Ile Val Val Leu Asp Ser 210 215 220		
Arg Gly Ile Ile His Asp Ser Arg Glu Asp Leu Ser Pro Val Lys Ala 225 230 235 240		
Ala Leu Ala Glu Lys Thr Asn Pro Arg Gly Ile Ser Gly Gly Ile Asn 245 250 255		
Glu Ala Phe Thr Gly Ala Asp Leu Phe Ile Gly Val Ser Gly Gly Asn 260 265 270		
Ile Gly Glu Asp Ala Leu Lys Leu Met Ala Pro Glu Pro Ile Leu Phe 275 280 285		
Thr Leu Ala Asn Pro Thr Pro Glu Ile Asp Pro Glu Leu Ser Gln Lys 290 295 300		
Tyr Gly Ala Ile Val Ala Thr Gly Pro Val Leu Thr Cys Leu Thr Arg 305 310 315 320		
Ser		

<210> 129
 <211> 1065
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS

<222> (101)..(1042)

<223> RXA02694

<400> 129

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tgggttggtcc ggtaggggaa atcaggaagt gggatcgaaa atg aaa gaa acc gtc 115
                                         Met Lys Glu Thr Val
                                         1                               5

ggt aac aag att gtc ctc att ggc gca gga gat gtt gga gtt gca tac 163
Gly Asn Lys Ile Val Leu Ile Gly Ala Gly Asp Val Gly Val Ala Tyr
                        10                               15                               20

gca tac gca ctg atc aac cag ggc atg gca gat cac ctt gcg atc atc 211
Ala Tyr Ala Leu Ile Asn Gln Gly Met Ala Asp His Leu Ala Ile Ile
                        25                               30                               35

gac atc gat gaa aag aaa ctc gaa ggc aac gtc atg gac tta aac cat 259
Asp Ile Asp Glu Lys Lys Leu Glu Gly Asn Val Met Asp Leu Asn His
                        40                               45                               50

ggt gtt gtg tgg gcc gat tcc cgc acc cgc gtc acc aag ggc acc tac 307
Gly Val Val Trp Ala Asp Ser Arg Thr Arg Val Thr Lys Gly Thr Tyr
                        55                               60                               65

gct gac tgc gaa gac gca gcc atg gtt gtc att tgt gcc ggc gca gcc 355
Ala Asp Cys Glu Asp Ala Ala Met Val Val Ile Cys Ala Gly Ala Ala
                        70                               75                               80                               85

caa aag cca ggc gag acc cgc ctc cag ctg gtg gac aaa aac gtc aag 403
Gln Lys Pro Gly Glu Thr Arg Leu Gln Leu Val Asp Lys Asn Val Lys
                        90                               95                               100

att atg aaa tcc atc gtc ggc gat gtc atg gac agc gga ttc gac ggc 451
Ile Met Lys Ser Ile Val Gly Asp Val Met Asp Ser Gly Phe Asp Gly
                        105                               110                               115

atc ttc ctc gtg gcg tcc aac cca gtg gat atc ctg acc tac gca gtg 499
Ile Phe Leu Val Ala Ser Asn Pro Val Asp Ile Leu Thr Tyr Ala Val
                        120                               125                               130

tgg aaa ttc tcc ggc ttg gaa tgg aac cgc gtg atc ggc tcc gga act 547
Trp Lys Phe Ser Gly Leu Glu Trp Asn Arg Val Ile Gly Ser Gly Thr
                        135                               140                               145

gtc ctg gac tcc gct cga ttc cgc tac atg ctg ggc gaa ctc tac gaa 595
Val Leu Asp Ser Ala Arg Phe Arg Tyr Met Leu Gly Glu Leu Tyr Glu
                        150                               155                               160                               165

gtg gca cca agc tcc gtc cac gcc tac atc atc ggc gaa cac ggc gac 643
Val Ala Pro Ser Ser Val His Ala Tyr Ile Ile Gly Glu His Gly Asp
                        170                               175                               180

act gaa ctt cca gtc ctg tcc tcc gcg acc atc gca ggc gta tcg ctt 691
Thr Glu Leu Pro Val Leu Ser Ser Ala Thr Ile Ala Gly Val Ser Leu
                        185                               190                               195

agc cga atg ctg gac aaa gac cca gag ctt gag ggc cgt cta gag aaa 739
Ser Arg Met Leu Asp Lys Asp Pro Glu Leu Glu Gly Arg Leu Glu Lys
                        200                               205                               210

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att ttc gaa gac acc cgc gac gct gcc tat cac att atc gac gcc aag 787
 Ile Phe Glu Asp Thr Arg Asp Ala Ala Tyr His Ile Ile Asp Ala Lys
 215 220 225
 ggc tcc act tcc tac ggc atc ggc atg ggt ctt gct cgc atc acc cgc 835
 Gly Ser Thr Ser Tyr Gly Ile Gly Met Gly Leu Ala Arg Ile Thr Arg
 230 235 240 245
 gca atc cta cag aac caa gac gtt gca gtc cca gtc tct gca ctg ctc 883
 Ala Ile Leu Gln Asn Gln Asp Val Ala Val Pro Val Ser Ala Leu Leu
 250 255 260
 cac ggt gaa tac ggt gag gaa gac atc tac atc ggc acc cca gct gtg 931
 His Gly Glu Tyr Gly Glu Glu Asp Ile Tyr Ile Gly Thr Pro Ala Val
 265 270 275
 gtg aac cgc cga ggc atc cgc cgc gtt gtc gaa cta gaa atc acc gac 979
 Val Asn Arg Arg Gly Ile Arg Arg Val Val Glu Leu Glu Ile Thr Asp
 280 285 290
 cac gag atg gaa cgc ttc aag cat tcc gca aat acc ctg cgc gaa att 1027
 His Glu Met Glu Arg Phe Lys His Ser Ala Asn Thr Leu Arg Glu Ile
 295 300 305
 cag aag cag ttc ttc taaatctttg gcgcctagtt ggc 1065
 Gln Lys Gln Phe Phe
 310

<210> 130

<211> 314

<212> PRT

<213> Corynebacterium glutamicum

<400> 130

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 20 25 30
 His Leu Ala Ile Ile Asp Ile Asp Glu Lys Lys Leu Glu Gly Asn Val
 35 40 45
 Met Asp Leu Asn His Gly Val Val Trp Ala Asp Ser Arg Thr Arg Val
 50 55 60
 Thr Lys Gly Thr Tyr Ala Asp Cys Glu Asp Ala Ala Met Val Val Ile
 65 70 75 80
 Cys Ala Gly Ala Ala Gln Lys Pro Gly Glu Thr Arg Leu Gln Leu Val
 85 90 95
 Asp Lys Asn Val Lys Ile Met Lys Ser Ile Val Gly Asp Val Met Asp
 100 105 110
 Ser Gly Phe Asp Gly Ile Phe Leu Val Ala Ser Asn Pro Val Asp Ile
 115 120 125
 Leu Thr Tyr Ala Val Trp Lys Phe Ser Gly Leu Glu Trp Asn Arg Val

aag ctg cgc acg gat atg aca acc cgt gca gca tat tct tct gat gca 211
Lys Leu Arg Thr Asp Met Thr Thr Arg Ala Ala Tyr Ser Ser Asp Ala
25 30 35

gga att ttt aga cgc gtc cct gca gct gta gct gaa cca gaa aat gtg	259
Gly Ile Phe Arg Arg Val Pro Ala Ala Val Ala Glu Pro Glu Asn Val	
40 45 50	
gaa caa att cgt gat gcc att gct gtt gcg gtg gca cga ggg tgg tct	307
Glu Gln Ile Arg Asp Ala Ile Ala Val Ala Val Ala Arg Gly Trp Ser	
55 60 65	
gtt gtt ggg cgc ggt gga gga agc tcg gtt gct gga aat gcg atc ggt	355
Val Val Gly Arg Gly Gly Gly Ser Ser Val Ala Gly Asn Ala Ile Gly	
70 75 80 85	
gaa ggt ttg atc atc gat acg tca cgc tat ttc aac cgc att tta gat	403
Glu Gly Leu Ile Ile Asp Thr Ser Arg Tyr Phe Asn Arg Ile Leu Asp	
90 95 100	
att gat cca gtt gca caa act gca gtt gtg gaa ccc ggt gtg gtg tgt	451
Ile Asp Pro Val Ala Gln Thr Ala Val Val Glu Pro Gly Val Val Cys	
105 110 115	
gat gcc ttg cgc gat gca gcc gca gaa ttc gga tta act tac ggc ccg	499
Asp Ala Leu Arg Asp Ala Ala Ala Glu Phe Gly Leu Thr Tyr Gly Pro	
120 125 130	
gat cct tcc acg cat tcc cgg tgc acg atc ggt ggc atg gtt gcc aac	547
Asp Pro Ser Thr His Ser Arg Cys Thr Ile Gly Gly Met Val Ala Asn	
135 140 145	
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Asn Ala Cys Gly Ser His Ser Val Ala Phe Gly Thr Ala Ala Glu Asn	
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ctc gtg gat gtc acg ctc atg ctc agc gat ggc cga gaa gtc act gtg	643
Leu Val Asp Val Thr Leu Met Leu Ser Asp Gly Arg Glu Val Thr Val	
170 175 180	
aca aaa gat ggc tgc gat gat gct gag atc aat cag aag ctc acc gac	691
Thr Lys Asp Gly Cys Asp Asp Ala Glu Ile Asn Gln Lys Leu Thr Asp	
185 190 195	
tta gcg tcc aag aat cag gac ctt att agt aaa gaa ctg ggt cgt ttc	739
Leu Ala Ser Lys Asn Gln Asp Leu Ile Ser Lys Glu Leu Gly Arg Phe	
200 205 210	
cct cgc caa gtg tcg ggc tac ggt ttg cat tat ctt gcc cac gac atg	787
Pro Arg Gln Val Ser Gly Tyr Gly Leu His Tyr Leu Ala His Asp Met	
215 220 225	
gcc aaa gca atg gcg ggc acc gag gga acc att gga atc att act cgg	835
Ala Lys Ala Met Ala Gly Thr Glu Gly Thr Ile Gly Ile Ile Thr Arg	
230 235 240 245	
ttg acg gtg aag ttg gtt cca aca ccc aaa gtg aaa gcg ctt gct gtc	883
Leu Thr Val Lys Leu Val Pro Thr Pro Lys Val Lys Ala Leu Ala Val	
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Leu Ala Phe Asp Thr Val Phe Asp Ala Ala Arg Ala Ala Lys Leu	
265 270 275	
cga ctg cct ggg gta gca acc att gaa ggc atg ggc gga gat ctc ctc	979

Arg	Leu	Pro	Gly	Val	Ala	Thr	Ile	Glu	Gly	Met	Gly	Gly	Asp	Leu	Leu	
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	295					300				305						
cca	gga	aac	cgc	atc	ggc	att	gaa	gcc	ggc	gga	tgg	ttg	tac	tgc	gag	1075
Pro	Gly	Asn	Arg	Ile	Gly	Ile	Glu	Ala	Gly	Gly	Trp	Leu	Tyr	Cys	Glu	
310					315					320					325	
aca	gga	agt	gac	acc	ctg	cag	gcc	gcg	gta	caa	gcc	gcc	gag	gaa	gtc	1123
Thr	Gly	Ser	Asp	Thr	Leu	Gln	Ala	Ala	Val	Gln	Ala	Ala	Glu	Glu	Val	
				330					335						340	
gca	acc	gcc	gtt	gac	acc	att	gat	tac	gtg	gtc	gtg	tct	gag	cct	tct	1171
Ala	Thr	Ala	Val	Asp	Thr	Ile	Asp	Tyr	Val	Val	Val	Ser	Glu	Pro	Ser	
			345					350					355			
gaa	atg	cgg	gaa	ttg	tgg	cgc	atc	cgt	gaa	tcc	tcg	gcg	ggc	att	gtc	1219
Glu	Met	Arg	Glu	Leu	Trp	Arg	Ile	Arg	Glu	Ser	Ser	Ala	Gly	Ile	Val	
		360					365					370				
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Thr	Arg	Leu	Ala	Asp	Gly	Gly	Glu	Ala	Trp	Pro	Asn	Trp	Glu	Asp	Ser	
		375				380					385					
gcg	gtg	cct	cca	gag	aat	tta	gct	gat	tat	ctc	cgc	gat	ctt	tat	gcg	1315
Ala	Val	Pro	Pro	Glu	Asn	Leu	Ala	Asp	Tyr	Leu	Arg	Asp	Leu	Tyr	Ala	
390					395					400					405	
ctg	atg	gat	aag	ttc	gat	tac	cag	ggt	att	cca	ttt	gga	cac	ttt	gga	1363
Leu	Met	Asp	Lys	Phe	Asp	Tyr	Gln	Gly	Ile	Pro	Phe	Gly	His	Phe	Gly	
				410					415					420		
gaa	ggc	tgc	gtc	cac	gtt	cgc	atc	agt	ttt	gat	ttc	tct	acc	aag	gaa	1411
Glu	Gly	Cys	Val	His	Val	Arg	Ile	Ser	Phe	Asp	Phe	Ser	Thr	Lys	Glu	
			425					430					435			
ggc	ctg	aag	aaa	ttc	gag	gcg	ttc	atg	aat	gaa	gcc	tcc	acc	ttg	gtg	1459
Gly	Leu	Lys	Lys	Phe	Glu	Ala	Phe	Met	Asn	Glu	Ala	Ser	Thr	Leu	Val	
		440					445					450				
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Ala	Ser	Tyr	Gly	Gly	Ser	Leu	Ser	Gly	Glu	His	Gly	Asp	Gly	Arg	Ala	
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Arg	Ser	Ser	Phe	Leu	Asp	Arg	Met	Tyr	Ser	Ala	Glu	Met	Arg	Ala	Leu	
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Phe	Glu	Glu	Phe	Lys	Leu	Ile	Phe	Asp	Pro	Gln	Arg	Ile	Phe	Asn	Pro	
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Pro	Gly	Gln	Arg	Ala	Leu	Asp	Ile	Thr	Pro	Val	His	Lys	Phe	Ser	Lys	

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Asp	Lys	Gly	Ser	Met	Ile	Asn	Ala	Val	Asn	Arg	Cys	Val	Gly	Val	Ser	
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Ala	Cys	Arg	Ser	Glu	Ser	Asp	Ala	Met	Cys	Pro	Ser	Phe	Gln	Ile	Thr	
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Gly	Asp	Glu	Val	His	Ser	Thr	Arg	Gly	Arg	Ala	Arg	Leu	Leu	Ser	Glu	
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Met	Phe	Arg	Gly	Glu	Ser	Ile	Ala	Asp	Gly	Tyr	Arg	Ser	Glu	Glu	Val	
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Asn	Glu	Ala	Leu	Asp	Leu	Cys	Leu	Ser	Cys	Lys	Ala	Cys	Ala	Ser	Glu	
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tgt	cca	gtc	aac	gtc	gac	atg	tcc	acc	tac	aaa	gcc	gaa	ttc	ctg	gac	1987
Cys	Pro	Val	Asn	Val	Asp	Met	Ser	Thr	Tyr	Lys	Ala	Glu	Phe	Leu	Asp	
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Lys	His	Tyr	Ala	Gly	Arg	Leu	Arg	Pro	Met	Ala	His	Tyr	Val	Met	Gly	
630					635					640					645	
tgg	ctg	ccg	ctt	ctg	gga	cac	gtt	gcc	cat	aaa	ata	ccg	ctt	ctt	cct	2083
Trp	Leu	Pro	Leu	Leu	Gly	His	Val	Ala	His	Lys	Ile	Pro	Leu	Leu	Pro	
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Thr	Leu	Ile	Asp	Ala	Thr	Met	Gln	Ser	Ala	Leu	Thr	Ala	Pro	Val	Val	
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cgc	aag	gtc	ggc	ggg	ctc	gct	gat	cgc	ccg	ttg	att	tcc	ttc	gcc	cac	2179
Arg	Lys	Val	Gly	Gly	Leu	Ala	Asp	Arg	Pro	Leu	Ile	Ser	Phe	Ala	His	
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Arg	Ser	Leu	Arg	Lys	Tyr	Lys	Pro	Lys	Lys	Asn	Ser	Gly	Glu	Thr	Val	
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cac	gca	gcg	atc	aaa	act	ctt	gaa	gcc	ctc	ggc	tac	aac	gtg	gtc	atc	2323
His	Ala	Ala	Ile	Lys	Thr	Leu	Glu	Ala	Leu	Gly	Tyr	Asn	Val	Val	Ile	
730					735					740						
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Pro	Asp	Gly	Phe	Val	Cys	Cys	Gly	Leu	Thr	Trp	His	Ser	Thr	Gly	Gln	
745					750					755						
ttg	agc	atg	aca	aag	aaa	gtc	cta	gaa	caa	acg	gcg	aaa	gtg	atg	aaa	2419
Leu	Ser	Met	Thr	Lys	Lys	Val	Leu	Glu	Gln	Thr	Ala	Lys	Val	Met	Lys	
760					765					770						

ccc tac ctg gac caa ggt cta aca gtc gtt ggt ttg gaa cct tcg tgc 2467
 Pro Tyr Leu Asp Gln Gly Leu Thr Val Val Gly Leu Glu Pro Ser Cys
 775 780 785

 acc gtc atg ctt caa gat gag gca aca gaa ctc tcc gat aac cct gat 2515
 Thr Val Met Leu Gln Asp Glu Ala Thr Glu Leu Ser Asp Asn Pro Asp
 790 795 800 805

 ctg gca cgc ctt gca gca ctg acc aaa cca ttc gct gag gtc atc gca 2563
 Leu Ala Arg Leu Ala Ala Leu Thr Lys Pro Phe Ala Glu Val Ile Ala
 810 815 820

 cca aag atc acc gag cta gtc gag tct gga agc ctc cag cta aca gaa 2611
 Pro Lys Ile Thr Glu Leu Val Glu Ser Gly Ser Leu Gln Leu Thr Glu
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 tca act gcg ctt acc cag gtg cac tgc cac gag cgt tcg cta ggc gac 2659
 Ser Thr Ala Leu Thr Gln Val His Cys His Glu Arg Ser Leu Gly Asp
 840 845 850

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 Pro Gln Gln Ser Ala Leu Val Leu Glu Ala Leu Gly Val Lys Asp Glu
 855 860 865

 caa att gcc act ggt tgt tgc ggg ctt gcc gga aac tgg ggc ttt gaa 2755
 Gln Ile Ala Thr Gly Cys Cys Gly Leu Ala Gly Asn Trp Gly Phe Glu
 870 875 880 885

 aaa gac cac gct gaa atg tcc ttc gca ctt ggt gaa cga gag ctg ttc 2803
 Lys Asp His Ala Glu Met Ser Phe Ala Leu Gly Glu Arg Glu Leu Phe
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 Pro Lys Val Arg Lys Ala Glu Gly His Val Ile Ala Asp Gly Phe Ser
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 Cys Arg Thr Gln Ile Glu Gln Gly Thr Gly Lys Gln Ala Thr His Leu
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 gca gag gtg gtc tta agc atc ttg gag caa aac aac atg gca caa 2944
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Asn	Arg	Ile	Leu	Asp	Ile	Asp	Pro	Val	Ala	Gln	Thr	Ala	Val	Val	Glu	
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Pro	Gly	Val	Val	Cys	Asp	Ala	Leu	Arg	Asp	Ala	Ala	Ala	Glu	Phe	Gly	
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Leu	Thr	Tyr	Gly	Pro	Asp	Pro	Ser	Thr	His	Ser	Arg	Cys	Thr	Ile	Gly	
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Gly	Met	Val	Ala	Asn	Asn	Ala	Cys	Gly	Ser	His	Ser	Val	Ala	Phe	Gly	
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Thr	Ala	Ala	Glu	Asn	Leu	Val	Asp	Val	Thr	Leu	Met	Leu	Ser	Asp	Gly	
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Arg	Glu	Val	Thr	Val	Thr	Lys	Asp	Gly	Cys	Asp	Asp	Ala	Glu	Ile	Asn	
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Gln	Lys	Leu	Thr	Asp	Leu	Ala	Ser	Lys	Asn	Gln	Asp	Leu	Ile	Ser	Lys	
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Gly	Ile	Ile	Thr	Arg	Leu	Thr	Val	Lys	Leu	Val	Pro	Thr	Pro	Lys	Val	
245					250					255						
Lys	Ala	Leu	Ala	Val	Leu	Ala	Phe	Asp	Thr	Val	Phe	Asp	Ala	Ala	Arg	
260					265					270						
Ala	Ala	Ala	Lys	Leu	Arg	Leu	Pro	Gly	Val	Ala	Thr	Ile	Glu	Gly	Met	
275					280					285						
Gly	Gly	Asp	Leu	Leu	Ala	Ala	Leu	Arg	Ser	Lys	Gln	Gly	Gln	Ser	Glu	
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Trp	Leu	Tyr	Cys	Glu	Thr	Gly	Ser	Asp	Thr	Leu	Gln	Ala	Ala	Val	Gln	
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Val	Ser	Glu	Pro	Ser	Glu	Met	Arg	Glu	Leu	Trp	Arg	Ile	Arg	Glu	Ser	
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 Asn Trp Glu Asp Ser Ala Val Pro Pro Glu Asn Leu Ala Asp Tyr Leu
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 Arg Asp Leu Tyr Ala Leu Met Asp Lys Phe Asp Tyr Gln Gly Ile Pro
 405 410 415
 Phe Gly His Phe Gly Glu Gly Cys Val His Val Arg Ile Ser Phe Asp
 420 425 430
 Phe Ser Thr Lys Glu Gly Leu Lys Lys Phe Glu Ala Phe Met Asn Glu
 435 440 445
 Ala Ser Thr Leu Val Ala Ser Tyr Gly Gly Ser Leu Ser Gly Glu His
 450 455 460
 Gly Asp Gly Arg Ala Arg Ser Ser Phe Leu Asp Arg Met Tyr Ser Ala
 465 470 475 480
 Glu Met Arg Ala Leu Phe Glu Glu Phe Lys Leu Ile Phe Asp Pro Gln
 485 490 495
 Arg Ile Phe Asn Pro Gly Val Leu Val Trp Ala Asp Pro Val Met Gln
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 Gly Leu Arg Met Asp Pro Gly Gln Arg Ala Leu Asp Ile Thr Pro Val
 515 520 525
 His Lys Phe Ser Lys Asp Lys Gly Ser Met Ile Asn Ala Val Asn Arg
 530 535 540
 Cys Val Gly Val Ser Ala Cys Arg Ser Glu Ser Asp Ala Met Cys Pro
 545 550 555 560
 Ser Phe Gln Ile Thr Gly Asp Glu Val His Ser Thr Arg Gly Arg Ala
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 Arg Leu Leu Ser Glu Met Phe Arg Gly Glu Ser Ile Ala Asp Gly Tyr
 580 585 590
 Arg Ser Glu Glu Val Asn Glu Ala Leu Asp Leu Cys Leu Ser Cys Lys
 595 600 605
 Ala Cys Ala Ser Glu Cys Pro Val Asn Val Asp Met Ser Thr Tyr Lys
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 Ala Glu Phe Leu Asp Lys His Tyr Ala Gly Arg Leu Arg Pro Met Ala
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 His Tyr Val Met Gly Trp Leu Pro Leu Leu Gly His Val Ala His Lys
 645 650 655
 Ile Pro Leu Leu Pro Thr Leu Ile Asp Ala Thr Met Gln Ser Ala Leu
 660 665 670
 Thr Ala Pro Val Val Arg Lys Val Gly Gly Leu Ala Asp Arg Pro Leu
 675 680 685

Ile Ser Phe Ala His Arg Ser Leu Arg Lys Tyr Lys Pro Lys Lys Asn
 690 695 700
 Ser Gly Glu Thr Val Val Leu Trp Pro Asp Ser Phe Asn Thr Asn Leu
 705 710 715 720
 Asp Thr Gly Pro Ala His Ala Ala Ile Lys Thr Leu Glu Ala Leu Gly
 725 730 735
 Tyr Asn Val Val Ile Pro Asp Gly Phe Val Cys Cys Gly Leu Thr Trp
 740 745 750
 His Ser Thr Gly Gln Leu Ser Met Thr Lys Lys Val Leu Glu Gln Thr
 755 760 765
 Ala Lys Val Met Lys Pro Tyr Leu Asp Gln Gly Leu Thr Val Val Gly
 770 775 780
 Leu Glu Pro Ser Cys Thr Val Met Leu Gln Asp Glu Ala Thr Glu Leu
 785 790 795 800
 Ser Asp Asn Pro Asp Leu Ala Arg Leu Ala Ala Leu Thr Lys Pro Phe
 805 810 815
 Ala Glu Val Ile Ala Pro Lys Ile Thr Glu Leu Val Glu Ser Gly Ser
 820 825 830
 Leu Gln Leu Thr Glu Ser Thr Ala Leu Thr Gln Val His Cys His Glu
 835 840 845
 Arg Ser Leu Gly Asp Pro Gln Gln Ser Ala Leu Val Leu Glu Ala Leu
 850 855 860
 Gly Val Lys Asp Glu Gln Ile Ala Thr Gly Cys Cys Gly Leu Ala Gly
 865 870 875 880
 Asn Trp Gly Phe Glu Lys Asp His Ala Glu Met Ser Phe Ala Leu Gly
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 Glu Arg Glu Leu Phe Pro Lys Val Arg Lys Ala Glu Gly His Val Ile
 900 905 910
 Ala Asp Gly Phe Ser Cys Arg Thr Gln Ile Glu Gln Gly Thr Gly Lys
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Arg Ala Lys Leu Arg Thr Asp Met Thr Arg Ala Ala Tyr Ser Ser	
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Asp Ala Gly Ile Phe Arg Arg Val Pro Ala Ala Val Ala Glu Pro Glu	
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aat gtg gaa caa att cgt gat gcc att gct gtt gcg gtg gca cga ggg	192
Asn Val Glu Gln Ile Arg Asp Ala Ile Ala Val Ala Val Ala Arg Gly	
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tgg tct gtt gtt ggg cgc ggt gga gga agc tcg gtt gct gga aat gcg	240
Trp Ser Val Val Gly Arg Gly Gly Gly Ser Ser Val Ala Gly Asn Ala	
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Ile Gly Glu Gly Leu Ile Ile Asp Thr Ser Arg Tyr Phe Asn Arg Ile	
85 90 95	
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Leu Asp Ile Asp Pro Val Ala Gln Thr Ala Val Val Glu Pro Gly Val	
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Val Cys Asp Ala Leu Arg Asp Ala Ala Ala Glu Phe Gly Leu Thr Tyr	
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Gly Pro Asp Pro Ser Thr His Ser Arg Cys Thr Ile Gly Gly Met Val	
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gcc aac aat gcg tgt ggt tca cac tcg gtt gca ttc ggt aca gct gcg	480
Ala Asn Asn Ala Cys Gly Ser His Ser Val Ala Phe Gly Thr Ala Ala	
145 150 155 160	
gaa aat ctc gtg gat gtc acg ctc atg ctc agc gat ggc cga gaa gtc	528
Glu Asn Leu Val Asp Val Thr Leu Met Leu Ser Asp Gly Arg Glu Val	
165 170 175	
act gtg aca aaa gat ggc tgc gat gat gct gag atc aat cag aag ctc	576
Thr Val Thr Lys Asp Gly Cys Asp Asp Ala Glu Ile Asn Gln Lys Leu	
180 185 190	
acc gac tta gcg tcc aag aat cag gac ctt att agt aaa gaa ctg ggt	624
Thr Asp Leu Ala Ser Lys Asn Gln Asp Leu Ile Ser Lys Glu Leu Gly	
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cgt ttc cct cgc caa gtg tcg ggc tac ggt ttg cat tat ctt gcc cac	672
Arg Phe Pro Arg Gln Val Ser Gly Tyr Gly Leu His Tyr Leu Ala His	
210 215 220	
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Asp Met Ala Lys Ala Met Ala Gly Thr Glu Gly Thr Ile Gly Ile Ile	
225 230 235 240	

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Thr	Arg	Leu	Thr	Val	Lys	Leu	Val	Pro	Thr	Pro	Lys	Val	Lys	Ala	Leu	
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gct	gtc	ctg	gct	ttc	gac	acg	gtt	ttt	gac	gcc	gcc	cga	gca	gcc	gcc	816
Ala	Val	Leu	Ala	Phe	Asp	Thr	Val	Phe	Asp	Ala	Ala	Arg	Ala	Ala	Ala	
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aaa	ttg	cga	ctg	cct	ggg	gta	gca	acc	att	gaa	ggc	atg	ggc	gga	gat	864
Lys	Leu	Arg	Leu	Pro	Gly	Val	Ala	Thr	Ile	Glu	Gly	Met	Gly	Gly	Asp	
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ctc	ctc	gct	gcg	ctg	cgc	agt	aaa	cag	gga	caa	tca	gaa	gct	ggg	cag	912
Leu	Leu	Ala	Ala	Leu	Arg	Ser	Lys	Gln	Gly	Gln	Ser	Glu	Ala	Gly	Gln	
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Cys	Glu	Thr	Gly	Ser	Asp	Thr	Leu	Gln	Ala	Ala	Val	Gln	Ala	Ala	Glu	
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Pro	Ser	Glu	Met	Arg	Glu	Leu	Trp	Arg	Ile	Arg	Glu	Ser	Ser	Ala	Gly	
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Ile	Val	Thr	Arg	Leu	Ala	Asp	Gly	Gly	Glu	Ala	Trp	Pro	Asn	Trp	Glu	
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gac	tcg	gcg	gtg	cct	cca	gag	aat	tta	gct	gat	tat	ctc	cgc	gat	ctt	1200
Asp	Ser	Ala	Val	Pro	Pro	Glu	Asn	Leu	Ala	Asp	Tyr	Leu	Arg	Asp	Leu	
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Tyr	Ala	Leu	Met	Asp	Lys	Phe	Asp	Tyr	Gln	Gly	Ile	Pro	Phe	Gly	His	
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Phe	Gly	Glu	Gly	Cys	Val	His	Val	Arg	Ile	Ser	Phe	Asp	Phe	Ser	Thr	
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Lys	Glu	Gly	Leu	Lys	Lys	Phe	Glu	Ala	Phe	Met	Asn	Glu	Ala	Ser	Thr	
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Leu	Val	Ala	Ser	Tyr	Gly	Gly	Ser	Leu	Ser	Gly	Glu	His	Gly	Asp	Gly	
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Ala Leu Phe Glu Glu Phe Lys Leu Ile Phe Asp Pro Gln Arg Ile Phe	
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Asn Pro Gly Val Leu Val Trp Ala Asp Pro Val Met Gln Gly Leu Arg	
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Met Asp Pro Gly Gln Arg Ala Leu Asp Ile Thr Pro Val His Lys Phe	
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Ser Lys Asp Lys Gly Ser Met Ile Asn Ala Val Asn Arg Cys Val Gly	
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Val Ser Ala Cys Arg Ser Glu Ser Asp Ala Met Cys Pro Ser Phe Gln	
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Ile Thr Gly Asp Glu Val His Ser Thr Arg Gly Arg Ala Arg Leu Leu	
565 570 575	
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Ser Glu Met Phe Arg Gly Glu Ser Ile Ala Asp Gly Tyr Arg Ser Glu	
580 585 590	
gaa gtc aat gaa gcc ctt gac ctg tgc ctt tcc tgc aaa gca tgc gca	1824
Glu Val Asn Glu Ala Leu Asp Leu Cys Leu Ser Cys Lys Ala Cys Ala	
595 600 605	
tcg gaa tgt cca gtc aac gtc gac atg tcc acc tac aaa gcc gaa ttc	1872
Ser Glu Cys Pro Val Asn Val Asp Met Ser Thr Tyr Lys Ala Glu Phe	
610 615 620	
ctg gac aaa cac tac gcc ggc cga ctt cgc ccc atg gcc cat tac gtc	1920
Leu Asp Lys His Tyr Ala Gly Arg Leu Arg Pro Met Ala His Tyr Val	
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Met Gly Trp Leu Pro Leu Leu Gly His Val Ala His Lys Ile Pro Leu	
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Val Val Arg Lys Val Gly Gly Leu Ala Asp Arg Pro Leu Ile Ser Phe	
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gcc cac cgc tcg ctg cgc aag tac aag ccg aag aaa aac tca ggt gaa	2112
Ala His Arg Ser Leu Arg Lys Tyr Lys Pro Lys Lys Asn Ser Gly Glu	
690 695 700	
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Thr Val Val Leu Trp Pro Asp Ser Phe Asn Thr Asn Leu Asp Thr Gly	
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cca gct cac gca gcg atc aaa act ctt gaa gcc ctc ggt tac aac gtg	2208

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Val	Ile	Pro	Asp	Gly	Phe	Val	Cys	Cys	Gly	Leu	Thr	Trp	His	Ser	Thr	
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ggc	caa	ttg	agc	atg	aca	aag	aaa	gtc	cta	gaa	caa	acg	gcg	aaa	gtg	2304
Gly	Gln	Leu	Ser	Met	Thr	Lys	Lys	Val	Leu	Glu	Gln	Thr	Ala	Lys	Val	
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Met	Lys	Pro	Tyr	Leu	Asp	Gln	Gly	Leu	Thr	Val	Val	Gly	Leu	Glu	Pro	
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Ser	Cys	Thr	Val	Met	Leu	Gln	Asp	Glu	Ala	Thr	Glu	Leu	Ser	Asp	Asn	
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cct	gat	ctg	gca	cgc	ctt	gca	gca	ctg	acc	aaa	cca	ttc	gct	gag	gtc	2448
Pro	Asp	Leu	Ala	Arg	Leu	Ala	Ala	Leu	Thr	Lys	Pro	Phe	Ala	Glu	Val	
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Ile	Ala	Pro	Lys	Ile	Thr	Glu	Leu	Val	Glu	Ser	Gly	Ser	Leu	Gln	Leu	
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Thr	Glu	Ser	Thr	Ala	Leu	Thr	Gln	Val	His	Cys	His	Glu	Arg	Ser	Leu	
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Gly	Asp	Pro	Gln	Gln	Ser	Ala	Leu	Val	Leu	Glu	Ala	Leu	Gly	Val	Lys	
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gat	gaa	caa	att	gcc	act	ggg	tgt	tgc	ggg	ctt	gcc	gga	aac	tgg	ggc	2640
Asp	Glu	Gln	Ile	Ala	Thr	Gly	Cys	Cys	Gly	Leu	Ala	Gly	Asn	Trp	Gly	
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ttt	gaa	aaa	gac	cac	gct	gaa	atg	tcc	ttc	gca	ctt	ggg	gaa	cga	gag	2688
Phe	Glu	Lys	Asp	His	Ala	Glu	Met	Ser	Phe	Ala	Leu	Gly	Glu	Arg	Glu	
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Leu	Phe	Pro	Lys	Val	Arg	Lys	Ala	Glu	Gly	His	Val	Ile	Ala	Asp	Gly	
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Phe	Ser	Cys	Arg	Thr	Gln	Ile	Glu	Gln	Gly	Thr	Gly	Lys	Gln	Ala	Thr	
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cac	ctt	gca	gag	gtg	gtc	tta	agc	atc	ttg	gag	caa	aac	aac	atg	gca	2832
His	Leu	Ala	Glu	Val	Val	Leu	Ser	Ile	Leu	Glu	Gln	Asn	Asn	Met	Ala	
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Gln																
945																

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<211> 945

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 134

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Asp Ala Gly Ile Phe Arg Arg Val Pro Ala Ala Val Ala Glu Pro Glu
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Asn Val Glu Gln Ile Arg Asp Ala Ile Ala Val Ala Val Ala Arg Gly
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Trp Ser Val Val Gly Arg Gly Gly Gly Ser Ser Val Ala Gly Asn Ala
 65           70           75           80

Ile Gly Glu Gly Leu Ile Ile Asp Thr Ser Arg Tyr Phe Asn Arg Ile
          85           90           95

Leu Asp Ile Asp Pro Val Ala Gln Thr Ala Val Val Glu Pro Gly Val
      100           105           110

Val Cys Asp Ala Leu Arg Asp Ala Ala Ala Glu Phe Gly Leu Thr Tyr
      115           120           125

Gly Pro Asp Pro Ser Thr His Ser Arg Cys Thr Ile Gly Gly Met Val
 130           135           140

Ala Asn Asn Ala Cys Gly Ser His Ser Val Ala Phe Gly Thr Ala Ala
 145           150           155           160

Glu Asn Leu Val Asp Val Thr Leu Met Leu Ser Asp Gly Arg Glu Val
          165           170           175

Thr Val Thr Lys Asp Gly Cys Asp Asp Ala Glu Ile Asn Gln Lys Leu
      180           185           190

Thr Asp Leu Ala Ser Lys Asn Gln Asp Leu Ile Ser Lys Glu Leu Gly
      195           200           205

Arg Phe Pro Arg Gln Val Ser Gly Tyr Gly Leu His Tyr Leu Ala His
      210           215           220

Asp Met Ala Lys Ala Met Ala Gly Thr Glu Gly Thr Ile Gly Ile Ile
 225           230           235           240

Thr Arg Leu Thr Val Lys Leu Val Pro Thr Pro Lys Val Lys Ala Leu
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Ala Val Leu Ala Phe Asp Thr Val Phe Asp Ala Ala Arg Ala Ala Ala
      260           265           270

Lys Leu Arg Leu Pro Gly Val Ala Thr Ile Glu Gly Met Gly Gly Asp
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Leu Leu Ala Ala Leu Arg Ser Lys Gln Gly Gln Ser Glu Ala Gly Gln
      290           295           300

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Asn Leu Pro Gly Asn Arg Ile Gly Ile Glu Ala Gly Gly Trp Leu Tyr
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 Cys Glu Thr Gly Ser Asp Thr Leu Gln Ala Ala Val Gln Ala Ala Glu
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 Glu Val Ala Thr Ala Val Asp Thr Ile Asp Tyr Val Val Val Ser Glu
 340 345 350
 Pro Ser Glu Met Arg Glu Leu Trp Arg Ile Arg Glu Ser Ser Ala Gly
 355 360 365
 Ile Val Thr Arg Leu Ala Asp Gly Gly Glu Ala Trp Pro Asn Trp Glu
 370 375 380
 Asp Ser Ala Val Pro Pro Glu Asn Leu Ala Asp Tyr Leu Arg Asp Leu
 385 390 395 400
 Tyr Ala Leu Met Asp Lys Phe Asp Tyr Gln Gly Ile Pro Phe Gly His
 405 410 415
 Phe Gly Glu Gly Cys Val His Val Arg Ile Ser Phe Asp Phe Ser Thr
 420 425 430
 Lys Glu Gly Leu Lys Lys Phe Glu Ala Phe Met Asn Glu Ala Ser Thr
 435 440 445
 Leu Val Ala Ser Tyr Gly Gly Ser Leu Ser Gly Glu His Gly Asp Gly
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 Arg Ala Arg Ser Ser Phe Leu Asp Arg Met Tyr Ser Ala Glu Met Arg
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 Ala Leu Phe Glu Glu Phe Lys Leu Ile Phe Asp Pro Gln Arg Ile Phe
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 Asn Pro Gly Val Leu Val Trp Ala Asp Pro Val Met Gln Gly Leu Arg
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 Met Asp Pro Gly Gln Arg Ala Leu Asp Ile Thr Pro Val His Lys Phe
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 Ser Lys Asp Lys Gly Ser Met Ile Asn Ala Val Asn Arg Cys Val Gly
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 Val Ser Ala Cys Arg Ser Glu Ser Asp Ala Met Cys Pro Ser Phe Gln
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 Ile Thr Gly Asp Glu Val His Ser Thr Arg Gly Arg Ala Arg Leu Leu
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 Ser Glu Met Phe Arg Gly Glu Ser Ile Ala Asp Gly Tyr Arg Ser Glu
 580 585 590
 Glu Val Asn Glu Ala Leu Asp Leu Cys Leu Ser Cys Lys Ala Cys Ala
 595 600 605
 Ser Glu Cys Pro Val Asn Val Asp Met Ser Thr Tyr Lys Ala Glu Phe
 610 615 620

Leu Asp Lys His Tyr Ala Gly Arg Leu Arg Pro Met Ala His Tyr Val
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 Met Gly Trp Leu Pro Leu Leu Gly His Val Ala His Lys Ile Pro Leu
 645 650 655
 Leu Pro Thr Leu Ile Asp Ala Thr Met Gln Ser Ala Leu Thr Ala Pro
 660 665 670
 Val Val Arg Lys Val Gly Gly Leu Ala Asp Arg Pro Leu Ile Ser Phe
 675 680 685
 Ala His Arg Ser Leu Arg Lys Tyr Lys Pro Lys Lys Asn Ser Gly Glu
 690 695 700
 Thr Val Val Leu Trp Pro Asp Ser Phe Asn Thr Asn Leu Asp Thr Gly
 705 710 715 720
 Pro Ala His Ala Ala Ile Lys Thr Leu Glu Ala Leu Gly Tyr Asn Val
 725 730 735
 Val Ile Pro Asp Gly Phe Val Cys Cys Gly Leu Thr Trp His Ser Thr
 740 745 750
 Gly Gln Leu Ser Met Thr Lys Lys Val Leu Glu Gln Thr Ala Lys Val
 755 760 765
 Met Lys Pro Tyr Leu Asp Gln Gly Leu Thr Val Val Gly Leu Glu Pro
 770 775 780
 Ser Cys Thr Val Met Leu Gln Asp Glu Ala Thr Glu Leu Ser Asp Asn
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 Pro Asp Leu Ala Arg Leu Ala Ala Leu Thr Lys Pro Phe Ala Glu Val
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 Ile Ala Pro Lys Ile Thr Glu Leu Val Glu Ser Gly Ser Leu Gln Leu
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 Thr Glu Ser Thr Ala Leu Thr Gln Val His Cys His Glu Arg Ser Leu
 835 840 845
 Gly Asp Pro Gln Gln Ser Ala Leu Val Leu Glu Ala Leu Gly Val Lys
 850 855 860
 Asp Glu Gln Ile Ala Thr Gly Cys Cys Gly Leu Ala Gly Asn Trp Gly
 865 870 875 880
 Phe Glu Lys Asp His Ala Glu Met Ser Phe Ala Leu Gly Glu Arg Glu
 885 890 895
 Leu Phe Pro Lys Val Arg Lys Ala Glu Gly His Val Ile Ala Asp Gly
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 Phe Ser Cys Arg Thr Gln Ile Glu Gln Gly Thr Gly Lys Gln Ala Thr
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 His Leu Ala Glu Val Val Leu Ser Ile Leu Glu Gln Asn Asn Met Ala
 930 935 940

Gln

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Thr	Leu	Met	Phe	Thr	Val	Asp	Thr	Pro	Ile	Ala	Gly	Tyr	Arg	Ile	Arg	
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Val	Leu	Asn	Ala	Ile	Pro	Arg	Pro	Trp	Trp	Trp	Ile	Asp	Phe	Leu	Thr	
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Gly	Asp	Leu	Leu	Asn	Ser	Ala	Met	Asp	Pro	Thr	Ile	Ser	Tyr	Glu	Asp	
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Leu	Lys	Val	Ile	Arg	Glu	Met	Trp	Pro	Gly	Lys	Leu	Val	Val	Lys	Gly	
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Val	Gln	Asn	Val	Glu	Asp	Ser	Val	Lys	Leu	Leu	Asp	Gln	Gly	Val	Asp	
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ggc	ctc	atc	ctc	tcc	aac	cac	ggc	ggc	cgt	caa	ctc	gac	cgc	gca	cca	1027
Gly	Leu	Ile	Leu	Ser	Asn	His	Gly	Gly	Arg	Gln	Leu	Asp	Arg	Ala	Pro	
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Val	Pro	Phe	His	Leu	Leu	Pro	Gln	Val	Arg	Lys	Glu	Val	Gly	Ser	Glu	
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cca	acc	atc	atg	atc	gac	acc	ggc	atc	atg	aac	ggc	gcc	gac	atc	gtc	1123
Pro	Thr	Ile	Met	Ile	Asp	Thr	Gly	Ile	Met	Asn	Gly	Ala	Asp	Ile	Val	
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gca	gcc	gta	gcc	atg	ggc	gct	gac	ttc	acc	ctc	atc	ggc	cgt	gcc	tac	1171
Ala	Ala	Val	Ala	Met	Gly	Ala	Asp	Phe	Thr	Leu	Ile	Gly	Arg	Ala	Tyr	
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Leu	Tyr	Gly	Leu	Met	Ala	Gly	Gly	Arg	Glu	Gly	Val	Asp	Arg	Thr	Ile	
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gcc	att	ctc	cgc	agc	gag	atc	acc	cgc	acc	atg	gct	ctc	ctc	ggc	gtt	1267
Ala	Ile	Leu	Arg	Ser	Glu	Ile	Thr	Arg	Thr	Met	Ala	Leu	Leu	Gly	Val	
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Ser	Ser	Leu	Glu	Glu	Leu	Glu	Pro	Arg	His	Val	Thr	Gln	Leu	Ala	Lys	
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atg	gtt	cca	gtt	tct	gac	gca	act	cgt	tct	gca	gcg	gcg	gag	att		1360
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 Ala Ala Ala Phe Asp Tyr Thr Asp Gly Ala Ala Glu Ala Glu Leu Ser
 50 55 60
 Ile Thr Arg Ala Arg Glu Ala Phe Glu Asn Ile Glu Phe His Pro Asp
 65 70 75 80
 Ile Leu Lys Pro Ala Glu His Val Asp Thr Thr Thr Gln Ile Leu Gly
 85 90 95
 Gly Thr Ser Ser Met Pro Phe Gly Ile Ala Pro Thr Gly Phe Thr Arg
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 Leu Met Gln Thr Glu Gly Glu Ile Ala Gly Ala Gly Ala Ala Gly Ala
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 Ala Gly Ile Pro Phe Thr Leu Ser Thr Leu Gly Thr Thr Ser Ile Glu
 130 135 140
 Asp Val Lys Ala Thr Asn Pro Asn Gly Arg Asn Trp Phe Gln Leu Tyr
 145 150 155 160
 Val Met Arg Asp Arg Glu Ile Ser Tyr Gly Leu Val Glu Arg Ala Ala
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 Lys Ala Gly Phe Asp Thr Leu Met Phe Thr Val Asp Thr Pro Ile Ala
 180 185 190
 Gly Tyr Arg Ile Arg Asp Ser Arg Asn Gly Phe Ser Ile Pro Pro Gln
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 Leu Thr Pro Ser Thr Val Leu Asn Ala Ile Pro Arg Pro Trp Trp Trp
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 Ile Asp Phe Leu Thr Thr Pro Thr Leu Glu Phe Ala Ser Leu Ser Ser
 225 230 235 240
 Thr Gly Gly Thr Val Gly Asp Leu Leu Asn Ser Ala Met Asp Pro Thr
 245 250 255
 Ile Ser Tyr Glu Asp Leu Lys Val Ile Arg Glu Met Trp Pro Gly Lys
 260 265 270

Leu Val Val Lys Gly Val Gln Asn Val Glu Asp Ser Val Lys Leu Leu
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 Leu Asp Arg Ala Pro Val Pro Phe His Leu Leu Pro Gln Val Arg Lys
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 Glu Val Gly Ser Glu Pro Thr Ile Met Ile Asp Thr Gly Ile Met Asn
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 Gly Ala Asp Ile Val Ala Ala Val Ala Met Gly Ala Asp Phe Thr Leu
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 Ile Gly Arg Ala Tyr Leu Tyr Gly Leu Met Ala Gly Gly Arg Glu Gly
 355 360 365
 Val Asp Arg Thr Ile Ala Ile Leu Arg Ser Glu Ile Thr Arg Thr Met
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 Ala Ala Glu Ile
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 Gln Thr Thr Thr Thr Ser His Glu Ala Ile Asp Ala Phe Lys Arg Ile
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 Val Gly Asp Glu His Val Leu Thr Ser Glu Arg Ala Thr Met Pro Phe
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 Ser Lys Gly Tyr Arg Phe Gly Gly Gly Pro Val Phe Ala Val Val Arg
 40 45 50

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Pro Gly Thr Leu Val Glu Met Trp Arg Ala Leu Gln Val Ser Val Asp	
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Asn Asn Leu Ile Val Ile Pro Gln Ala Ser Asn Thr Gly Leu Thr Gly	
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Gly Ser Gly Pro Gly Phe Gln Asp Tyr Asp Arg Pro Ile Val Ile Ile	
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Ser Thr His Arg Ile Asp Glu Val His Leu Ile Asn Asp Ala Arg Glu	
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gcg atc tcg ctc gcg ggc acc ccg ctg aca cac ctg acc gac gcg ctc	499
Ala Ile Ser Leu Ala Gly Thr Pro Leu Thr His Leu Thr Asp Ala Leu	
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Ala Lys His Gln Arg Glu Pro His Ser Val Ile Gly Ser Thr Ser Ile	
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Gly Ala Ser Val Ile Gly Gly Ile Ala Asn Asn Ser Gly Gly Ser Gln	
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Ile Arg Lys Gly Pro Ala Phe Thr Arg Glu Ala Ile Phe Ala Arg Val	
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Asn Asp Asp Gly Lys Val Glu Leu Val Asn His Leu Gly Ile Ser Leu	
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gga gac gac cct gag gtc gca ctc gac cgt cta cag cgc ggc gag tgg	739
Gly Asp Asp Pro Glu Val Ala Leu Asp Arg Leu Gln Arg Gly Glu Trp	
200 205 210	
tct ccc gag gat gtc acc cca gct ccc gaa gac tcg aac gag acc gag	787
Ser Pro Glu Asp Val Thr Pro Ala Pro Glu Asp Ser Asn Glu Thr Glu	
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Tyr Ala Glu His Leu Arg Lys Ile Val Pro Ser Pro Ala Arg Tyr Asn	
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Ala Asn Pro Glu Tyr Leu Phe Glu Ala Ser Gly Ser Ala Gly Lys Leu	
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Met Val Phe Ala Val Arg Thr Arg Thr Phe Pro Arg Glu Val His Pro	
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acc gtg ttt tac atc ggc acg aac aac acg cac gag ctc gaa gag atc	979
Thr Val Phe Tyr Ile Gly Thr Asn Asn Thr His Glu Leu Glu Glu Ile	
280 285 290	
cgt cgg ttg ttc ctc gaa gcc gac atg ccg ctg cct atc tct ggt gag	1027

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Tyr	Met	Gly	Arg	Ser	Ala	Phe	Asp	Leu	Ala	Glu	Lys	Tyr	Gly	Lys	Asp		
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Thr	Phe	Val	Phe	Leu	Lys	Phe	Met	Ser	Pro	Ala	Leu	Gln	Thr	Arg	Met		
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Phe	Ser	Phe	Lys	Thr	Trp	Ala	Asn	Gly	Leu	Phe	Ser	Lys	Ile	Pro	Gly		
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Ile	Gly	Pro	Thr	Phe	Ala	Asp	Thr	Val	Ser	Gln	Ala	Met	Phe	Ser	Val		
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Leu	Pro	Asn	Gln	Leu	Pro	Lys	Arg	Met	Met	Glu	Tyr	Arg	Asn	Arg	Phe		
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Glu	His	His	Leu	Leu	Leu	Thr	Val	Ser	Glu	Ser	Gln	Lys	Ala	Ala	Ser		
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Phe	Phe	Ile	Cys	Thr	Ser	Asp	Glu	Glu	Lys	Ser	Ala	Ser	Leu	Asn	Arg		
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Phe	Gly	Ala	Ala	Ser	Ala	Ala	Thr	Arg	Tyr	Ala	Ala	Leu	Lys	Arg	Arg		
		440					445					450					
cac	atc	gca	ggg	ctc	atc	ccc	atc	gat	gtg	gcc	ctg	cgt	cgc	gac	gat	1507	
His	Ile	Ala	Gly	Leu	Ile	Pro	Ile	Asp	Val	Ala	Leu	Arg	Arg	Asp	Asp		
		455				460					465						
tgg	aac	tgg	ctc	gag	gtg	ctg	ccg	gag	gag	atc	gac	gac	cag	ctt	gag	1555	
Trp	Asn	Trp	Leu	Glu	Val	Leu	Pro	Glu	Glu	Ile	Asp	Asp	Gln	Leu	Glu		
470					475					480					485		
gtc	aag	gcg	tat	tac	ggg	cac	ttc	ttc	tgc	cat	gtg	atg	cac	cag	gac	1603	
Val	Lys	Ala	Tyr	Tyr	Gly	His	Phe	Phe	Cys	His	Val	Met	His	Gln	Asp		
				490					495					500			
tat	gtc	gcc	aag	cag	ggc	gtg	gat	ctc	gag	gcg	ctg	cac	gac	cgc	atc	1651	
Tyr	Val	Ala	Lys	Gln	Gly	Val	Asp	Leu	Glu	Ala	Leu	His	Asp	Arg	Ile		
			505					510					515				
cag	cac	ctg	ctg	gag	gag	cgc	ggc	gcg	aag	ctg	ccc	gcc	gag	cac	aac	1699	
Gln	His	Leu	Leu	Glu	Glu	Arg	Gly	Ala	Lys	Leu	Pro	Ala	Glu	His	Asn		
		520					525					530					
tac	ggt	cgc	atg	tac	aag	ctg	ccg	gag	tcc	atg	gaa	gag	cac	ttc	aag	1747	
Tyr	Gly	Arg	Met	Tyr	Lys	Leu	Pro	Glu	Ser	Met	Glu	Glu	His	Phe	Lys		

535 540 545

gag ctc gat ccg acg aat acg ttc aac gcc ggt atc ggc ggc acg tcg 1795
 Glu Leu Asp Pro Thr Asn Thr Phe Asn Ala Gly Ile Gly Gly Thr Ser
 550 555 560 565

ccg cac aag gac tgg gcc taagtcccca aggtagcgcg acg 1836
 Pro His Lys Asp Trp Ala
 570

<210> 138
 <211> 571
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 138
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Ala Phe Lys Arg Ile Val Gly Asp Glu His Val Leu Thr Ser Glu Arg
 20 25 30

Ala Thr Met Pro Phe Ser Lys Gly Tyr Arg Phe Gly Gly Gly Pro Val
 35 40 45

Phe Ala Val Val Arg Pro Gly Thr Leu Val Glu Met Trp Arg Ala Leu
 50 55 60

Gln Val Ser Val Asp Asn Asn Leu Ile Val Ile Pro Gln Ala Ser Asn
 65 70 75 80

Thr Gly Leu Thr Gly Gly Ser Gly Pro Gly Phe Gln Asp Tyr Asp Arg
 85 90 95

Pro Ile Val Ile Ile Ser Thr His Arg Ile Asp Glu Val His Leu Ile
 100 105 110

Asn Asp Ala Arg Glu Ala Ile Ser Leu Ala Gly Thr Pro Leu Thr His
 115 120 125

Leu Thr Asp Ala Leu Ala Lys His Gln Arg Glu Pro His Ser Val Ile
 130 135 140

Gly Ser Thr Ser Ile Gly Ala Ser Val Ile Gly Gly Ile Ala Asn Asn
 145 150 155 160

Ser Gly Gly Ser Gln Ile Arg Lys Gly Pro Ala Phe Thr Arg Glu Ala
 165 170 175

Ile Phe Ala Arg Val Asn Asp Asp Gly Lys Val Glu Leu Val Asn His
 180 185 190

Leu Gly Ile Ser Leu Gly Asp Asp Pro Glu Val Ala Leu Asp Arg Leu
 195 200 205

Gln Arg Gly Glu Trp Ser Pro Glu Asp Val Thr Pro Ala Pro Glu Asp
 210 215 220

Ser Asn Glu Thr Glu Tyr Ala Glu His Leu Arg Lys Ile Val Pro Ser
 225 230 235 240

Pro Ala Arg Tyr Asn Ala Asn Pro Glu Tyr Leu Phe Glu Ala Ser Gly
 245 250 255
 Ser Ala Gly Lys Leu Met Val Phe Ala Val Arg Thr Arg Thr Phe Pro
 260 265 270
 Arg Glu Val His Pro Thr Val Phe Tyr Ile Gly Thr Asn Asn Thr His
 275 280 285
 Glu Leu Glu Glu Ile Arg Arg Leu Phe Leu Glu Ala Asp Met Pro Leu
 290 295 300
 Pro Ile Ser Gly Glu Tyr Met Gly Arg Ser Ala Phe Asp Leu Ala Glu
 305 310 315 320
 Lys Tyr Gly Lys Asp Thr Phe Val Phe Leu Lys Phe Met Ser Pro Ala
 325 330 335
 Leu Gln Thr Arg Met Phe Ser Phe Lys Thr Trp Ala Asn Gly Leu Phe
 340 345 350
 Ser Lys Ile Pro Gly Ile Gly Pro Thr Phe Ala Asp Thr Val Ser Gln
 355 360 365
 Ala Met Phe Ser Val Leu Pro Asn Gln Leu Pro Lys Arg Met Met Glu
 370 375 380
 Tyr Arg Asn Arg Phe Glu His His Leu Leu Leu Thr Val Ser Glu Ser
 385 390 395 400
 Gln Lys Ala Ala Ser Glu Lys Met Leu Lys Glu Phe Phe Ala Glu Pro
 405 410 415
 Glu His Thr Gly Glu Phe Phe Ile Cys Thr Ser Asp Glu Glu Lys Ser
 420 425 430
 Ala Ser Leu Asn Arg Phe Gly Ala Ala Ser Ala Ala Thr Arg Tyr Ala
 435 440 445
 Ala Leu Lys Arg Arg His Ile Ala Gly Leu Ile Pro Ile Asp Val Ala
 450 455 460
 Leu Arg Arg Asp Asp Trp Asn Trp Leu Glu Val Leu Pro Glu Glu Ile
 465 470 475 480
 Asp Asp Gln Leu Glu Val Lys Ala Tyr Tyr Gly His Phe Phe Cys His
 485 490 495
 Val Met His Gln Asp Tyr Val Ala Lys Gln Gly Val Asp Leu Glu Ala
 500 505 510
 Leu His Asp Arg Ile Gln His Leu Leu Glu Glu Arg Gly Ala Lys Leu
 515 520 525
 Pro Ala Glu His Asn Tyr Gly Arg Met Tyr Lys Leu Pro Glu Ser Met
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 Glu Glu His Phe Lys Glu Leu Asp Pro Thr Asn Thr Phe Asn Ala Gly
 545 550 555 560

Ile Gly Gly Thr Ser Pro His Lys Asp Trp Ala
 565 570

<210> 139
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 <212> DNA
 <213> Corynebacterium glutamicum

<220>
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 <222> (1)..(216)
 <223> FRXA01952

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 Pro Gly Leu Cys Arg Gln Ala Gly Arg Gly Ser Gln Gly Ala Asp Asp
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 cgc atc cag cac ttg ctg gag gag cac ggc aag aag ctg ccc gcc gag 96
 Arg Ile Gln His Leu Leu Glu Glu His Gly Lys Lys Leu Pro Ala Glu
 20 25 30

 cac aac tac ggt cgc atg tac aag ctg ccg gag tcc atg gaa gag cac 144
 His Asn Tyr Gly Arg Met Tyr Lys Leu Pro Glu Ser Met Glu Glu His
 35 40 45

 ttc aag gag ctc gat ccg acg aat acg ttc aac gcc ggt atc ggc ggc 192
 Phe Lys Glu Leu Asp Pro Thr Asn Thr Phe Asn Ala Gly Ile Gly Gly
 50 55 60

 acg tcg ccg cac aag gac tgg gcc taagtcccca aggtagcgcg acg 239
 Thr Ser Pro His Lys Asp Trp Ala
 65 70

<210> 140
 <211> 72
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 140
 Pro Gly Leu Cys Arg Gln Ala Gly Arg Gly Ser Gln Gly Ala Asp Asp
 1 5 10 15

 Arg Ile Gln His Leu Leu Glu Glu His Gly Lys Lys Leu Pro Ala Glu
 20 25 30

 His Asn Tyr Gly Arg Met Tyr Lys Leu Pro Glu Ser Met Glu Glu His
 35 40 45

 Phe Lys Glu Leu Asp Pro Thr Asn Thr Phe Asn Ala Gly Ile Gly Gly
 50 55 60

 Thr Ser Pro His Lys Asp Trp Ala
 65 70

<210> 141
 <211> 1699
 <212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1699)

<223> FRXA01955

<400> 141

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tgacgcgctt gtgatgcaac tgaatatagg aagcttagag atg acg caa cca gga 115
                                         Met Thr Gln Pro Gly
                                         1      5

cag acc acc acg act tcg cac gaa gcg atc gat gcg ttc aag aga atc 163
Gln Thr Thr Thr      Ser His Glu Ala Ile Asp Ala Phe Lys Arg Ile
                        10      15      20

gtc ggc gac gaa cat gta ctg acc tct gag cgt gcc acg atg cca ttc 211
Val Gly Asp Glu His Val Leu Thr Ser Glu Arg Ala Thr Met Pro Phe
                        25      30      35

agc aaa ggc tat cga ttc ggc gga gga cca gtc ttc gcc gtg gtg cgc 259
Ser Lys Gly Tyr Arg Phe Gly Gly Gly Pro Val Phe Ala Val Val Arg
                        40      45      50

ccc ggc acg ctg gtc gag atg tgg cgg gcg ctg cag gta tcc gtc gac 307
Pro Gly Thr Leu Val Glu Met Trp Arg Ala Leu Gln Val Ser Val Asp
                        55      60      65

aac aac ctc atc gtc atc ccg cag gca tcg aac acg ggc ctg act ggt 355
Asn Asn Leu Ile Val Ile Pro Gln Ala Ser Asn Thr Gly Leu Thr Gly
                        70      75      80      85

gga tcc ggc ccc ggc ttc caa gac tac gat cgc ccc att gtg atc atc 403
Gly Ser Gly Pro Gly Phe Gln Asp Tyr Asp Arg Pro Ile Val Ile Ile
                        90      95      100

tcg act cac cgc atc gat gag gtg cac ctc atc aac gac gcg cgc gag 451
Ser Thr His Arg Ile Asp Glu Val His Leu Ile Asn Asp Ala Arg Glu
                        105      110      115

gcg atc tcg ctc gcg ggc acc ccg ctg aca cac ctg acc gac gcg ctc 499
Ala Ile Ser Leu Ala Gly Thr Pro Leu Thr His Leu Thr Asp Ala Leu
                        120      125      130

gcc aag cac cag cgc gag ccg cac tcg gtg atc ggg tcg aca tca atc 547
Ala Lys His Gln Arg Glu Pro His Ser Val Ile Gly Ser Thr Ser Ile
                        135      140      145

ggc gcc tcg gtc atc ggc ggc atc gcg aac aac tcg ggc ggc agc cag 595
Gly Ala Ser Val Ile Gly Gly Ile Ala Asn Asn Ser Gly Gly Ser Gln
                        150      155      160      165

att cgc aag ggt ccg gca ttc acg cgc gaa gcg atc ttc gcc cgc gtc 643
Ile Arg Lys Gly Pro Ala Phe Thr Arg Glu Ala Ile Phe Ala Arg Val
                        170      175      180

aac gac gac ggc aag gtc gag ctg gtc aat cac ctg ggc atc tcg ctc 691
Asn Asp Asp Gly Lys Val Glu Leu Val Asn His Leu Gly Ile Ser Leu
                        185      190      195

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gga gac gac cct gag gtc gca ctc gac cgt cta cag cgc ggc gag tgg	739
Gly Asp Asp Pro Glu Val Ala Leu Asp Arg Leu Gln Arg Gly Glu Trp	
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tct ccc gag gat gtc acc cca gct ccc gaa gac tcg aac gag acc gag	787
Ser Pro Glu Asp Val Thr Pro Ala Pro Glu Asp Ser Asn Glu Thr Glu	
215 220 225	
tac gcc gag cac ttg cgc aag atc gtg cct tcg cct gct cgc tac aat	835
Tyr Ala Glu His Leu Arg Lys Ile Val Pro Ser Pro Ala Arg Tyr Asn	
230 235 240 245	
gcg aac ccc gag tac ctg ttc gag gct tcc ggc tcg gcc ggc aag ctg	883
Ala Asn Pro Glu Tyr Leu Phe Glu Ala Ser Gly Ser Ala Gly Lys Leu	
250 255 260	
atg gtg ttc gcg gtg cgc acc cgc acc ttc cct cgc gaa gtg cac ccg	931
Met Val Phe Ala Val Arg Thr Arg Thr Phe Pro Arg Glu Val His Pro	
265 270 275	
acc gtg ttt tac atc ggc acg aac aac acg cac gag ctc gaa gag atc	979
Thr Val Phe Tyr Ile Gly Thr Asn Asn Thr His Glu Leu Glu Glu Ile	
280 285 290	
cgt cgg ttg ttc ctc gaa gcc gac atg ccg ctg cct atc tct ggt gag	1027
Arg Arg Leu Phe Leu Glu Ala Asp Met Pro Leu Pro Ile Ser Gly Glu	
295 300 305	
tac atg ggc cgc agt gcc ttc gac ttg gcc gag aag tac ggc aaa gac	1075
Tyr Met Gly Arg Ser Ala Phe Asp Leu Ala Glu Lys Tyr Gly Lys Asp	
310 315 320 325	
acc ttc gtc ttc ctg aag ttc atg agt cca gcg ctg cag acg cgc atg	1123
Thr Phe Val Phe Leu Lys Phe Met Ser Pro Ala Leu Gln Thr Arg Met	
330 335 340	
ttc tcg ttc aag acg tgg gcc aac ggc ttg ttc tcg aag att ccc ggc	1171
Phe Ser Phe Lys Thr Trp Ala Asn Gly Leu Phe Ser Lys Ile Pro Gly	
345 350 355	
att ggt ccg acc ttc gcc gac acg gta tcg caa gcc atg ttc agc gtg	1219
Ile Gly Pro Thr Phe Ala Asp Thr Val Ser Gln Ala Met Phe Ser Val	
360 365 370	
ctg ccc aac cag ctg ccc aag cgc atg atg gag tac cgc aac cgt ttc	1267
Leu Pro Asn Gln Leu Pro Lys Arg Met Met Glu Tyr Arg Asn Arg Phe	
375 380 385	
gag cat cac ctg ctg ctc acc gtc agc gag tcg cag aag gcc gcg agc	1315
Glu His His Leu Leu Thr Val Ser Glu Ser Gln Lys Ala Ala Ser	
390 395 400 405	
gag aag atg ctc aag gag ttc ttc gca gag ccc gag cac act ggt gag	1363
Glu Lys Met Leu Lys Glu Phe Phe Ala Glu Pro Glu His Thr Gly Glu	
410 415 420	
ttc ttc atc tgc acg tct gat gaa gaa aag agc gcg tcg ctc aac cgg	1411
Phe Phe Ile Cys Thr Ser Asp Glu Glu Lys Ser Ala Ser Leu Asn Arg	
425 430 435	

ttc ggc gcg gcc agt gcc gcc act cgc tac gcc gcg ttg aag cgc cgg 1459
 Phe Gly Ala Ala Ser Ala Ala Thr Arg Tyr Ala Ala Leu Lys Arg Arg
 440 445 450

 cac atc gca ggg ctc atc ccc atc gat gtg gcc ctg cgt cgc gac gat 1507
 His Ile Ala Gly Leu Ile Pro Ile Asp Val Ala Leu Arg Arg Asp Asp
 455 460 465

 tgg aac tgg ctc gag gtg ctg ccg gag gag atc gac gac cag ctt gag 1555
 Trp Asn Trp Leu Glu Val Leu Pro Glu Glu Ile Asp Asp Gln Leu Glu
 470 475 480 485

 gtc aag gcg tat tac ggg cac ttc ttc tgc cat gtg atg cac cag gac 1603
 Val Lys Ala Tyr Tyr Gly His Phe Phe Cys His Val Met His Gln Asp
 490 495 500

 tat gtc gcc aag cag ggc gtg gat ctc gag gcg ctg cac gac cgc atc 1651
 Tyr Val Ala Lys Gln Gly Val Asp Leu Glu Ala Leu His Asp Arg Ile
 505 510 515

 cag cac ctg ctg gag gag cgc ggc gcg aag ctg ccc gcc gag cac aac 1699
 Gln His Leu Leu Glu Glu Arg Gly Ala Lys Leu Pro Ala Glu His Asn
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<210> 142

<211> 533

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 142

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 Ala Phe Lys Arg Ile Val Gly Asp Glu His Val Leu Thr Ser Glu Arg
 20 25 30

 Ala Thr Met Pro Phe Ser Lys Gly Tyr Arg Phe Gly Gly Gly Pro Val
 35 40 45

 Phe Ala Val Val Arg Pro Gly Thr Leu Val Glu Met Trp Arg Ala Leu
 50 55 60

 Gln Val Ser Val Asp Asn Asn Leu Ile Val Ile Pro Gln Ala Ser Asn
 65 70 75 80

 Thr Gly Leu Thr Gly Gly Ser Gly Pro Gly Phe Gln Asp Tyr Asp Arg
 85 90 95

 Pro Ile Val Ile Ile Ser Thr His Arg Ile Asp Glu Val His Leu Ile
 100 105 110

 Asn Asp Ala Arg Glu Ala Ile Ser Leu Ala Gly Thr Pro Leu Thr His
 115 120 125

 Leu Thr Asp Ala Leu Ala Lys His Gln Arg Glu Pro His Ser Val Ile
 130 135 140

 Gly Ser Thr Ser Ile Gly Ala Ser Val Ile Gly Gly Ile Ala Asn Asn
 145 150 155 160

Ser Gly Gly Ser Gln Ile Arg Lys Gly Pro Ala Phe Thr Arg Glu Ala
 165 170 175
 Ile Phe Ala Arg Val Asn Asp Asp Gly Lys Val Glu Leu Val Asn His
 180 185 190
 Leu Gly Ile Ser Leu Gly Asp Asp Pro Glu Val Ala Leu Asp Arg Leu
 195 200 205
 Gln Arg Gly Glu Trp Ser Pro Glu Asp Val Thr Pro Ala Pro Glu Asp
 210 215 220
 Ser Asn Glu Thr Glu Tyr Ala Glu His Leu Arg Lys Ile Val Pro Ser
 225 230 235 240
 Pro Ala Arg Tyr Asn Ala Asn Pro Glu Tyr Leu Phe Glu Ala Ser Gly
 245 250 255
 Ser Ala Gly Lys Leu Met Val Phe Ala Val Arg Thr Arg Thr Phe Pro
 260 265 270
 Arg Glu Val His Pro Thr Val Phe Tyr Ile Gly Thr Asn Asn Thr His
 275 280 285
 Glu Leu Glu Glu Ile Arg Arg Leu Phe Leu Glu Ala Asp Met Pro Leu
 290 295 300
 Pro Ile Ser Gly Glu Tyr Met Gly Arg Ser Ala Phe Asp Leu Ala Glu
 305 310 315 320
 Lys Tyr Gly Lys Asp Thr Phe Val Phe Leu Lys Phe Met Ser Pro Ala
 325 330 335
 Leu Gln Thr Arg Met Phe Ser Phe Lys Thr Trp Ala Asn Gly Leu Phe
 340 345 350
 Ser Lys Ile Pro Gly Ile Gly Pro Thr Phe Ala Asp Thr Val Ser Gln
 355 360 365
 Ala Met Phe Ser Val Leu Pro Asn Gln Leu Pro Lys Arg Met Met Glu
 370 375 380
 Tyr Arg Asn Arg Phe Glu His His Leu Leu Leu Thr Val Ser Glu Ser
 385 390 395 400
 Gln Lys Ala Ala Ser Glu Lys Met Leu Lys Glu Phe Phe Ala Glu Pro
 405 410 415
 Glu His Thr Gly Glu Phe Phe Ile Cys Thr Ser Asp Glu Glu Lys Ser
 420 425 430
 Ala Ser Leu Asn Arg Phe Gly Ala Ala Ser Ala Ala Thr Arg Tyr Ala
 435 440 445
 Ala Leu Lys Arg Arg His Ile Ala Gly Leu Ile Pro Ile Asp Val Ala
 450 455 460
 Leu Arg Arg Asp Asp Trp Asn Trp Leu Glu Val Leu Pro Glu Glu Ile
 465 470 475 480
 Asp Asp Gln Leu Glu Val Lys Ala Tyr Tyr Gly His Phe Phe Cys His

485						490						495					
Val	Met	His	Gln	Asp	Tyr	Val	Ala	Lys	Gln	Gly	Val	Asp	Leu	Glu	Ala		
500						505						510					
Leu	His	Asp	Arg	Ile	Gln	His	Leu	Leu	Glu	Glu	Arg	Gly	Ala	Lys	Leu		
515						520						525					
Pro	Ala	Glu	His	Asn													
530																	

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<210> 143
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<212> DNA
<213> Corynebacterium glutamicum
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<222> (101)..(1012)  
<223> RXA00293
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Met Lys Ile Phe Val 1 5															
ggt ttt ggc gat tat cca ctc acc acc aag gcc ctt aag gag gca ggc 163															
Gly Phe Gly Asp Tyr Pro Leu Thr Thr Lys Ala Leu Lys Glu Ala Gly 10 15 20															
gca gaa ata gtg gac tcc ctc gaa aaa gcc gag ggg ttt gtc ttc act 211															
Ala Glu Ile Val Asp Ser Leu Glu Lys Ala Glu Gly Phe Val Phe Thr 25 30 35															
caa aca cca ggc aca gaa ttt ccc cta ctt ccc gac gga gtg agg tgg 259															
Gln Thr Pro Gly Thr Glu Phe Pro Leu Leu Pro Asp Gly Val Arg Trp 40 45 50															
gtg caa ttt ccc aat gcg ggg ctc aac gca tat ttc aca gct ggg cag 307															
Val Gln Phe Pro Asn Ala Gly Leu Asn Ala Tyr Phe Thr Ala Gly Gln 55 60 65															
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Ile Asp Asp Lys Arg Arg Trp Ser Asn Ala Ser Gly Val Tyr Gly Gln 70 75 80 85															
cag gta gcc gaa gca gca atg gct ctt ttg ctg gga ctg att cat atg 403															
Gln Val Ala Glu Ala Ala Met Ala Leu Leu Leu Gly Leu Ile His Met 90 95 100															
cac ccc acc atg gtg cgt gcc gat agt tgg gca cca agc act caa ata 451															
His Pro Thr Met Val Arg Ala Asp Ser Trp Ala Pro Ser Thr Gln Ile 105 110 115															
gat cag cag acc aga tgg ctt gat ggt gca aca gtt gcc att gtg gga 499															
Asp Gln Gln Thr Arg Trp Leu Asp Gly Ala Thr Val Ala Ile Val Gly 120 125 130															

gct ggt gga atc ggt aaa cat ctg gca gcc atg ttg aaa cct ttt ggc 547
 Ala Gly Gly Ile Gly Lys His Leu Ala Ala Met Leu Lys Pro Phe Gly
 135 140 145

gca aag tct tta gca gta agc agg acc ggt aca ccc acc caa gat ttt 595
 Ala Lys Ser Leu Ala Val Ser Arg Thr Gly Thr Pro Thr Gln Asp Phe
 150 155 160 165

gat gca acg gaa cct ata tcc aac ctg cac caa gta ctt gcc gac gcc 643
 Asp Ala Thr Glu Pro Ile Ser Asn Leu His Gln Val Leu Ala Asp Ala
 170 175 180

gac cat gtg gtg ttg tgc gta ccg ctt acc gca gac acc tat cat ctg 691
 Asp His Val Val Leu Cys Val Pro Leu Thr Ala Asp Thr Tyr His Leu
 185 190 195

atc gga aaa gca gag ctt aaa gca atg cag tcc act gca att ttg atc 739
 Ile Gly Lys Ala Glu Leu Lys Ala Met Gln Ser Thr Ala Ile Leu Ile
 200 205 210

aac gtg gct cgc gga gaa gta gta gat aca gaa gca tta gtt gac gcc 787
 Asn Val Ala Arg Gly Glu Val Val Asp Thr Glu Ala Leu Val Asp Ala
 215 220 225

tta gat gcc caa gaa ata tcc ggg gca ggc tta gat gtc acc gat cct 835
 Leu Asp Ala Gln Glu Ile Ser Gly Ala Gly Leu Asp Val Thr Asp Pro
 230 235 240 245

gaa cca ttg ccg gac gat cat cca ctg tgg ggg cgc agc aat gtg atc 883
 Glu Pro Leu Pro Asp Asp His Pro Leu Trp Gly Arg Ser Asn Val Ile
 250 255 260

att acc ccg cac gta gcc aac acg ttg acc tcg atg gat cgc atg ctt 931
 Ile Thr Pro His Val Ala Asn Thr Leu Thr Ser Met Asp Arg Met Leu
 265 270 275

gcc cca gtg gtg gca gaa aac tac cga cgg ttt ctc gct gga gaa aag 979
 Ala Pro Val Val Ala Glu Asn Tyr Arg Arg Phe Leu Ala Gly Glu Lys
 280 285 290

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 Met Leu Thr Glu Val Asp Ile His Lys Gly Tyr
 295 300

tag 1035

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<211> 304

<212> PRT

<213> Corynebacterium glutamicum

<400> 144

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 20 25 30

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 35 40 45

Asp Gly Val Arg Trp Val Gln Phe Pro Asn Ala Gly Leu Asn Ala Tyr
 50 55 60
 Phe Thr Ala Gly Gln Ile Asp Asp Lys Arg Arg Trp Ser Asn Ala Ser
 65 70 75 80
 Gly Val Tyr Gly Gln Gln Val Ala Glu Ala Ala Met Ala Leu Leu Leu
 85 90 95
 Gly Leu Ile His Met His Pro Thr Met Val Arg Ala Asp Ser Trp Ala
 100 105 110
 Pro Ser Thr Gln Ile Asp Gln Gln Thr Arg Trp Leu Asp Gly Ala Thr
 115 120 125
 Val Ala Ile Val Gly Ala Gly Gly Ile Gly Lys His Leu Ala Ala Met
 130 135 140
 Leu Lys Pro Phe Gly Ala Lys Ser Leu Ala Val Ser Arg Thr Gly Thr
 145 150 155 160
 Pro Thr Gln Asp Phe Asp Ala Thr Glu Pro Ile Ser Asn Leu His Gln
 165 170 175
 Val Leu Ala Asp Ala Asp His Val Val Leu Cys Val Pro Leu Thr Ala
 180 185 190
 Asp Thr Tyr His Leu Ile Gly Lys Ala Glu Leu Lys Ala Met Gln Ser
 195 200 205
 Thr Ala Ile Leu Ile Asn Val Ala Arg Gly Glu Val Val Asp Thr Glu
 210 215 220
 Ala Leu Val Asp Ala Leu Asp Ala Gln Glu Ile Ser Gly Ala Gly Leu
 225 230 235 240
 Asp Val Thr Asp Pro Glu Pro Leu Pro Asp Asp His Pro Leu Trp Gly
 245 250 255
 Arg Ser Asn Val Ile Ile Thr Pro His Val Ala Asn Thr Leu Thr Ser
 260 265 270
 Met Asp Arg Met Leu Ala Pro Val Val Ala Glu Asn Tyr Arg Arg Phe
 275 280 285
 Leu Ala Gly Glu Lys Met Leu Thr Glu Val Asp Ile His Lys Gly Tyr
 290 295 300

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<211> 687

<212> DNA

<213> Corynebacterium glutamicum

<220>

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<222> (62)..(664)

<223> RXN01130

<400> 145

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gatg gat ctg gct cgc aag ctt ggt ctt ctt gct ggc aag ctt gtc gac 109
Met Asp Leu Ala Arg Lys Leu Gly Leu Leu Ala Gly Lys Leu Val Asp
  1           5           10           15

gcc gcc cca gtc tcc att gag gtt gag gct cga ggc gag ctt tct tcc 157
Ala Ala Pro Val Ser Ile Glu Val Glu Ala Arg Gly Glu Leu Ser Ser
          20           25           30

gag cag gtc aat gca ctt ggt ttg tcc gct gtt cgt ggt ttg ttc tcc 205
Glu Gln Val Asn Ala Leu Gly Leu Ser Ala Val Arg Gly Leu Phe Ser
          35           40           45

gga att atc gaa gag tcc gtt act ttc gtc aac gct cct cgc att gct 253
Gly Ile Ile Glu Glu Ser Val Thr Phe Val Asn Ala Pro Arg Ile Ala
          50           55           60

gaa gag cgt ggc ctg gac atc tcc gtg aag acc aac tct gag tct gtt 301
Glu Glu Arg Gly Leu Asp Ile Ser Val Lys Thr Asn Ser Glu Ser Val
          65           70           75           80

act cac cgt tcc gtc ctg cag gtc aag gtc att act ggc agc ggc gcg 349
Thr His Arg Ser Val Leu Gln Val Lys Val Ile Thr Gly Ser Gly Ala
          85           90           95

agc gca act gtt gtt ggt gcc ctg act ggt ctt gag cgc gtt gag aag 397
Ser Ala Thr Val Val Gly Ala Leu Thr Gly Leu Glu Arg Val Glu Lys
          100           105           110

atc acc cgc atc aat ggc cgt ggc ctg gat ctg cgc gca gag ggt ctg 445
Ile Thr Arg Ile Asn Gly Arg Gly Leu Asp Leu Arg Ala Glu Gly Leu
          115           120           125

aac ctc ttc ctg cag tac act gac gct cct ggt gca ctg ggt acc gtt 493
Asn Leu Phe Leu Gln Tyr Thr Asp Ala Pro Gly Ala Leu Gly Thr Val
          130           135           140

ggt acc aag ctg ggt gct gct ggc atc aac atc gag gct gct gcg ttg 541
Gly Thr Lys Leu Gly Ala Ala Gly Ile Asn Ile Glu Ala Ala Ala Leu
          145           150           155           160

act cag gct gag aag ggt gac ggc gct gtc ctg atc ctg cgt gtt gag 589
Thr Gln Ala Glu Lys Gly Asp Gly Ala Val Leu Ile Leu Arg Val Glu
          165           170           175

tcc gct gtc tct gaa gag ctg gaa gct gaa atc aac gct gag ttg ggt 637
Ser Ala Val Ser Glu Glu Leu Glu Ala Glu Ile Asn Ala Glu Leu Gly
          180           185           190

gct act tcc ttc cag gtt gat ctt gac taattagaga tccatttgct 684
Ala Thr Ser Phe Gln Val Asp Leu Asp
          195           200

tga 687

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<210> 146

<211> 201
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 146

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Met Asp Leu Ala Arg Lys Leu Gly Leu Leu Ala Gly Lys Leu Val Asp
 1              5              10              15

Ala Ala Pro Val Ser Ile Glu Val Glu Ala Arg Gly Glu Leu Ser Ser
          20              25              30

Glu Gln Val Asn Ala Leu Gly Leu Ser Ala Val Arg Gly Leu Phe Ser
          35              40              45

Gly Ile Ile Glu Glu Ser Val Thr Phe Val Asn Ala Pro Arg Ile Ala
 50              55              60

Glu Glu Arg Gly Leu Asp Ile Ser Val Lys Thr Asn Ser Glu Ser Val
 65              70              75              80

Thr His Arg Ser Val Leu Gln Val Lys Val Ile Thr Gly Ser Gly Ala
          85              90              95

Ser Ala Thr Val Val Gly Ala Leu Thr Gly Leu Glu Arg Val Glu Lys
          100             105             110

Ile Thr Arg Ile Asn Gly Arg Gly Leu Asp Leu Arg Ala Glu Gly Leu
          115             120             125

Asn Leu Phe Leu Gln Tyr Thr Asp Ala Pro Gly Ala Leu Gly Thr Val
          130             135             140

Gly Thr Lys Leu Gly Ala Ala Gly Ile Asn Ile Glu Ala Ala Ala Leu
          145             150             155             160

Thr Gln Ala Glu Lys Gly Asp Gly Ala Val Leu Ile Leu Arg Val Glu
          165             170             175

Ser Ala Val Ser Glu Glu Leu Glu Ala Glu Ile Asn Ala Glu Leu Gly
          180             185             190

Ala Thr Ser Phe Gln Val Asp Leu Asp
          195             200
  
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<210> 147
 <211> 326
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (1)..(303)
 <223> FRXA01130

<400> 147

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gtt ggt gcc ctg act ggt ctt gag cgc gtt gag aag atc acc cgc atc   48
Val Gly Ala Leu Thr Gly Leu Glu Arg Val Glu Lys Ile Thr Arg Ile
 1              5              10              15

aat ggc cgt ggc ctg gat ctg cgc gca gag ggt ctg aac ctc ttc ctg   96
  
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Asn Gly Arg Gly Leu Asp Leu Arg Ala Glu Gly Leu Asn Leu Phe Leu
 20 25 30
 cag tac act gac gct cct ggt gca ctg ggt acc gtt ggt acc aag ctg 144
 Gln Tyr Thr Asp Ala Pro Gly Ala Leu Gly Thr Val Gly Thr Lys Leu
 35 40 45
 ggt gct gct ggc atc aac atc gag gct gct gcg ttg act cag gct gag 192
 Gly Ala Ala Gly Ile Asn Ile Glu Ala Ala Ala Leu Thr Gln Ala Glu
 50 55 60
 aag ggt gac ggc gct gtc ctg atc ctg cgt gtt gag tcc gct gtc tct 240
 Lys Gly Asp Gly Ala Val Leu Ile Leu Arg Val Glu Ser Ala Val Ser
 65 70 75 80
 gaa gag ctg gaa gct gaa atc aac gct gag ttg ggt gct act tcc ttc 288
 Glu Glu Leu Glu Ala Glu Ile Asn Ala Glu Leu Gly Ala Thr Ser Phe
 85 90 95
 cag gtt gat ctt gac taattagaga tccatttgct tga 326
 Gln Val Asp Leu Asp
 100

<210> 148
 <211> 101
 <212> PRT
 <213> *Corynebacterium glutamicum*

<400> 148
 Val Gly Ala Leu Thr Gly Leu Glu Arg Val Glu Lys Ile Thr Arg Ile
 1 5 10 15
 Asn Gly Arg Gly Leu Asp Leu Arg Ala Glu Gly Leu Asn Leu Phe Leu
 20 25 30
 Gln Tyr Thr Asp Ala Pro Gly Ala Leu Gly Thr Val Gly Thr Lys Leu
 35 40 45
 Gly Ala Ala Gly Ile Asn Ile Glu Ala Ala Ala Leu Thr Gln Ala Glu
 50 55 60
 Lys Gly Asp Gly Ala Val Leu Ile Leu Arg Val Glu Ser Ala Val Ser
 65 70 75 80
 Glu Glu Leu Glu Ala Glu Ile Asn Ala Glu Leu Gly Ala Thr Ser Phe
 85 90 95
 Gln Val Asp Leu Asp
 100

<210> 149
 <211> 604
 <212> DNA
 <213> *Corynebacterium glutamicum*
 <220>
 <221> CDS
 <222> (101)..(604)
 <223> RXN03112

<400> 149

gtgagcacgc aatttctttg ctgctgtcta ctgctcgcca gatcctgctg ctgatgcgac 60

gctgcgtgag ggcgagtgga agcgggtcttc tttcaacggt gtg gaa att ttc gga 115
 Val Glu Ile Phe Gly
 1 5

aaa act gtc ggt atc gtc ggt ttt ggc cac att ggt cag ttg ttt gct 163
 Lys Thr Val Gly Ile Val Gly Phe Gly His Ile Gly Gln Leu Phe Ala
 10 15 20

cag cgt ctt gct gcg ttt gag acc acc att gtt gct tac gat cct tac 211
 Gln Arg Leu Ala Ala Phe Glu Thr Thr Ile Val Ala Tyr Asp Pro Tyr
 25 30 35

gct aac cct gct cgt gcg gct cag ctg aac gtt gag ttg gtt gag ttg 259
 Ala Asn Pro Ala Arg Ala Ala Gln Leu Asn Val Glu Leu Val Glu Leu
 40 45 50

gat gag ctg atg agc cgt tct gac ttt gtc acc att cac ctt cct aag 307
 Asp Glu Leu Met Ser Arg Ser Asp Phe Val Thr Ile His Leu Pro Lys
 55 60 65

acc aag gaa act gct ggc atg ttt gat gcg cac ctc ctt gct aag tcc 355
 Thr Lys Glu Thr Ala Gly Met Phe Asp Ala His Leu Leu Ala Lys Ser
 70 75 80 85

aag aag ggc cag atc atc atc aac gct gct cgt ggt ggc ctt gtt gat 403
 Lys Lys Gly Gln Ile Ile Ile Asn Ala Ala Arg Gly Gly Leu Val Asp
 90 95 100

gag cag gct ttg gct gat gcg att gag tcc ggt cac att cgt ggc gct 451
 Glu Gln Ala Leu Ala Asp Ala Ile Glu Ser Gly His Ile Arg Gly Ala
 105 110 115

ggt ttc gat gtg tac tcc acc gag cct tgc act gat tct cct ttg ttc 499
 Gly Phe Asp Val Tyr Ser Thr Glu Pro Cys Thr Asp Ser Pro Leu Phe
 120 125 130

aag ttg cct cag gtt gtt gtg act cct cac ttg ggt gct tct act gaa 547
 Lys Leu Pro Gln Val Val Val Thr Pro His Leu Gly Ala Ser Thr Glu
 135 140 145

gag gct caa gat cgt gcg ggt act gac att gct gat tct gtg ctc aag 595
 Glu Ala Gln Asp Arg Ala Gly Thr Asp Ile Ala Asp Ser Val Leu Lys
 150 155 160 165

gcg ctg gct 604
 Ala Leu Ala

<210> 150

<211> 168

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 150

Val Glu Ile Phe Gly Lys Thr Val Gly Ile Val Gly Phe Gly His Ile
 1 5 10 15

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<210> 151
<211> 649
<212> DNA
<213> Corynebacterium glutamicum
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<220>  
<221> CDS  
<222> (101)..(649)  
<223> FRXA01133
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[illegible]

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tct gct acc act gtc gat gct gaa gtc atc gcc gct gcc cct aac ttg 307
Ser Ala Thr Thr Val Asp Ala Glu Val Ile Ala Ala Ala Pro Asn Leu
    55                60                65

aag atc gtc ggt cgt gcc ggc gtg ggc ttg gac aac gtt gac atc cct 355
Lys Ile Val Gly Arg Ala Gly Val Gly Leu Asp Asn Val Asp Ile Pro
    70                75                80                85

gct gcc act gaa gct ggc gtc atg gtt gct aac gca ccg acc tct aat 403
Ala Ala Thr Glu Ala Gly Val Met Val Ala Asn Ala Pro Thr Ser Asn
                90                95                100

att cac tcc gct tgt gag cac gca att tct ttg ctg ctg tct act gct 451
Ile His Ser Ala Cys Glu His Ala Ile Ser Leu Leu Leu Ser Thr Ala
                105                110                115

cgc cag atc ctg ctg ctg atg cga cgc tgc gtg agg gcg agt gga agc 499
Arg Gln Ile Leu Leu Leu Met Arg Arg Cys Val Arg Ala Ser Gly Ser
                120                125                130

ggg ctt ctt tca acg gtg tgg aaa ttt tgc gaa aaa ctg tgc gta tgc 547
Gly Leu Leu Ser Thr Val Trp Lys Phe Ser Glu Lys Leu Ser Val Ser
                135                140                145

tcg gtt ttg gcc aca ttg gtc agt tgt ttg ctc agc gtc ttg ctg cgt 595
Ser Val Leu Ala Thr Leu Val Ser Cys Leu Leu Ser Val Leu Leu Arg
    150                155                160                165

ttg aga cca cca ttg ttg ctt acg atc ctt acg cta acc ctg ctt cgt 643
Leu Arg Pro Pro Leu Leu Leu Thr Ile Leu Thr Leu Thr Leu Leu Arg
                170                175                180

gcg ggt 649
Ala Gly

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<210> 152

<211> 183

<212> PRT

<213> Corynebacterium glutamicum

<400> 152

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Val Ser Gln Asn Gly Arg Pro Val Val Leu Ile Ala Asp Lys Leu Ala
    1                5                10                15

Gln Ser Thr Val Asp Ala Leu Gly Asp Ala Val Glu Val Arg Trp Val
                20                25                30

Asp Gly Pro Asn Arg Pro Glu Leu Leu Asp Ala Val Lys Glu Ala Asp
    35                40                45

Ala Leu Leu Val Arg Ser Ala Thr Thr Val Asp Ala Glu Val Ile Ala
    50                55                60

Ala Ala Pro Asn Leu Lys Ile Val Gly Arg Ala Gly Val Gly Leu Asp
    65                70                75                80

Asn Val Asp Ile Pro Ala Ala Thr Glu Ala Gly Val Met Val Ala Asn
                85                90                95

```


Ala Pro Thr Ser Asn Ile His Ser Ala Cys Glu His Ala Ile Ser Leu
 100 105 110

Leu Leu Ser Thr Ala Arg Gln Ile Leu Leu Leu Met Arg Arg Cys Val
 115 120 125

Arg Ala Ser Gly Ser Gly Leu Leu Ser Thr Val Trp Lys Phe Ser Glu
 130 135 140

Lys Leu Ser Val Ser Ser Val Leu Ala Thr Leu Val Ser Cys Leu Leu
 145 150 155 160

Ser Val Leu Leu Arg Leu Arg Pro Pro Leu Leu Leu Thr Ile Leu Thr
 165 170 175

Leu Thr Leu Leu Arg Ala Gly
 180

<210> 153
 <211> 1011
 <212> DNA
 <213> *Corynebacterium glutamicum*

<220>
 <221> CDS
 <222> (101)..(988)
 <223> RXN00871

<400> 153
 gggaaaaggc gatcaccagc cggttggtcg acccagcaac ccacggtggc attaacctcg 60

gtttccca gaacgattaa ttgaaggaga gcacaggact atg cgt tgg ttc cat 115
 Met Arg Trp Phe His
 1 5

aag aag ggc gaa ctg gcc cga gat ggt tgg caa agc gtt gtc gat gcc 163
 Lys Lys Gly Glu Leu Ala Arg Asp Gly Trp Gln Ser Val Val Asp Ala
 10 15 20

acc acc cca ggt tgg gaa tat acc ggc atc cgc att gcc gaa ctg ggc 211
 Thr Thr Pro Gly Trp Glu Tyr Thr Gly Ile Arg Ile Ala Glu Leu Gly
 25 30 35

agt ggt gaa tcg ctt gaa ctg aat gac act ggt gtg gaa cgc atc ttc 259
 Ser Gly Glu Ser Leu Glu Leu Asn Asp Thr Gly Val Glu Arg Ile Phe
 40 45 50

att cca ctt cag ggc agc ttc gat gtt gcc cac cat ggt cag gtg acc 307
 Ile Pro Leu Gln Gly Ser Phe Asp Val Ala His His Gly Gln Val Thr
 55 60 65

cat ctt cac gga aga aag tca gtc ttt gat gga cca acc gat gtg ctc 355
 His Leu His Gly Arg Lys Ser Val Phe Asp Gly Pro Thr Asp Val Leu
 70 75 80 85

tac ctc ccc act gga caa aca gca acg ctc agt ggt cag gga cga gtc 403
 Tyr Leu Pro Thr Gly Gln Thr Ala Thr Leu Ser Gly Gln Gly Arg Val
 90 95 100

gcc gtg gcg gaa gct ccc act cag gaa ccc aag gag tgg aag tac atc 451

Ala	Val	Ala	Glu	Ala	Pro	Thr	Gln	Glu	Pro	Lys	Glu	Trp	Lys	Tyr	Ile		
			105					110					115				
gct	cca	gca	gaa	act	cct	gtg	gag	ttg	cgt	gga	gct	ggc	cgc	tcg	agc	499	
Ala	Pro	Ala	Glu	Thr	Pro	Val	Glu	Leu	Arg	Gly	Ala	Gly	Arg	Ser	Ser		
			120				125					130					
cga	caa	gtc	cac	aac	ttt	ggc	acc	ccg	gaa	gct	ctc	gat	gct	gct	cga	547	
Arg	Gln	Val	His	Asn	Phe	Gly	Thr	Pro	Glu	Ala	Leu	Asp	Ala	Ala	Arg		
			135			140					145						
cta	atc	gtg	tgt	gaa	gta	atc	acc	cca	ggg	gaa	aac	tgg	agc	tct	tac	595	
Leu	Ile	Val	Cys	Glu	Val	Ile	Thr	Pro	Gly	Glu	Asn	Trp	Ser	Ser	Tyr		
					155					160					165		
cct	cca	cac	aag	cat	gat	gag	cac	atc	cca	gga	cac	gag	tcc	aag	ctg	643	
Pro	Pro	His	Lys	His	Asp	Glu	His	Ile	Pro	Gly	His	Glu	Ser	Lys	Leu		
				170				175						180			
gag	gaa	atc	tac	tac	ttc	gaa	agc	gcc	cca	tcg	cga	gtt	ggt	ggc	agg	691	
Glu	Glu	Ile	Tyr	Tyr	Phe	Glu	Ser	Ala	Pro	Ser	Arg	Val	Gly	Gly	Arg		
			185					190					195				
gcc	gaa	gca	gca	gaa	gga	gct	ttc	gga	atg	ttt	tcc	acc	tac	tcc	tca	739	
Ala	Glu	Ala	Ala	Glu	Gly	Ala	Phe	Gly	Met	Phe	Ser	Thr	Tyr	Ser	Ser		
			200				205					210					
cca	gcg	ggg	gag	atc	gat	atc	aac	gcc	atg	gtg	tac	agc	ggc	gat	atc	787	
Pro	Ala	Gly	Glu	Ile	Asp	Ile	Asn	Ala	Met	Val	Tyr	Ser	Gly	Asp	Ile		
			215			220					225						
gcg	cta	gtt	cct	ttc	gga	tac	cac	ggc	cct	gcc	gtg	gca	gca	cct	ggc	835	
Ala	Leu	Val	Pro	Phe	Gly	Tyr	His	Gly	Pro	Ala	Val	Ala	Ala	Pro	Gly		
					235					240					245		
tat	gac	ttg	tac	tac	ctc	aac	gtc	atg	gca	gga	cct	gat	ccg	gag	aga	883	
Tyr	Asp	Leu	Tyr	Tyr	Leu	Asn	Val	Met	Ala	Gly	Pro	Asp	Pro	Glu	Arg		
				250					255					260			
atc	tgg	ctg	att	aac	gat	gac	cca	gcg	cac	gcc	tgg	gtt	cga	gat	aca	931	
Ile	Trp	Leu	Ile	Asn	Asp	Asp	Pro	Ala	His	Ala	Trp	Val	Arg	Asp	Thr		
			265				270						275				
tgg	acc	ggg	caa	gca	ttt	gat	gat	cgc	ttg	cca	tat	gag	aac	gca	aac	979	
Trp	Thr	Gly	Gln	Ala	Phe	Asp	Asp	Arg	Leu	Pro	Tyr	Glu	Asn	Ala	Asn		
			280				285					290					
aag	gag	gga	taaaatttca	tggtgaaac	gaa											1011	
Lys	Glu	Gly															
			295														

<210> 154

<211> 296

<212> PRT

<213> Corynebacterium glutamicum

<400> 154

Met	Arg	Trp	Phe	His	Lys	Lys	Gly	Glu	Leu	Ala	Arg	Asp	Gly	Trp	Gln		
1				5					10					15			

Ser Val Val Asp Ala Thr Thr Pro Gly Trp Glu Tyr Thr Gly Ile Arg
 20 25 30
 Ile Ala Glu Leu Gly Ser Gly Glu Ser Leu Glu Leu Asn Asp Thr Gly
 35 40 45
 Val Glu Arg Ile Phe Ile Pro Leu Gln Gly Ser Phe Asp Val Ala His
 50 55 60
 His Gly Gln Val Thr His Leu His Gly Arg Lys Ser Val Phe Asp Gly
 65 70 75 80
 Pro Thr Asp Val Leu Tyr Leu Pro Thr Gly Gln Thr Ala Thr Leu Ser
 85 90 95
 Gly Gln Gly Arg Val Ala Val Ala Glu Ala Pro Thr Gln Glu Pro Lys
 100 105 110
 Glu Trp Lys Tyr Ile Ala Pro Ala Glu Thr Pro Val Glu Leu Arg Gly
 115 120 125
 Ala Gly Arg Ser Ser Arg Gln Val His Asn Phe Gly Thr Pro Glu Ala
 130 135 140
 Leu Asp Ala Ala Arg Leu Ile Val Cys Glu Val Ile Thr Pro Gly Glu
 145 150 155 160
 Asn Trp Ser Ser Tyr Pro Pro His Lys His Asp Glu His Ile Pro Gly
 165 170 175
 His Glu Ser Lys Leu Glu Glu Ile Tyr Tyr Phe Glu Ser Ala Pro Ser
 180 185 190
 Arg Val Gly Gly Arg Ala Glu Ala Ala Glu Gly Ala Phe Gly Met Phe
 195 200 205
 Ser Thr Tyr Ser Ser Pro Ala Gly Glu Ile Asp Ile Asn Ala Met Val
 210 215 220
 Tyr Ser Gly Asp Ile Ala Leu Val Pro Phe Gly Tyr His Gly Pro Ala
 225 230 235 240
 Val Ala Ala Pro Gly Tyr Asp Leu Tyr Tyr Leu Asn Val Met Ala Gly
 245 250 255
 Pro Asp Pro Glu Arg Ile Trp Leu Ile Asn Asp Asp Pro Ala His Ala
 260 265 270
 Trp Val Arg Asp Thr Trp Thr Gly Gln Ala Phe Asp Asp Arg Leu Pro
 275 280 285
 Tyr Glu Asn Ala Asn Lys Glu Gly
 290 295

<210> 155

<211> 964

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(964)

<223> FRXA00871

<400> 155

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gggaaaaggc gatcaccagc cggttggtcg acccagcaac ccacggtggc attaacctcg 60

gtttcccaca gaacgattaa ttgaaggaga gcacaggact atg cgt tgg ttc cat 115
                                         Met Arg Trp Phe His
                                         1                               5

aag aag ggc gaa ctg gcc cga gat ggt tgg caa agc gtt gtc gat gcc 163
Lys Lys Gly Glu Leu Ala Arg Asp Gly Trp Gln Ser Val Val Asp Ala
                        10                               15                               20

acc acc cca ggt tgg gaa tat acc ggc atc cgc att gcc gaa ctg ggc 211
Thr Thr Pro Gly Trp Glu Tyr Thr Gly Ile Arg Ile Ala Glu Leu Gly
                        25                               30                               35

agt ggt gaa tcg ctt gaa ctg aat gac act ggt gtg gaa cgc atc ttc 259
Ser Gly Glu Ser Leu Glu Leu Asn Asp Thr Gly Val Glu Arg Ile Phe
                        40                               45                               50

att cca ctt cag ggc agc ttc gat gtt gcc cac cat ggt cag gtg acc 307
Ile Pro Leu Gln Gly Ser Phe Asp Val Ala His His Gly Gln Val Thr
                        55                               60                               65

cat ctt cac gga aga aag tca gtc ttt gat gga cca acc gat gtg ctc 355
His Leu His Gly Arg Lys Ser Val Phe Asp Gly Pro Thr Asp Val Leu
                        70                               75                               80                               85

tac ctc ccc act gga caa aca gca acg ctc agt ggt cag gga cga gtc 403
Tyr Leu Pro Thr Gly Gln Thr Ala Thr Leu Ser Gly Gln Gly Arg Val
                        90                               95                               100

gcc gtg gcg gaa gct ccc act cag gaa ccc aag gag tgg aag tac atc 451
Ala Val Ala Glu Ala Pro Thr Gln Glu Pro Lys Glu Trp Lys Tyr Ile
                        105                               110                               115

gct cca gca gaa act cct gtg gag ttg cgt gga gct ggc cgc tcg agc 499
Ala Pro Ala Glu Thr Pro Val Glu Leu Arg Gly Ala Gly Arg Ser Ser
                        120                               125                               130

cga caa gtc cac aac ttt ggc acc ccg gaa gct ctc gat gct gct cga 547
Arg Gln Val His Asn Phe Gly Thr Pro Glu Ala Leu Asp Ala Ala Arg
                        135                               140                               145

cta atc gtg tgt gaa gta atc acc cca ggt gaa aac tgg agc tct tac 595
Leu Ile Val Cys Glu Val Ile Thr Pro Gly Glu Asn Trp Ser Ser Tyr
                        150                               155                               160                               165

cct cca cac aag cat gat gag cac atc cca gga cac gag tcc aag ctg 643
Pro Pro His Lys His Asp Glu His Ile Pro Gly His Glu Ser Lys Leu
                        170                               175                               180

gag gaa atc tac tac ttc gaa agc gcc cca tcg cga gtt ggt ggc agg 691
Glu Glu Ile Tyr Tyr Phe Glu Ser Ala Pro Ser Arg Val Gly Gly Arg
                        185                               190                               195

gcc gaa gca gca gaa gga gct ttc gga atg ttt tcc acc tac tcc tca 739
Ala Glu Ala Ala Glu Gly Ala Phe Gly Met Phe Ser Thr Tyr Ser Ser

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200	205	210	
cca gcg ggg gag atc gat atc aac gcc atg gtg tac agc ggc gat atc			787
Pro Ala Gly Glu Ile Asp Ile Asn Ala Met Val Tyr Ser Gly Asp Ile			
215	220	225	
gcg cta gtt cct ttc gga tac cac ggc cct gcc gtg gca gca cct ggc			835
Ala Leu Val Pro Phe Gly Tyr His Gly Pro Ala Val Ala Ala Pro Gly			
230	235	240	245
tat gac ttg tac tac ctc aac gtc atg gca gga cct gat ccg gag aga			883
Tyr Asp Leu Tyr Tyr Leu Asn Val Met Ala Gly Pro Asp Pro Glu Arg			
250	255	260	
atc tgg ctg att aac gat gac cca gcg cac gcc tgg gtt cga gat aca			931
Ile Trp Leu Ile Asn Asp Asp Pro Ala His Ala Trp Val Arg Asp Thr			
265	270	275	
tgg acc ggg caa gca ttt gat gat cgc ttg cca			964
Trp Thr Gly Gln Ala Phe Asp Asp Arg Leu Pro			
280	285		

<210> 156

<211> 288

<212> PRT

<213> Corynebacterium glutamicum

<400> 156

Met Arg Trp Phe His Lys Lys Gly Glu Leu Ala Arg Asp Gly Trp Gln			
1	5	10	15
Ser Val Val Asp Ala Thr Thr Pro Gly Trp Glu Tyr Thr Gly Ile Arg			
20	25	30	
Ile Ala Glu Leu Gly Ser Gly Glu Ser Leu Glu Leu Asn Asp Thr Gly			
35	40	45	
Val Glu Arg Ile Phe Ile Pro Leu Gln Gly Ser Phe Asp Val Ala His			
50	55	60	
His Gly Gln Val Thr His Leu His Gly Arg Lys Ser Val Phe Asp Gly			
65	70	75	80
Pro Thr Asp Val Leu Tyr Leu Pro Thr Gly Gln Thr Ala Thr Leu Ser			
85	90	95	
Gly Gln Gly Arg Val Ala Val Ala Glu Ala Pro Thr Gln Glu Pro Lys			
100	105	110	
Glu Trp Lys Tyr Ile Ala Pro Ala Glu Thr Pro Val Glu Leu Arg Gly			
115	120	125	
Ala Gly Arg Ser Ser Arg Gln Val His Asn Phe Gly Thr Pro Glu Ala			
130	135	140	
Leu Asp Ala Ala Arg Leu Ile Val Cys Glu Val Ile Thr Pro Gly Glu			
145	150	155	160
Asn Trp Ser Ser Tyr Pro Pro His Lys His Asp Glu His Ile Pro Gly			
165	170	175	

His Glu Ser Lys Leu Glu Glu Ile Tyr Tyr Phe Glu Ser Ala Pro Ser
 180 185 190

Arg Val Gly Gly Arg Ala Glu Ala Glu Gly Ala Phe Gly Met Phe
 195 200 205

Ser Thr Tyr Ser Ser Pro Ala Gly Glu Ile Asp Ile Asn Ala Met Val
 210 215 220

Tyr Ser Gly Asp Ile Ala Leu Val Pro Phe Gly Tyr His Gly Pro Ala
 225 230 235 240

Val Ala Ala Pro Gly Tyr Asp Leu Tyr Tyr Leu Asn Val Met Ala Gly
 245 250 255

Pro Asp Pro Glu Arg Ile Trp Leu Ile Asn Asp Asp Pro Ala His Ala
 260 265 270

Trp Val Arg Asp Thr Trp Thr Gly Gln Ala Phe Asp Asp Arg Leu Pro
 275 280 285

<210> 157
 <211> 373
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(373)
 <223> RXN02829

<400> 157
 tttttcgttt aatctcatat ttaaacacgt tccttttaat tggttttata aattgataaa 60

ctgaattcgt cagttaaagt gtatcgaaag gagactggac atg caa aaa aat att 115
 Met Gln Lys Asn Ile
 1 5

cta aaa agt ggc atc gaa att tct gaa ctt ggg tta ggt tgc atg agt 163
 Leu Lys Ser Gly Ile Glu Ile Ser Glu Leu Gly Leu Gly Cys Met Ser
 10 15 20

tta ggc aca gat tat aaa aaa gcg caa cca att att gaa agt gca att 211
 Leu Gly Thr Asp Tyr Lys Lys Ala Gln Pro Ile Ile Glu Ser Ala Ile
 25 30 35

gat aat ggt att acg tat ttt gat act gca gat att tac gat caa gga 259
 Asp Asn Gly Ile Thr Tyr Phe Asp Thr Ala Asp Ile Tyr Asp Gln Gly
 40 45 50

gtt aat gaa gaa att gtt ggt aaa gcc tta aaa aaa tat caa aat cgt 307
 Val Asn Glu Glu Ile Val Gly Lys Ala Leu Lys Lys Tyr Gln Asn Arg
 55 60 65

gat gac atc gtt atc gga act aaa gtt gga aat cga tta act gac gat 355
 Asp Asp Ile Val Ile Gly Thr Lys Val Gly Asn Arg Leu Thr Asp Asp

70 75 80 85 373
 gga cat atg acg tgg gat
 Gly His Met Thr Trp Asp
 90

<210> 158
 <211> 91
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 158
 Met Gln Lys Asn Ile Leu Lys Ser Gly Ile Glu Ile Ser Glu Leu Gly
 1 5 10 15
 Leu Gly Cys Met Ser Leu Gly Thr Asp Tyr Lys Lys Ala Gln Pro Ile
 20 25 30
 Ile Glu Ser Ala Ile Asp Asn Gly Ile Thr Tyr Phe Asp Thr Ala Asp
 35 40 45
 Ile Tyr Asp Gln Gly Val Asn Glu Glu Ile Val Gly Lys Ala Leu Lys
 50 55 60
 Lys Tyr Gln Asn Arg Asp Asp Ile Val Ile Gly Thr Lys Val Gly Asn
 65 70 75 80
 Arg Leu Thr Asp Asp Gly His Met Thr Trp Asp
 85 90

<210> 159
 <211> 376
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(376)
 <223> FRXA02829

<400> 159
 tttttcgttt aatctcatat ttaaacacgt tccttttaaat tggttttata aattgataaa 60
 ctgaattcgt cagttaaagt gtatcgaaag gagactggac atg caa aaa aat att 115
 Met Gln Lys Asn Ile
 1 5
 cta aaa agt ggc atc gaa att tct gaa ctt ggg tta ggt tgc atg agt 163
 Leu Lys Ser Gly Ile Glu Ile Ser Glu Leu Gly Leu Gly Cys Met Ser
 10 15 20
 tta ggc aca gat tat aaa aaa gcg caa cca att att gaa agt gca att 211
 Leu Gly Thr Asp Tyr Lys Lys Ala Gln Pro Ile Ile Glu Ser Ala Ile
 25 30 35
 gat aat ggt att acg tat ttt gat act gca gat att tac gat caa gga 259
 Asp Asn Gly Ile Thr Tyr Phe Asp Thr Ala Asp Ile Tyr Asp Gln Gly
 40 45 50

ggt aat gaa gaa att gtt ggt aaa gcc tta aaa aaa tat caa aat cgt 307
Val Asn Glu Glu Ile Val Gly Lys Ala Leu Lys Lys Tyr Gln Asn Arg
55 60 65

gat gac atc gtt atc gga act aaa gtt gga aat cga tta act gac gat 355
Asp Asp Ile Val Ile Gly Thr Lys Val Gly Asn Arg Leu Thr Asp Asp
70 75 80 85

gga cat atg acg tgg gga tcc 376
Gly His Met Thr Trp Gly Ser
90

<210> 160

<211> 92

<212> PRT

<213> Corynebacterium glutamicum

<400> 160

Met Gln Lys Asn Ile Leu Lys Ser Gly Ile Glu Ile Ser Glu Leu Gly
1 5 10 15

Leu Gly Cys Met Ser Leu Gly Thr Asp Tyr Lys Lys Ala Gln Pro Ile
20 25 30

Ile Glu Ser Ala Ile Asp Asn Gly Ile Thr Tyr Phe Asp Thr Ala Asp
35 40 45

Ile Tyr Asp Gln Gly Val Asn Glu Glu Ile Val Gly Lys Ala Leu Lys
50 55 60

Lys Tyr Gln Asn Arg Asp Asp Ile Val Ile Gly Thr Lys Val Gly Asn
65 70 75 80

Arg Leu Thr Asp Asp Gly His Met Thr Trp Gly Ser
85 90

<210> 161

<211> 948

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101) . . (925)

<223> RXN01468

<400> 161

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ttagcgggaa aatttcgcc aaaacaggga caatggtgtt atg aca gtg aac att 115
Met Thr Val Asn Ile
 1 5

tca tat ctg acc gac atg gac ggc gtc ctc atc aaa gag ggc gag ata 163
Ser Tyr Leu Thr Asp Met Asp Gly Val Leu Ile Lys Glu Gly Glu Ile
10 15 20

att ccg ggt gca gat cgt ttt ctt cag tct ctc acc gat aac aat gtg 211
Ile Pro Gly Ala Asp Arg Phe Leu Gln Ser Leu Thr Asp Asn Asn Val

25					30					35						
gag	ttt	atg	gtt	ttg	acc	aac	aac	tcc	att	ttc	acc	ccg	agg	gat	ctt	259
Glu	Phe	Met	Val	Leu	Thr	Asn	Asn	Ser	Ile	Phe	Thr	Pro	Arg	Asp	Leu	
		40					45					50				
tct	gca	cgt	ctt	aag	act	tcc	ggc	ttg	gat	atc	ccg	ccg	gag	cgt	att	307
Ser	Ala	Arg	Leu	Lys	Thr	Ser	Gly	Leu	Asp	Ile	Pro	Pro	Glu	Arg	Ile	
		55					60					65				
tg	act	tct	gca	acc	gcc	act	gct	cac	ttc	ctg	aaa	tcc	cag	gtc	aag	355
Trp	Thr	Ser	Ala	Thr	Ala	Thr	Ala	His	Phe	Leu	Lys	Ser	Gln	Val	Lys	
		70				75				80					85	
gag	ggc	aca	gcc	tat	gtt	gtt	ggc	gag	tcc	ggc	ctg	acc	act	gcg	ttg	403
Glu	Gly	Thr	Ala	Tyr	Val	Val	Gly	Glu	Ser	Gly	Leu	Thr	Thr	Ala	Leu	
				90					95					100		
cat	acc	gcg	ggc	ttg	att	ttg	acg	gat	gca	aat	cct	gag	ttt	gtt	gtc	451
His	Thr	Ala	Gly	Trp	Ile	Leu	Thr	Asp	Ala	Asn	Pro	Glu	Phe	Val	Val	
			105					110					115			
ctg	ggc	gaa	acc	cgc	aca	tat	tcc	ttc	gag	gca	atc	act	act	gcg	ata	499
Leu	Gly	Glu	Thr	Arg	Thr	Tyr	Ser	Phe	Glu	Ala	Ile	Thr	Thr	Ala	Ile	
		120					125					130				
aat	ctg	att	ttg	ggc	ggc	gct	cgc	ttt	att	tgc	acc	aac	ccg	gat	gtc	547
Asn	Leu	Ile	Leu	Gly	Gly	Ala	Arg	Phe	Ile	Cys	Thr	Asn	Pro	Asp	Val	
		135				140					145					
act	gga	cct	tca	cca	agt	ggc	att	ttg	cct	gct	act	ggc	tct	gtc	gcc	595
Thr	Gly	Pro	Ser	Pro	Ser	Gly	Ile	Leu	Pro	Ala	Thr	Gly	Ser	Val	Ala	
		150			155					160					165	
gca	ctt	att	acc	gca	gct	act	ggc	gct	gag	cct	tat	tac	atc	ggc	aag	643
Ala	Leu	Ile	Thr	Ala	Ala	Thr	Gly	Ala	Glu	Pro	Tyr	Tyr	Ile	Gly	Lys	
				170					175					180		
cca	aac	cct	gtg	atg	atg	cgc	agt	gcg	ctg	aac	acc	atc	ggg	gcg	cat	691
Pro	Asn	Pro	Val	Met	Met	Arg	Ser	Ala	Leu	Asn	Thr	Ile	Gly	Ala	His	
			185					190					195			
tcc	gag	cac	act	gtc	atg	atc	ggc	gac	cgc	atg	gac	acc	gac	gtg	aaa	739
Ser	Glu	His	Thr	Val	Met	Ile	Gly	Asp	Arg	Met	Asp	Thr	Asp	Val	Lys	
		200					205					210				
tct	ggc	ttg	gaa	gcc	ggc	ctg	agc	acc	gtg	ctg	gtt	cga	agc	gga	att	787
Ser	Gly	Leu	Glu	Ala	Gly	Leu	Ser	Thr	Val	Leu	Val	Arg	Ser	Gly	Ile	
		215				220					225					
tcc	gac	gac	gcc	gag	atc	cgc	cgc	tac	ccc	ttc	cgc	cca	act	cac	gtg	835
Ser	Asp	Asp	Ala	Glu	Ile	Arg	Arg	Tyr	Pro	Phe						

tagtattctg taggtcatgg cat

948

<210> 162

<211> 275

<212> PRT

<213> Corynebacterium glutamicum

<400> 162

Met Thr Val Asn Ile Ser Tyr Leu Thr Asp Met Asp Gly Val Leu Ile
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Lys Glu Gly Glu Ile Ile Pro Gly Ala Asp Arg Phe Leu Gln Ser Leu
 20 25 30

Thr Asp Asn Asn Val Glu Phe Met Val Leu Thr Asn Asn Ser Ile Phe
 35 40 45

Thr Pro Arg Asp Leu Ser Ala Arg Leu Lys Thr Ser Gly Leu Asp Ile
 50 55 60

Pro Pro Glu Arg Ile Trp Thr Ser Ala Thr Ala Thr Ala His Phe Leu
 65 70 75 80

Lys Ser Gln Val Lys Glu Gly Thr Ala Tyr Val Val Gly Glu Ser Gly
 85 90 95

Leu Thr Thr Ala Leu His Thr Ala Gly Trp Ile Leu Thr Asp Ala Asn
 100 105 110

Pro Glu Phe Val Val Leu Gly Glu Thr Arg Thr Tyr Ser Phe Glu Ala
 115 120 125

Ile Thr Thr Ala Ile Asn Leu Ile Leu Gly Gly Ala Arg Phe Ile Cys
 130 135 140

Thr Asn Pro Asp Val Thr Gly Pro Ser Pro Ser Gly Ile Leu Pro Ala
 145 150 155 160

Thr Gly Ser Val Ala Ala Leu Ile Thr Ala Ala Thr Gly Ala Glu Pro
 165 170 175

Tyr Tyr Ile Gly Lys Pro Asn Pro Val Met Met Arg Ser Ala Leu Asn
 180 185 190

Thr Ile Gly Ala His Ser Glu His Thr Val Met Ile Gly Asp Arg Met
 195 200 205

Asp Thr Asp Val Lys Ser Gly Leu Glu Ala Gly Leu Ser Thr Val Leu
 210 215 220

Val Arg Ser Gly Ile Ser Asp Asp Ala Glu Ile Arg Arg Tyr Pro Phe
 225 230 235 240

Arg Pro Thr His Val Ile Asn Ser Ile Ala Asp Leu Ala Asp Cys Trp
 245 250 255

Asp Asp Pro Phe Gly Asp Gly Ala Phe His Val Pro Asp Glu Gln Gln
 260 265 270

Phe Thr Asp
275

<210> 163
<211> 948
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(925)
<223> FRXA01468

<400> 163
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ttagcgggaa aatttcgccc aaaacagggga caatggtggt atg aca gtg aac att 115
Met Thr Val Asn Ile
1 5
tca tat ctg acc gac atg gac ggc gtc ctc atc aaa gag ggc gag ata 163
Ser Tyr Leu Thr Asp Met Asp Gly Val Leu Ile Lys Glu Gly Glu Ile
10 15 20
att ccg ggt gca gat cgt ttt ctt cag tct ctc acc gat aac aat gtg 211
Ile Pro Gly Ala Asp Arg Phe Leu Gln Ser Leu Thr Asp Asn Asn Val
25 30 35
gag ttt atg gtt ttg acc aac aac tcc att ttc acc ccg agg gat ctt 259
Glu Phe Met Val Leu Thr Asn Asn Ser Ile Phe Thr Pro Arg Asp Leu
40 45 50
tct gca cgt ctt aag act tcc ggt ttg gat atc ccg ccg gag cgt att 307
Ser Ala Arg Leu Lys Thr Ser Gly Leu Asp Ile Pro Pro Glu Arg Ile
55 60 65
tgg act tct gca acc gcc act gct cac ttc ctg aaa tcc cag gtc aag 355
Trp Thr Ser Ala Thr Ala Thr Ala His Phe Leu Lys Ser Gln Val Lys
70 75 80 85
gag ggc aca gcc tat gtt gtt ggc gag tcc ggt ctg acc act gcg ttg 403
Glu Gly Thr Ala Tyr Val Val Gly Glu Ser Gly Leu Thr Thr Ala Leu
90 95 100
cat acc gcg ggt tgg att ttg acg gat gca aat cct gag ttt gtt gtc 451
His Thr Ala Gly Trp Ile Leu Thr Asp Ala Asn Pro Glu Phe Val Val
105 110 115
ctg ggc gaa acc cgc aca tat tcc ttc gag gca atc act act gcg ata 499
Leu Gly Glu Thr Arg Thr Tyr Ser Phe Glu Ala Ile Thr Thr Ala Ile
120 125 130
aat ctg att ttg ggt ggc gct cgc ttt att tgc acc aac ccg gat gtc 547
Asn Leu Ile Leu Gly Gly Ala Arg Phe Ile Cys Thr Asn Pro Asp Val
135 140 145
act gga cct tca cca agt ggc att ttg cct gct act ggc tct gtc gcc 595
Thr Gly Pro Ser Pro Ser Gly Ile Leu Pro Ala Thr Gly Ser Val Ala
150 155 160 165

gca ctt att acc gca gct act ggc gct gag cct tat tac atc ggc aag 643
 Ala Leu Ile Thr Ala Ala Thr Gly Ala Glu Pro Tyr Tyr Ile Gly Lys
 170 175 180
 cca aac cct gtg atg atg cgc agt gcg ctg aac acc atc ggg gcg cat 691
 Pro Asn Pro Val Met Met Arg Ser Ala Leu Asn Thr Ile Gly Ala His
 185 190 195
 tcc gag cac act gtc atg atc ggc gac cgc atg gac acc gac gtg aaa 739
 Ser Glu His Thr Val Met Ile Gly Asp Arg Met Asp Thr Asp Val Lys
 200 205 210
 tct ggt ttg gaa gcc ggc ctg agc acc gtg ctg gtt cga agc gga att 787
 Ser Gly Leu Glu Ala Gly Leu Ser Thr Val Leu Val Arg Ser Gly Ile
 215 220 225
 tcc gac gac gcc gag atc cgc cgc tac ccc ttc cgc cca act cac gtg 835
 Ser Asp Asp Ala Glu Ile Arg Arg Tyr Pro Phe Arg Pro Thr His Val
 230 235 240 245
 atc aat tcc atc gcc gat ctt gcc gat tgc tgg gac gat cct ttc ggt 883
 Ile Asn Ser Ile Ala Asp Leu Ala Asp Cys Trp Asp Asp Pro Phe Gly
 250 255 260
 gac ggt gca ttt cac gta cca gat gag cag cag ttc act gac 925
 Asp Gly Ala Phe His Val Pro Asp Glu Gln Gln Phe Thr Asp
 265 270 275
 tagtattctg taggtcatgg cat 948

<210> 164

<211> 275

<212> PRT

<213> Corynebacterium glutamicum

<400> 164

Met Thr Val Asn Ile Ser Tyr Leu Thr Asp Met Asp Gly Val Leu Ile
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 Lys Glu Gly Glu Ile Ile Pro Gly Ala Asp Arg Phe Leu Gln Ser Leu
 20 25 30
 Thr Asp Asn Asn Val Glu Phe Met Val Leu Thr Asn Asn Ser Ile Phe
 35 40 45
 Thr Pro Arg Asp Leu Ser Ala Arg Leu Lys Thr Ser Gly Leu Asp Ile
 50 55 60
 Pro Pro Glu Arg Ile Trp Thr Ser Ala Thr Ala Thr Ala His Phe Leu
 65 70 75 80
 Lys Ser Gln Val Lys Glu Gly Thr Ala Tyr Val Val Gly Glu Ser Gly
 85 90 95
 Leu Thr Thr Ala Leu His Thr Ala Gly Trp Ile Leu Thr Asp Ala Asn
 100 105 110
 Pro Glu Phe Val Val Leu Gly Glu Thr Arg Thr Tyr Ser Phe Glu Ala
 115 120 125

Ile Thr Thr Ala Ile Asn Leu Ile Leu Gly Gly Ala Arg Phe Ile Cys
 130 135 140

Thr Asn Pro Asp Val Thr Gly Pro Ser Pro Ser Gly Ile Leu Pro Ala
 145 150 155 160

Thr Gly Ser Val Ala Ala Leu Ile Thr Ala Ala Thr Gly Ala Glu Pro
 165 170 175

Tyr Tyr Ile Gly Lys Pro Asn Pro Val Met Met Arg Ser Ala Leu Asn
 180 185 190

Thr Ile Gly Ala His Ser Glu His Thr Val Met Ile Gly Asp Arg Met
 195 200 205

Asp Thr Asp Val Lys Ser Gly Leu Glu Ala Gly Leu Ser Thr Val Leu
 210 215 220

Val Arg Ser Gly Ile Ser Asp Asp Ala Glu Ile Arg Arg Tyr Pro Phe
 225 230 235 240

Arg Pro Thr His Val Ile Asn Ser Ile Ala Asp Leu Ala Asp Cys Trp
 245 250 255

Asp Asp Pro Phe Gly Asp Gly Ala Phe His Val Pro Asp Glu Gln Gln
 260 265 270

Phe Thr Asp
 275

<210> 165

<211> 1128

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1105)

<223> RXA00794

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cgtaaccagg tcagatcaag tgccccagga ggcccttcag atg aac cta aag aac 115
 Met Asn Leu Lys Asn
 1 5

ccc gaa acg cca gac cgt aac ctt gct atg gag ctg gtg cga gtt acg 163
 Pro Glu Thr Pro Asp Arg Asn Leu Ala Met Glu Leu Val Arg Val Thr
 10 15 20

gaa gca gct gca ctg gct tct gga cgt tgg gtt gga cgt ggc atg aag 211
 Glu Ala Ala Ala Leu Ala Ser Gly Arg Trp Val Gly Arg Gly Met Lys
 25 30 35

aat gaa ggc gac ggt gcc gct gtt gac gcc atg cgc cag ctc atc aac 259
 Asn Glu Gly Asp Gly Ala Ala Val Asp Ala Met Arg Gln Leu Ile Asn
 40 45 50

tca gtg acc atg aag ggc gtc gtt gtt atc ggc gag ggc gaa aaa gac 307

Ser	Val	Thr	Met	Lys	Gly	Val	Val	Val	Ile	Gly	Glu	Gly	Glu	Lys	Asp		
	55					60					65						
gaa	gct	cca	atg	ctg	tac	aac	ggc	gaa	gag	gtc	gga	acc	ggc	ttt	gga	355	
Glu	Ala	Pro	Met	Leu	Tyr	Asn	Gly	Glu	Glu	Val	Gly	Thr	Gly	Phe	Gly		
	70				75					80					85		
cct	gag	gtt	gat	atc	gca	gtt	gac	cca	gtt	gac	ggc	acc	acc	ctg	atg	403	
Pro	Glu	Val	Asp	Ile	Ala	Val	Asp	Pro	Val	Asp	Gly	Thr	Thr	Leu	Met		
				90					95					100			
gct	gag	ggt	cgc	ccc	aac	gca	att	tcc	att	ctc	gca	gct	gca	gag	cgt	451	
Ala	Glu	Gly	Arg	Pro	Asn	Ala	Ile	Ser	Ile	Leu	Ala	Ala	Ala	Glu	Arg		
			105					110					115				
ggc	acc	atg	tac	gat	cca	tcc	tcc	gtc	ttc	tac	atg	aag	aag	atc	gcc	499	
Gly	Thr	Met	Tyr	Asp	Pro	Ser	Ser	Val	Phe	Tyr	Met	Lys	Lys	Ile	Ala		
	120						125					130					
gtg	gga	cct	gag	gcc	gca	ggc	aag	atc	gac	atc	gaa	gct	cca	gtt	gcc	547	
Val	Gly	Pro	Glu	Ala	Ala	Gly	Lys	Ile	Asp	Ile	Glu	Ala	Pro	Val	Ala		
	135					140					145						
cac	aac	atc	aac	gcg	gtg	gca	aag	tcc	aag	gga	atc	aac	cct	tcc	gac	595	
His	Asn	Ile	Asn	Ala	Val	Ala	Lys	Ser	Lys	Gly	Ile	Asn	Pro	Ser	Asp		
	150				155					160					165		
gtc	acc	gtt	gtc	gtg	ctt	gac	cgt	cct	cgc	cac	atc	gaa	ctg	atc	gca	643	
Val	Thr	Val	Val	Val	Leu	Asp	Arg	Pro	Arg	His	Ile	Glu	Leu	Ile	Ala		
				170					175					180			
gac	att	cgt	cgt	gca	ggc	gca	aag	gtt	cgt	ctc	atc	tcc	gac	ggc	gac	691	
Asp	Ile	Arg	Arg	Ala	Gly	Ala	Lys	Val	Arg	Leu	Ile	Ser	Asp	Gly	Asp		
			185					190					195				
gtt	gca	ggt	gca	gtt	gca	gca	gct	cag	gat	tcc	aac	tcc	gtg	gac	atc	739	
Val	Ala	Gly	Ala	Val	Ala	Ala	Ala	Gln	Asp	Ser	Asn	Ser	Val	Asp	Ile		
	200						205					210					
atg	atg	ggc	acc	ggc	gga	acc	cca	gaa	ggc	atc	atc	act	gcg	tgc	gcc	787	
Met	Met	Gly	Thr	Gly	Gly	Thr	Pro	Glu	Gly	Ile	Ile	Thr	Ala	Cys	Ala		
	215					220					225						
atg	aag	tgc	atg	ggt	ggc	gaa	atc	cag	ggc	atc	ctg	gcc	cca	atg	aac	835	
Met	Lys	Cys	Met	Gly	Gly	Glu	Ile	Gln	Gly	Ile	Leu	Ala	Pro	Met	Asn		
	230				235					240					245		
gat	ttc	gag	cgc	cag	aag	gca	cac	gac	gct	ggt	ctg	gtt	ctt	gat	cag	883	
Asp	Phe	Glu	Arg	Gln	Lys	Ala	His	Asp	Ala	Gly	Leu	Val	Leu	Asp	Gln		
				250					255				260				
gtt	ctg	cac	acc	aac	gat	ctg	gtg	agc	tcc	gac	aac	tgc	tac	ttc	gtg	931	
Val	Leu	His	Thr	Asn	Asp	Leu	Val	Ser	Ser	Asp	Asn	Cys	Tyr	Phe	Val		
			265					270				275					
gca	acc	ggt	gtg	acc	aac	ggt	gac	atg	ctc	cgt	ggc	gtt	tcc	tac	cgc	979	
Ala	Thr	Gly	Val	Thr	Asn	Gly	Asp	Met	Leu	Arg	Gly	Val	Ser	Tyr	Arg		
	280					285						290					
gca	aac	ggc	gca	acc	acc	cgt	tcc	ctg	gtt	atg	cgc	gca	aag	tca	ggc	1027	
Ala	Asn	Gly	Ala	Thr	Thr	Arg	Ser	Leu	Val	Met	Arg	Ala	Lys	Ser	Gly		

295 300 305

acc atc cgc cac atc gag tct gtc cac cag ctg tcc aag ctg cag gaa 1075
 Thr Ile Arg His Ile Glu Ser Val His Gln Leu Ser Lys Leu Gln Glu
 310 315 320 325

tac tcc gtg gtt gac tac acc acc gcg acc taagagctct tagttcgaaa 1125
 Tyr Ser Val Val Asp Tyr Thr Thr Ala Thr
 330 335

aac 1128

<210> 166

<211> 335

<212> PRT

<213> Corynebacterium glutamicum

<400> 166

Met Asn Leu Lys Asn Pro Glu Thr Pro Asp Arg Asn Leu Ala Met Glu
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Leu Val Arg Val Thr Glu Ala Ala Ala Leu Ala Ser Gly Arg Trp Val
 20 25 30

Gly Arg Gly Met Lys Asn Glu Gly Asp Gly Ala Ala Val Asp Ala Met
 35 40 45

Arg Gln Leu Ile Asn Ser Val Thr Met Lys Gly Val Val Val Ile Gly
 50 55 60

Glu Gly Glu Lys Asp Glu Ala Pro Met Leu Tyr Asn Gly Glu Glu Val
 65 70 75 80

Gly Thr Gly Phe Gly Pro Glu Val Asp Ile Ala Val Asp Pro Val Asp
 85 90 95

Gly Thr Thr Leu Met Ala Glu Gly Arg Pro Asn Ala Ile Ser Ile Leu
 100 105 110

Ala Ala Ala Glu Arg Gly Thr Met Tyr Asp Pro Ser Ser Val Phe Tyr
 115 120 125

Met Lys Lys Ile Ala Val Gly Pro Glu Ala Ala Gly Lys Ile Asp Ile
 130 135 140

Glu Ala Pro Val Ala His Asn Ile Asn Ala Val Ala Lys Ser Lys Gly
 145 150 155 160

Ile Asn Pro Ser Asp Val Thr Val Val Val Leu Asp Arg Pro Arg His
 165 170 175

Ile Glu Leu Ile Ala Asp Ile Arg Arg Ala Gly Ala Lys Val Arg Leu
 180 185 190

Ile Ser Asp Gly Asp Val Ala Gly Ala Val Ala Ala Gln Asp Ser
 195 200 205

Asn Ser Val Asp Ile Met Met Gly Thr Gly Gly Thr Pro Glu Gly Ile
 210 215 220

Ile Thr Ala Cys Ala Met Lys Cys Met Gly Gly Glu Ile Gln Gly Ile
 225 230 235 240

Leu Ala Pro Met Asn Asp Phe Glu Arg Gln Lys Ala His Asp Ala Gly
 245 250 255

Leu Val Leu Asp Gln Val Leu His Thr Asn Asp Leu Val Ser Ser Asp
 260 265 270

Asn Cys Tyr Phe Val Ala Thr Gly Val Thr Asn Gly Asp Met Leu Arg
 275 280 285

Gly Val Ser Tyr Arg Ala Asn Gly Ala Thr Thr Arg Ser Leu Val Met
 290 295 300

Arg Ala Lys Ser Gly Thr Ile Arg His Ile Glu Ser Val His Gln Leu
 305 310 315 320

Ser Lys Leu Gln Glu Tyr Ser Val Val Asp Tyr Thr Thr Ala Thr
 325 330 335

<210> 167
 <211> 1035
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1012)
 <223> RXN02920

<400> 167
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cgggtggcgt cgaaaagcat ttttaaagga gtttaagacg atg aag ttt gtt atg 115
 Met Lys Phe Val Met
 1 5

tat ccg cat ttg tgg gag tcc acg acc gct gtc att gag ggt ggc gga 163
 Tyr Pro His Leu Trp Glu Ser Thr Thr Ala Val Ile Glu Gly Gly Gly
 10 15 20

cat gag cgg gtt gag gat att aaa gat gca gac ttc att ttc ttt aat 211
 His Glu Arg Val Glu Asp Ile Lys Asp Ala Asp Phe Ile Phe Phe Asn
 25 30 35

ggt tca gcg ccg gag ttc ccg gat ttg ccg gag aac atc aag ttc gtg 259
 Gly Ser Ala Pro Glu Phe Pro Asp Leu Pro Glu Asn Ile Lys Phe Val
 40 45 50

cag gcc tcc atg gcg ggt att gat gcg ctg gtc aag cgt ggt gtc gtc 307
 Gln Ala Ser Met Ala Gly Ile Asp Ala Leu Val Lys Arg Gly Val Val
 55 60 65

aat gag aag gca cgt tgg gca aac gcg gct ggc ctg tac gct gac acc 355
 Asn Glu Lys Ala Arg Trp Ala Asn Ala Ala Gly Leu Tyr Ala Asp Thr
 70 75 80 85

gtt gct gag tcc acc att ggt tta att ctg gcg cag atg cac atg cat 403
 Val Ala Glu Ser Thr Ile Gly Leu Ile Leu Ala Gln Met His Met His

90										95					100					
gcg	acg	act	cgt	ttg	gct	aag	tcg	tgg	agc	gtg	cgg	cct	gag	gtg	gaa	451				
Ala	Thr	Thr	Arg	Leu	Ala	Lys	Ser	Trp	Ser	Val	Arg	Pro	Glu	Val	Glu					
			105					110					115							
aac	aac	aag	tca	tgg	ctg	cat	gac	aat	aaa	act	gtc	gct	att	ttg	ggc	499				
Asn	Asn	Lys	Ser	Trp	Leu	His	Asp	Asn	Lys	Thr	Val	Ala	Ile	Leu	Gly					
		120					125					130								
gdc	ggt	ggc	att	ggc	gtg	cgt	ctg	ctg	gaa	atg	ctc	aag	ccg	ttc	aac	547				
Ala	Gly	Gly	Ile	Gly	Val	Arg	Leu	Leu	Glu	Met	Leu	Lys	Pro	Phe	Asn					
	135					140					145									
gtg	aag	acc	att	gcg	gtt	aat	aac	tct	ggt	cgt	ccg	gtg	gaa	ggt	gca	595				
Val	Lys	Thr	Ile	Ala	Val	Asn	Asn	Ser	Gly	Arg	Pro	Val	Glu	Gly	Ala					
	150				155				160						165					
gat	gaa	acc	ttc	gcc	atg	gat	aag	gct	gag	cac	gtg	tgg	gct	gag	gct	643				
Asp	Glu	Thr	Phe	Ala	Met	Asp	Lys	Ala	Glu	His	Val	Trp	Ala	Glu	Ala					
				170					175						180					
gat	gtg	ttt	gtg	ctc	atc	ctg	ccg	ctg	act	gat	gcc	act	tat	cag	atc	691				
Asp	Val	Phe	Val	Leu	Ile	Leu	Pro	Leu	Thr	Asp	Ala	Thr	Tyr	Gln	Ile					
			185					190					195							
gtc	aat	gca	gaa	act	ttg	ggc	aag	atg	aag	cct	tct	gcc	gtg	gtg	gtc	739				
Val	Asn	Ala	Glu	Thr	Leu	Gly	Lys	Met	Lys	Pro	Ser	Ala	Val	Val	Val					
		200					205					210								
aat	gtg	ggg	cgt	ggc	ccg	ctg	atc	aac	acc	gat	gat	ctg	gtg	gat	gca	787				
Asn	Val	Gly	Arg	Gly	Pro	Leu	Ile	Asn	Thr	Asp	Asp	Leu	Val	Asp	Ala					
	215					220					225									
ttg	aac	aac	ggc	acc	att	gcg	ggt	gct	gcg	ctg	gac	gtt	acc	gat	cct	835				
Leu	Asn	Asn	Gly	Thr	Ile	Ala	Gly	Ala	Ala	Leu	Asp	Val	Thr	Asp	Pro					
	230				235					240					245					
gag	cca	ctt	cct	gac	agc	cac	ccg	ctg	tgg	gag	atg	gac	aat	gtg	gtt	883				
Glu	Pro	Leu	Pro	Asp	Ser	His	Pro	Leu	Trp	Glu	Met	Asp	Asn	Val	Val					
				250					255						260					
atc	act	cct	cat	act	gca	aac	acg	aat	gag	agg	att	cgt	gct	ttg	acc	931				
Ile	Thr	Pro	His	Thr	Ala	Asn	Thr	Asn	Glu	Arg	Ile	Arg	Ala	Leu	Thr					
			265					270					275							
ggc	gaa	ctc	acc	ttg	cgc	aac	att	gag	ttg	ttt	gag	gca	ggc	gag	cag	979				
Gly	Glu	Leu	Thr	Leu	Arg	Asn	Ile	Glu	Leu	Phe	Glu	Ala	Gly	Glu	Gln					
		280					285					290								
atg	gcc	acc	gag	gtc	gat	gtg	gtg	gct	ggc	tac	taggcctttt	atggtgtgat	1032							
Met	Ala	Thr	Glu	Val	Asp	Val	Val	Ala	Gly	Tyr										
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ccg																1035				

<210> 168

<211> 304

<212> PRT

<213> Corynebacterium glutamicum

<400> 168

Met Lys Phe Val Met Tyr Pro His Leu Trp Glu Ser Thr Thr Ala Val
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 Ile Glu Gly Gly Gly His Glu Arg Val Glu Asp Ile Lys Asp Ala Asp
 20 25 30
 Phe Ile Phe Phe Asn Gly Ser Ala Pro Glu Phe Pro Asp Leu Pro Glu
 35 40 45
 Asn Ile Lys Phe Val Gln Ala Ser Met Ala Gly Ile Asp Ala Leu Val
 50 55 60
 Lys Arg Gly Val Val Asn Glu Lys Ala Arg Trp Ala Asn Ala Ala Gly
 65 70 75 80
 Leu Tyr Ala Asp Thr Val Ala Glu Ser Thr Ile Gly Leu Ile Leu Ala
 85 90 95
 Gln Met His Met His Ala Thr Thr Arg Leu Ala Lys Ser Trp Ser Val
 100 105 110
 Arg Pro Glu Val Glu Asn Asn Lys Ser Trp Leu His Asp Asn Lys Thr
 115 120 125
 Val Ala Ile Leu Gly Ala Gly Gly Ile Gly Val Arg Leu Leu Glu Met
 130 135 140
 Leu Lys Pro Phe Asn Val Lys Thr Ile Ala Val Asn Asn Ser Gly Arg
 145 150 155 160
 Pro Val Glu Gly Ala Asp Glu Thr Phe Ala Met Asp Lys Ala Glu His
 165 170 175
 Val Trp Ala Glu Ala Asp Val Phe Val Leu Ile Leu Pro Leu Thr Asp
 180 185 190
 Ala Thr Tyr Gln Ile Val Asn Ala Glu Thr Leu Gly Lys Met Lys Pro
 195 200 205
 Ser Ala Val Val Val Asn Val Gly Arg Gly Pro Leu Ile Asn Thr Asp
 210 215 220
 Asp Leu Val Asp Ala Leu Asn Asn Gly Thr Ile Ala Gly Ala Ala Leu
 225 230 235 240
 Asp Val Thr Asp Pro Glu Pro Leu Pro Asp Ser His Pro Leu Trp Glu
 245 250 255
 Met Asp Asn Val Val Ile Thr Pro His Thr Ala Asn Thr Asn Glu Arg
 260 265 270
 Ile Arg Ala Leu Thr Gly Glu Leu Thr Leu Arg Asn Ile Glu Leu Phe
 275 280 285
 Glu Ala Gly Glu Gln Met Ala Thr Glu Val Asp Val Val Ala Gly Tyr
 290 295 300

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<210> 169
<211> 779
<212> DNA
<213> Corynebacterium glutamicum
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<220>
<221> CDS
<222> (52) .. (756)
<223> FRXA02379
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<400> 169																
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Met Arg																
1																
aag	cac	cgt	tgg	gca	aac	gcg	gct	ggc	ctg	tac	gct	gac	acc	gtt	gct	105
Lys	His	Arg	Trp	Ala	Asn	Ala	Ala	Gly	Leu	Tyr	Ala	Asp	Thr	Val	Ala	
5																
10																
15																
gag	tcc	acc	att	ggg	tta	att	ctg	gcg	cag	atg	cac	atg	cat	gcg	acg	153
Glu	Ser	Thr	Ile	Gly	Leu	Ile	Leu	Ala	Gln	Met	His	Met	His	Ala	Thr	
20																
25																
30																
act	cgt	ttg	gct	aag	tgc	tgg	agc	gtg	cgg	cct	gag	gtg	gaa	aac	aac	201
Thr	Arg	Leu	Ala	Lys	Ser	Trp	Ser	Val	Arg	Pro	Glu	Val	Glu	Asn	Asn	
35																
40																
45																
aag	tca	tgg	ctg	cat	gac	aat	aaa	act	gtc	gct	att	ttg	ggc	gcc	ggg	249
Lys	Ser	Trp	Leu	His	Asp	Asn	Lys	Thr	Val	Ala	Ile	Leu	Gly	Ala	Gly	
55																
60																
65																
ggc	att	ggc	gtg	cgt	ctg	ctg	gaa	atg	ctc	aag	ccg	ttc	aac	gtg	aag	297
Gly	Ile	Gly	Val	Arg	Leu	Leu	Glu	Met	Leu	Lys	Pro	Phe	Asn	Val	Lys	
70																
75																
80																
acc	att	gcg	gtt	aat	aac	tct	ggg	cgt	ccg	gtg	gaa	ggg	gca	gat	gaa	345
Thr	Ile	Ala	Val	Asn	Asn	Ser	Gly	Arg	Pro	Val	Glu	Gly	Ala	Asp	Glu	
85																
90																
95																
acc	ttc	gcc	atg	gat	aag	gct	gag	cac	gtg	tgg	gct	gag	gct	gat	gtg	393
Thr	Phe	Ala	Met	Asp	Lys	Ala	Glu	His	Val	Trp	Ala	Glu	Ala	Asp	Val	
100																
105																
110																
ttt	gtg	ctc	atc	ctg	ccg	ctg	act	gat	gcc	act	tat	cag	atc	gtc	aat	441
Phe	Val	Leu	Ile	Leu	Pro	Leu	Thr	Asp	Ala	Thr	Tyr	Gln	Ile	Val	Asn	
115																
120																
125																
gca	gaa	act	ttg	ggc	aag	atg	aag	cct	tct	gcc	gtg	gtg	gtc	aat	gtg	489
Ala	Glu	Thr	Leu	Gly	Lys	Met	Lys	Pro	Ser	Ala	Val	Val	Val	Asn	Val	
135																
140																
145																
ggg	cgt	ggc	ccg	ctg	atc	aac	acc	gat	gat	ctg	gtg	gat	gca	ttg	aac	537
Gly	Arg	Gly	Pro	Leu	Ile	Asn	Thr	Asp	Asp	Leu	Val	Asp	Ala	Leu	Asn	
150																
155																
160																
aac	ggc	acc	att	gcg	ggg	gct	gcg	ctg	gac	gtt	acc	gat	cct	gag	cca	585
Asn	Gly	Thr	Ile	Ala	Gly	Ala	Ala	Leu	Asp	Val	Thr	Asp	Pro	Glu	Pro	
165																
170																
175																

ctt cct gac agc cac ccg ctg tgg gag atg gac aat gtg gtt atc act 633
 Leu Pro Asp Ser His Pro Leu Trp Glu Met Asp Asn Val Val Ile Thr
 180 185 190

cct cat act gca aac acg aat gag agg att cgt gct ttg acc ggc gaa 681
 Pro His Thr Ala Asn Thr Asn Glu Arg Ile Arg Ala Leu Thr Gly Glu
 195 200 205 210

ctc acc ttg cgc aac att gag ttg ttt gag gca ggc gag cag atg gcc 729
 Leu Thr Leu Arg Asn Ile Glu Leu Phe Glu Ala Gly Glu Gln Met Ala
 215 220 225

acc gag gtc gat gtg gtg gct ggc tac taggcctttt atggtgtgat 776
 Thr Glu Val Asp Val Val Ala Gly Tyr
 230 235

ccg 779

<210> 170

<211> 235

<212> PRT

<213> Corynebacterium glutamicum

<400> 170

Met Arg Lys His Arg Trp Ala Asn Ala Ala Gly Leu Tyr Ala Asp Thr
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Val Ala Glu Ser Thr Ile Gly Leu Ile Leu Ala Gln Met His Met His
 20 25 30

Ala Thr Thr Arg Leu Ala Lys Ser Trp Ser Val Arg Pro Glu Val Glu
 35 40 45

Asn Asn Lys Ser Trp Leu His Asp Asn Lys Thr Val Ala Ile Leu Gly
 50 55 60

Ala Gly Gly Ile Gly Val Arg Leu Leu Glu Met Leu Lys Pro Phe Asn
 65 70 75 80

Val Lys Thr Ile Ala Val Asn Asn Ser Gly Arg Pro Val Glu Gly Ala
 85 90 95

Asp Glu Thr Phe Ala Met Asp Lys Ala Glu His Val Trp Ala Glu Ala
 100 105 110

Asp Val Phe Val Leu Ile Leu Pro Leu Thr Asp Ala Thr Tyr Gln Ile
 115 120 125

Val Asn Ala Glu Thr Leu Gly Lys Met Lys Pro Ser Ala Val Val Val
 130 135 140

Asn Val Gly Arg Gly Pro Leu Ile Asn Thr Asp Asp Leu Val Asp Ala
 145 150 155 160

Leu Asn Asn Gly Thr Ile Ala Gly Ala Ala Leu Asp Val Thr Asp Pro
 165 170 175

Glu Pro Leu Pro Asp Ser His Pro Leu Trp Glu Met Asp Asn Val Val
 180 185 190

Ile Thr Pro His Thr Ala Asn Thr Asn Glu Arg Ile Arg Ala Leu Thr
 195 200 205

Gly Glu Leu Thr Leu Arg Asn Ile Glu Leu Phe Glu Ala Gly Glu Gln
 210 215 220

Met Ala Thr Glu Val Asp Val Val Ala Gly Tyr
 225 230 235

<210> 171
 <211> 792
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(769)
 <223> RXN02688

<400> 171
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gggttcgcgc agcaagcgaa ggaaggaaac ttaactagcc atg gcc ggc cgg att 115
 Met Ala Gly Arg Ile
 1 5

att ttg cta cga cac ggg cag act cac aac aac gtc aaa cac ctc ctg 163
 Ile Leu Leu Arg His Gly Gln Thr His Asn Asn Val Lys His Leu Leu
 10 15 20

gac acc cgc cca cca gga gct gaa ctc acc gac ctg ggc cgt aaa caa 211
 Asp Thr Arg Pro Pro Gly Ala Glu Leu Thr Asp Leu Gly Arg Lys Gln
 25 30 35

gcc ctt gaa gtt ggc cac gaa cta gcc acc tac tcc ggt gag cgc ctc 259
 Ala Leu Glu Val Gly His Glu Leu Ala Thr Tyr Ser Gly Glu Arg Leu
 40 45 50

gcc cat gtg tac agc tcc atc gtg ttg cgc gcc caa caa acc gcc gtg 307
 Ala His Val Tyr Ser Ser Ile Val Leu Arg Ala Gln Gln Thr Ala Val
 55 60 65

ctt gcc acc tct acc ttt gaa aaa gct cgc gac atg cag tcc ggt gcg 355
 Leu Ala Thr Ser Thr Phe Glu Lys Ala Arg Asp Met Gln Ser Gly Ala
 70 75 80 85

att cca ctc gac gtt gtg gaa ggc att cag gaa atc aac gtc ggc gac 403
 Ile Pro Leu Asp Val Val Glu Gly Ile Gln Glu Ile Asn Val Gly Asp
 90 95 100

ttt gaa atg cgc ggc gat gaa gaa gcc cac atg aat tac tcc cgc gca 451
 Phe Glu Met Arg Gly Asp Glu Glu Ala His Met Asn Tyr Ser Arg Ala
 105 110 115

ctc aac ggc tgg ctt cac ggg gat cct gcc gct ggt ctt ccc ggc ggt 499
 Leu Asn Gly Trp Leu His Gly Asp Pro Ala Ala Gly Leu Pro Gly Gly
 120 125 130

gag acc tac aaa gac gtg ctg aac cgc tac cag ccg act ctt gat cga 547
 Glu Thr Tyr Lys Asp Val Leu Asn Arg Tyr Gln Pro Thr Leu Asp Arg

135	140	145	
atc atg gac agc cac gac ctt gac gac gac cgc gac gtt gcc gtt gtc			595
Ile Met Asp Ser His Asp Leu Asp Asp Asp Arg Asp Val Ala Val Val			
150	155	160	165
agc cac ggc gcc gtc atc cgc atc gtg gca aca cac gca act ggt gtg			643
Ser His Gly Ala Val Ile Arg Ile Val Ala Thr His Ala Thr Gly Val			
	170	175	180
gat ccc aac ttt gcg ttc aac acc tac ctg ggc aac tgc cgc ttc gtg			691
Asp Pro Asn Phe Ala Phe Asn Thr Tyr Leu Gly Asn Cys Arg Phe Val			
	185	190	195
gtg ctg gag cca aac ggt aag aaa ttc agc caa tgg gat gtt gtg cgc			739
Val Leu Glu Pro Asn Gly Lys Lys Phe Ser Gln Trp Asp Val Val Arg			
	200	205	210
tgg act gac agc cca ctg cca tgg cag gag taattgagac caaaggctcg			789
Trp Thr Asp Ser Pro Leu Pro Trp Gln Glu			
	215	220	
gat			792

<210> 172

<211> 223

<212> PRT

<213> Corynebacterium glutamicum

<400> 172

Met Ala Gly Arg Ile Ile Leu Leu Arg His Gly Gln Thr His Asn Asn		
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Val Lys His Leu Leu Asp Thr Arg Pro Pro Gly Ala Glu Leu Thr Asp		
	20	25
		30

Leu Gly Arg Lys Gln Ala Leu Glu Val Gly His Glu Leu Ala Thr Tyr		
	35	40
		45

Ser Gly Glu Arg Leu Ala His Val Tyr Ser Ser Ile Val Leu Arg Ala		
	50	55
		60

Gln Gln Thr Ala Val Leu Ala Thr Ser Thr Phe Glu Lys Ala Arg Asp		
	65	70
		75

Met Gln Ser Gly Ala Ile Pro Leu Asp Val Val Glu Gly Ile Gln Glu		
	85	90
		95

Ile Asn Val Gly Asp Phe Glu Met Arg Gly Asp Glu Glu Ala His Met		
	100	105
		110

Asn Tyr Ser Arg Ala Leu Asn Gly Trp Leu His Gly Asp Pro Ala Ala		
	115	120
		125

Gly Leu Pro Gly Gly Glu Thr Tyr Lys Asp Val Leu Asn Arg Tyr Gln		
	130	135
		140

Pro Thr Leu Asp Arg Ile Met Asp Ser His Asp Leu Asp Asp Asp Arg		
	145	150
		155
		160

20 25 30
 Ile Lys Leu Glu Ala Pro Ile Met Ala Pro Gly Pro Gly Ile Val Ala
 35 40 45
 Lys Val Ser Phe Asp Asp Phe Ser Asp Val Thr Gly Gly Asp Glu Leu
 50 55 60
 Leu Glu Leu Glu Ala Lys Asn
 65 70

 <210> 175
 <211> 310
 <212> DNA
 <213> *Corynebacterium glutamicum*

 <220>
 <221> CDS
 <222> (101)..(310)
 <223> RXN03186

 <400> 175
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 cgtataaacg aaataaaaca ttccaacagg aggtgtggaa atg gcc gat caa gca 115
 Met Ala Asp Gln Ala
 1 5
 aaa ctt ggt ggc aag ccc tcg gat gac tct aac ttc gcg atg atc cgc 163
 Lys Leu Gly Gly Lys Pro Ser Asp Asp Ser Asn Phe Ala Met Ile Arg
 10 15 20
 gat ggc gtg gca tct tat ttg aac gac tca gat ccg gag gag acc aac 211
 Asp Gly Val Ala Ser Tyr Leu Asn Asp Ser Asp Pro Glu Glu Thr Asn
 25 30 35
 gag tgg atg gat tca ctc gac gga tta ctc cag gag tct tct cca gaa 259
 Glu Trp Met Asp Ser Leu Asp Gly Leu Leu Gln Glu Ser Ser Pro Glu
 40 45 50
 cgt gct cgt tac ctc atg ctt cgt ttg ctt gag cgt gca tct gca aag 307
 Arg Ala Arg Tyr Leu Met Leu Arg Leu Leu Glu Arg Ala Ser Ala Lys
 55 60 65
 cgc 310
 Arg
 70

<210> 176
 <211> 70
 <212> PRT
 <213> *Corynebacterium glutamicum*

<400> 176
 Met Ala Asp Gln Ala Lys Leu Gly Gly Lys Pro Ser Asp Asp Ser Asn
 1 5 10 15
 Phe Ala Met Ile Arg Asp Gly Val Ala Ser Tyr Leu Asn Asp Ser Asp
 20 25 30

Pro Glu Glu Thr Asn Glu Trp Met Asp Ser Leu Asp Gly Leu Leu Gln
 35 40 45

Glu Ser Ser Pro Glu Arg Ala Arg Tyr Leu Met Leu Arg Leu Leu Glu
 50 55 60

Arg Ala Ser Ala Lys Arg
 65 70

<210> 177

<211> 302

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(279)

<223> RXN03187

<400> 177

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 Val Ala Val Ser Asp Phe Ser Thr Asp Leu Pro Asn Gln Ile Arg Glu
 1 5 10 15

tgg gtc cca ggc gac tac acc gtt ctc ggt gca gat ggc ttc ggt ttc 96
 Trp Val Pro Gly Asp Tyr Thr Val Leu Gly Ala Asp Gly Phe Gly Phe
 20 25 30

tct gat acc cgc cca gct gct cgt cgc ttc ttc aac atc gac gct gag 144
 Ser Asp Thr Arg Pro Ala Ala Arg Arg Phe Phe Asn Ile Asp Ala Glu
 35 40 45

tcc att gtt gtt gca gtg ctg aac tcc ctg gca cgc gaa ggc aag atc 192
 Ser Ile Val Val Ala Val Leu Asn Ser Leu Ala Arg Glu Gly Lys Ile
 50 55 60

gac gtc tcc gtt gct gct cag gct gct gag aag ttc aag ttg gat gat 240
 Asp Val Ser Val Ala Ala Gln Ala Ala Glu Lys Phe Lys Leu Asp Asp
 65 70 75 80

cct acg agt gtt tcc gta gat cca aac gct cct gag gaa taaatcacct 289
 Pro Thr Ser Val Ser Val Asp Pro Asn Ala Pro Glu Glu
 85 90

caagggacag ata 302

<210> 178

<211> 93

<212> PRT

<213> Corynebacterium glutamicum

<400> 178

Val Ala Val Ser Asp Phe Ser Thr Asp Leu Pro Asn Gln Ile Arg Glu
 1 5 10 15

Trp Val Pro Gly Asp Tyr Thr Val Leu Gly Ala Asp Gly Phe Gly Phe
 20 25 30

Ser Asp Thr Arg Pro Ala Ala Arg Arg Phe Phe Asn Ile Asp Ala Glu
 35 40 45

Ser Ile Val Val Ala Val Leu Asn Ser Leu Ala Arg Glu Gly Lys Ile
 50 55 60

Asp Val Ser Val Ala Ala Gln Ala Ala Glu Lys Phe Lys Leu Asp Asp
 65 70 75 80

Pro Thr Ser Val Ser Val Asp Pro Asn Ala Pro Glu Glu
 85 90

<210> 179
 <211> 1953
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1930)
 <223> RXN02591

<400> 179
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ggcgagaact ctgtcgaatg acacaaaatc tggagaagta atg act act gct gca 115
 Met Thr Thr Ala Ala
 1 5

atc agg ggc ctt cag ggc gag gcg ccg acc aag aat aag gaa ctg ctg 163
 Ile Arg Gly Leu Gln Gly Glu Ala Pro Thr Lys Asn Lys Glu Leu Leu
 10 15 20

aac tgg atc gca gac gcc gtc gag ctc ttc cag cct gag gct gtt gtg 211
 Asn Trp Ile Ala Asp Ala Val Glu Leu Phe Gln Pro Glu Ala Val Val
 25 30 35

ttc gtt gat gga tcc cag gct gag tgg gat cgc atg gcg gag gat ctt 259
 Phe Val Asp Gly Ser Gln Ala Glu Trp Asp Arg Met Ala Glu Asp Leu
 40 45 50

gtt gaa gcc ggt acc ctc atc aag ctc aac gag gaa aag cgt ccg aac 307
 Val Glu Ala Gly Thr Leu Ile Lys Leu Asn Glu Glu Lys Arg Pro Asn
 55 60 65

agc tac cta gct cgt tcc aac cca tct gac gtt gcg cgc gtt gag tcc 355
 Ser Tyr Leu Ala Arg Ser Asn Pro Ser Asp Val Ala Arg Val Glu Ser
 70 75 80 85

cgc acc ttc atc tgc tcc gag aag gaa gaa gat gct ggc cca acc aac 403
 Arg Thr Phe Ile Cys Ser Glu Lys Glu Glu Asp Ala Gly Pro Thr Asn
 90 95 100

aac tgg gct cca cca cag gca atg aag gac gaa atg tcc aag cat tac 451
 Asn Trp Ala Pro Pro Gln Ala Met Lys Asp Glu Met Ser Lys His Tyr
 105 110 115

gct ggt tcc atg aag ggg cgc acc atg tac gtc gtg cct ttc tgc atg 499
 Ala Gly Ser Met Lys Gly Arg Thr Met Tyr Val Val Pro Phe Cys Met
 120 125 130

ggt cca atc agc gat ccg gac cct aag ctt ggt gtg cag ctc act gac	547
Gly Pro Ile Ser Asp Pro Asp Pro Lys Leu Gly Val Gln Leu Thr Asp	
135 140 145	
tcc gag tac gtt gtc atg tcc atg cgc atc atg acc cgc atg ggt att	595
Ser Glu Tyr Val Val Met Ser Met Arg Ile Met Thr Arg Met Gly Ile	
150 155 160 165	
gaa gcg ctg gac aag atc ggc gcg aac ggc agc ttc gtc agg tgc ctc	643
Glu Ala Leu Asp Lys Ile Gly Ala Asn Gly Ser Phe Val Arg Cys Leu	
170 175 180	
cac tcc gtt ggt gct cct ttg gag cca ggc cag gaa gac gtt gca tgg	691
His Ser Val Gly Ala Pro Leu Glu Pro Gly Gln Glu Asp Val Ala Trp	
185 190 195	
cct tgc aac gac acc aag tac atc acc cag ttc cca gag acc aag gaa	739
Pro Cys Asn Asp Thr Lys Tyr Ile Thr Gln Phe Pro Glu Thr Lys Glu	
200 205 210	
att tgg tcc tac ggt tcc ggc tac ggc gga aac gca atc ctg gca aag	787
Ile Trp Ser Tyr Gly Ser Gly Tyr Gly Gly Asn Ala Ile Leu Ala Lys	
215 220 225	
aag tgc tac gca ctg cgt atc gca tct gtc atg gct cgc gaa gaa gga	835
Lys Cys Tyr Ala Leu Arg Ile Ala Ser Val Met Ala Arg Glu Glu Gly	
230 235 240 245	
tgg atg gct gag cac atg ctc atc ctg aag ctg atc aac cca gag ggc	883
Trp Met Ala Glu His Met Leu Ile Leu Lys Leu Ile Asn Pro Glu Gly	
250 255 260	
aag gcg tac cac atc gca gca gca ttc cca tct gct tgt ggc aag acc	931
Lys Ala Tyr His Ile Ala Ala Ala Phe Pro Ser Ala Cys Gly Lys Thr	
265 270 275	
aac ctc gcc atg atc act cca acc atc cca ggc tgg acc gct cag gtt	979
Asn Leu Ala Met Ile Thr Pro Thr Ile Pro Gly Trp Thr Ala Gln Val	
280 285 290	
gtt ggc gac gac atc gct tgg ctg aag ctg cgc gag gac ggc ctc tac	1027
Val Gly Asp Asp Ile Ala Trp Leu Lys Leu Arg Glu Asp Gly Leu Tyr	
295 300 305	
gca gtt aac cca gaa aat ggt ttc ttc ggt gtt gct cca ggc acc aac	1075
Ala Val Asn Pro Glu Asn Gly Phe Phe Gly Val Ala Pro Gly Thr Asn	
310 315 320 325	
tac gca tcc aac cca atc gcg atg aag acc atg gaa cca ggc aac acc	1123
Tyr Ala Ser Asn Pro Ile Ala Met Lys Thr Met Glu Pro Gly Asn Thr	
330 335 340	
ctg ttc acc aac gtg gca ctc acc gac gac ggc gac atc tgg tgg gaa	1171
Leu Phe Thr Asn Val Ala Leu Thr Asp Asp Gly Asp Ile Trp Trp Glu	
345 350 355	
ggc atg gac ggc gac gcc cca gct cac ctc att gac tgg atg ggc aac	1219
Gly Met Asp Gly Asp Ala Pro Ala His Leu Ile Asp Trp Met Gly Asn	
360 365 370	

gac tgg acc cca gag tcc gac gaa aac gct gct cac cct aac tcc cgt	1267
Asp Trp Thr Pro Glu Ser Asp Glu Asn Ala Ala His Pro Asn Ser Arg	
375 380 385	
tac tgc gta gca atc gac cag tcc cca gca gca gca cct gag ttc aac	1315
Tyr Cys Val Ala Ile Asp Gln Ser Pro Ala Ala Ala Pro Glu Phe Asn	
390 395 400 405	
gac tgg gaa ggc gtc aag atc gac gca atc ctc ttc ggt gga cgt cgc	1363
Asp Trp Glu Gly Val Lys Ile Asp Ala Ile Leu Phe Gly Gly Arg Arg	
410 415 420	
gca gac acc gtc cca ctg gtt acc cag acc tac gac tgg gag cac ggc	1411
Ala Asp Thr Val Pro Leu Val Thr Gln Thr Tyr Asp Trp Glu His Gly	
425 430 435	
acc atg gtt ggt gca ctg ctc gca tcc ggt cag acc gca gct tcc gca	1459
Thr Met Val Gly Ala Leu Leu Ala Ser Gly Gln Thr Ala Ala Ser Ala	
440 445 450	
gaa gca aag gtc ggc aca ctc cgc cac gac cca atg gca atg ctc cca	1507
Glu Ala Lys Val Gly Thr Leu Arg His Asp Pro Met Ala Met Leu Pro	
455 460 465	
ttc att ggc tac aac gct ggt gaa tac ctg cag aac tgg att gac atg	1555
Phe Ile Gly Tyr Asn Ala Gly Glu Tyr Leu Gln Asn Trp Ile Asp Met	
470 475 480 485	
ggt aac aag ggt ggc gac aag atg cca tcc atc ttc ctg gtc aac tgg	1603
Gly Asn Lys Gly Gly Asp Lys Met Pro Ser Ile Phe Leu Val Asn Trp	
490 495 500	
ttc cgc cgt ggc gaa gat gga cgc ttc ctg tgg cct ggc ttc ggc gac	1651
Phe Arg Arg Gly Glu Asp Gly Arg Phe Leu Trp Pro Gly Phe Gly Asp	
505 510 515	
aac tct cgc gtt ctg aag tgg gtc atc gac cgc atc gaa ggc cac gtt	1699
Asn Ser Arg Val Leu Lys Trp Val Ile Asp Arg Ile Glu Gly His Val	
520 525 530	
ggc gca gac gag acc gtt gtt gga cac acc gct aag gcc gaa gac ctc	1747
Gly Ala Asp Glu Thr Val Val Gly His Thr Ala Lys Ala Glu Asp Leu	
535 540 545	
gac ctc gac ggc ctc gac acc cca att gag gat gtc aag gaa gca ctg	1795
Asp Leu Asp Gly Leu Asp Thr Pro Ile Glu Asp Val Lys Glu Ala Leu	
550 555 560 565	
acc gct cct gca gag cag tgg gca aac gac gtt gaa gac aac gcc gag	1843
Thr Ala Pro Ala Glu Gln Trp Ala Asn Asp Val Glu Asp Asn Ala Glu	
570 575 580	
tac ctc act ttc ctc gga cca cgt gtt cct gca gag gtt cac agc cag	1891
Tyr Leu Thr Phe Leu Gly Pro Arg Val Pro Ala Glu Val His Ser Gln	
585 590 595	
ttc gat gct ctg aag gcc cgc att tca gca gct cac gct taaagttcac	1940
Phe Asp Ala Leu Lys Ala Arg Ile Ser Ala Ala His Ala	
600 605 610	
gcttaagaac tgc	1953

<210> 180

<211> 610

<212> PRT

<213> Corynebacterium glutamicum

<400> 180

Met Thr Thr Ala Ala Ile Arg Gly Leu Gln Gly Glu Ala Pro Thr Lys
 1 5 10 15

Asn Lys Glu Leu Leu Asn Trp Ile Ala Asp Ala Val Glu Leu Phe Gln
 20 25 30

Pro Glu Ala Val Val Phe Val Asp Gly Ser Gln Ala Glu Trp Asp Arg
 35 40 45

Met Ala Glu Asp Leu Val Glu Ala Gly Thr Leu Ile Lys Leu Asn Glu
 50 55 60

Glu Lys Arg Pro Asn Ser Tyr Leu Ala Arg Ser Asn Pro Ser Asp Val
 65 70 75 80

Ala Arg Val Glu Ser Arg Thr Phe Ile Cys Ser Glu Lys Glu Glu Asp
 85 90 95

Ala Gly Pro Thr Asn Asn Trp Ala Pro Pro Gln Ala Met Lys Asp Glu
 100 105 110

Met Ser Lys His Tyr Ala Gly Ser Met Lys Gly Arg Thr Met Tyr Val
 115 120 125

Val Pro Phe Cys Met Gly Pro Ile Ser Asp Pro Asp Pro Lys Leu Gly
 130 135 140

Val Gln Leu Thr Asp Ser Glu Tyr Val Val Met Ser Met Arg Ile Met
 145 150 155 160

Thr Arg Met Gly Ile Glu Ala Leu Asp Lys Ile Gly Ala Asn Gly Ser
 165 170 175

Phe Val Arg Cys Leu His Ser Val Gly Ala Pro Leu Glu Pro Gly Gln
 180 185 190

Glu Asp Val Ala Trp Pro Cys Asn Asp Thr Lys Tyr Ile Thr Gln Phe
 195 200 205

Pro Glu Thr Lys Glu Ile Trp Ser Tyr Gly Ser Gly Tyr Gly Gly Asn
 210 215 220

Ala Ile Leu Ala Lys Lys Cys Tyr Ala Leu Arg Ile Ala Ser Val Met
 225 230 235 240

Ala Arg Glu Glu Gly Trp Met Ala Glu His Met Leu Ile Leu Lys Leu
 245 250 255

Ile Asn Pro Glu Gly Lys Ala Tyr His Ile Ala Ala Ala Phe Pro Ser
 260 265 270

Ala Cys Gly Lys Thr Asn Leu Ala Met Ile Thr Pro Thr Ile Pro Gly
 275 280 285

Trp Thr Ala Gln Val Val Gly Asp Asp Ile Ala Trp Leu Lys Leu Arg
 290 295 300
 Glu Asp Gly Leu Tyr Ala Val Asn Pro Glu Asn Gly Phe Phe Gly Val
 305 310 315 320
 Ala Pro Gly Thr Asn Tyr Ala Ser Asn Pro Ile Ala Met Lys Thr Met
 325 330 335
 Glu Pro Gly Asn Thr Leu Phe Thr Asn Val Ala Leu Thr Asp Asp Gly
 340 345 350
 Asp Ile Trp Trp Glu Gly Met Asp Gly Asp Ala Pro Ala His Leu Ile
 355 360 365
 Asp Trp Met Gly Asn Asp Trp Thr Pro Glu Ser Asp Glu Asn Ala Ala
 370 375 380
 His Pro Asn Ser Arg Tyr Cys Val Ala Ile Asp Gln Ser Pro Ala Ala
 385 390 395 400
 Ala Pro Glu Phe Asn Asp Trp Glu Gly Val Lys Ile Asp Ala Ile Leu
 405 410 415
 Phe Gly Gly Arg Arg Ala Asp Thr Val Pro Leu Val Thr Gln Thr Tyr
 420 425 430
 Asp Trp Glu His Gly Thr Met Val Gly Ala Leu Leu Ala Ser Gly Gln
 435 440 445
 Thr Ala Ala Ser Ala Glu Ala Lys Val Gly Thr Leu Arg His Asp Pro
 450 455 460
 Met Ala Met Leu Pro Phe Ile Gly Tyr Asn Ala Gly Glu Tyr Leu Gln
 465 470 475 480
 Asn Trp Ile Asp Met Gly Asn Lys Gly Gly Asp Lys Met Pro Ser Ile
 485 490 495
 Phe Leu Val Asn Trp Phe Arg Arg Gly Glu Asp Gly Arg Phe Leu Trp
 500 505 510
 Pro Gly Phe Gly Asp Asn Ser Arg Val Leu Lys Trp Val Ile Asp Arg
 515 520 525
 Ile Glu Gly His Val Gly Ala Asp Glu Thr Val Val Gly His Thr Ala
 530 535 540
 Lys Ala Glu Asp Leu Asp Leu Asp Gly Leu Asp Thr Pro Ile Glu Asp
 545 550 555 560
 Val Lys Glu Ala Leu Thr Ala Pro Ala Glu Gln Trp Ala Asn Asp Val
 565 570 575
 Glu Asp Asn Ala Glu Tyr Leu Thr Phe Leu Gly Pro Arg Val Pro Ala
 580 585 590
 Glu Val His Ser Gln Phe Asp Ala Leu Lys Ala Arg Ile Ser Ala Ala
 595 600 605

His Ala
610

<210> 181
<211> 1305
<212> DNA
<213> *Corynebacterium glutamicum*

<220>
<221> CDS
<222> (101)..(1282)
<223> RXS01260

<400> 181
ctaaacgtgg gctgcattcc ttccaaagtc tctgatcaaa aacgctgaag ttgcccatac 60
ctttacccat gagaagaaga ccttcggcat caatggcgaa gtg acc ttc aac tat 115
Val Thr Phe Asn Tyr
1 5
gag gat gct cac aag cgt tcc cgt ggc gtt tcc gac aag atc gtt gga 163
Glu Asp Ala His Lys Arg Ser Arg Gly Val Ser Asp Lys Ile Val Gly
10 15 20
ggc gtt cat tac ttg atg aag aag aac aag atc atc gaa att cat ggt 211
Gly Val His Tyr Leu Met Lys Lys Asn Lys Ile Ile Glu Ile His Gly
25 30 35
ctt gga aac ttc aag gat gct aag act ctt gag gtc acc gac ggt aag 259
Leu Gly Asn Phe Lys Asp Ala Lys Thr Leu Glu Val Thr Asp Gly Lys
40 45 50
gat gct ggc aag acc atc acc ttt gat gac tgc atc atc gca acc ggt 307
Asp Ala Gly Lys Thr Ile Thr Phe Asp Asp Cys Ile Ile Ala Thr Gly
55 60 65
tcg gta gtc aac acc ctc cgt ggc gtt gac ttc tca gag aac gtt gtg 355
Ser Val Val Asn Thr Leu Arg Gly Val Asp Phe Ser Glu Asn Val Val
70 75 80 85
tct ttt gaa gag cag att ctt aac cct gtt gcg cca aag aag atg gtc 403
Ser Phe Glu Glu Gln Ile Leu Asn Pro Val Ala Pro Lys Lys Met Val
90 95 100
att gtt ggt gca ggc gca att gga atg gaa ttc gcc tac gtt ctt ggt 451
Ile Val Gly Ala Gly Ala Ile Gly Met Glu Phe Ala Tyr Val Leu Gly
105 110 115
aac tac ggt gta gat gta acc gtc atc gag ttc atg gat cgt gtg ctt 499
Asn Tyr Gly Val Asp Val Thr Val Ile Glu Phe Met Asp Arg Val Leu
120 125 130
cca aat gaa gat gct gaa gtc tcc aag gtt att gca aag gcc tac aag 547
Pro Asn Glu Asp Ala Glu Val Ser Lys Val Ile Ala Lys Ala Tyr Lys
135 140 145
aag atg ggc gtt aag ctt ctt cct ggc cat gca acc act gct gtt cgg 595
Lys Met Gly Val Lys Leu Leu Pro Gly His Ala Thr Thr Ala Val Arg
150 155 160 165

gac aac ggt gac ttt gtc gag gtt gat tac cag aag aag ggc tct gac	643
Asp Asn Gly Asp Phe Val Glu Val Asp Tyr Gln Lys Lys Gly Ser Asp	
170 175 180	
aag aca gag act ctt act gtt gat cga gtc atg gtt tcc gtt ggt ttc	691
Lys Thr Glu Thr Leu Thr Val Asp Arg Val Met Val Ser Val Gly Phe	
185 190 195	
cgt cca cgc gtt gag gga ttt ggt ctt gaa aac act ggc gtt aag ctc	739
Arg Pro Arg Val Glu Gly Phe Gly Leu Glu Asn Thr Gly Val Lys Leu	
200 205 210	
acc gag cgt ggc gca atc gag atc gat gat tac atg cgt acc aac gtc	787
Thr Glu Arg Gly Ala Ile Glu Ile Asp Asp Tyr Met Arg Thr Asn Val	
215 220 225	
gat ggc att tac gcc atc ggt gac gtg acc gcc aag ctt cag ctt gct	835
Asp Gly Ile Tyr Ala Ile Gly Asp Val Thr Ala Lys Leu Gln Leu Ala	
230 235 240 245	
cac gtc gca gaa gca cag ggc att gtt gcc gca gag act att gct ggt	883
His Val Ala Glu Ala Gln Gly Ile Val Ala Ala Glu Thr Ile Ala Gly	
250 255 260	
gca gaa act cag act ctt ggt gat tac atg atg atg cca cgt gca acc	931
Ala Glu Thr Gln Thr Leu Gly Asp Tyr Met Met Met Pro Arg Ala Thr	
265 270 275	
ttc tgc aac cca cag gtt tct tcc ttt ggt tac acc gaa gag cag gcc	979
Phe Cys Asn Pro Gln Val Ser Ser Phe Gly Tyr Thr Glu Glu Gln Ala	
280 285 290	
aag gag aag tgg cca gat cgt gag atc aag gtt gct tcc ttc cca ttc	1027
Lys Glu Lys Trp Pro Asp Arg Glu Ile Lys Val Ala Ser Phe Pro Phe	
295 300 305	
tct gca aac ggt aaa gca gtt ggc ctg gca gaa act gat ggt ttc gca	1075
Ser Ala Asn Gly Lys Ala Val Gly Leu Ala Glu Thr Asp Gly Phe Ala	
310 315 320 325	
aag atc gtt gct gat gca gaa ttc ggt gag ctg ctc ggt gca cac ctg	1123
Lys Ile Val Ala Asp Ala Glu Phe Gly Glu Leu Leu Gly Ala His Leu	
330 335 340	
gtt gga gca aat gca tca gag ctg atc aat gaa ttg gtg ctt gct cag	1171
Val Gly Ala Asn Ala Ser Glu Leu Ile Asn Glu Leu Val Leu Ala Gln	
345 350 355	
aac tgg gat ctc acc act gaa gag atc tct cgt agc gtc cat att cac	1219
Asn Trp Asp Leu Thr Thr Glu Glu Ile Ser Arg Ser Val His Ile His	
360 365 370	
cca acg cta tct gag gca gtt aag gaa gct gca cac ggt atc tct gga	1267
Pro Thr Leu Ser Glu Ala Val Lys Glu Ala Ala His Gly Ile Ser Gly	
375 380 385	
cac atg atc aac ttc tagaatccac ctgcttggcc ctg	1305
His Met Ile Asn Phe	
390	

<210> 182
 <211> 394
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 182

Val	Thr	Phe	Asn	Tyr	Glu	Asp	Ala	His	Lys	Arg	Ser	Arg	Gly	Val	Ser
1				5					10					15	
Asp	Lys	Ile	Val	Gly	Gly	Val	His	Tyr	Leu	Met	Lys	Lys	Asn	Lys	Ile
			20					25					30		
Ile	Glu	Ile	His	Gly	Leu	Gly	Asn	Phe	Lys	Asp	Ala	Lys	Thr	Leu	Glu
		35					40					45			
Val	Thr	Asp	Gly	Lys	Asp	Ala	Gly	Lys	Thr	Ile	Thr	Phe	Asp	Asp	Cys
	50					55					60				
Ile	Ile	Ala	Thr	Gly	Ser	Val	Val	Asn	Thr	Leu	Arg	Gly	Val	Asp	Phe
65					70					75					80
Ser	Glu	Asn	Val	Val	Ser	Phe	Glu	Glu	Gln	Ile	Leu	Asn	Pro	Val	Ala
			85						90					95	
Pro	Lys	Lys	Met	Val	Ile	Val	Gly	Ala	Gly	Ala	Ile	Gly	Met	Glu	Phe
			100					105					110		
Ala	Tyr	Val	Leu	Gly	Asn	Tyr	Gly	Val	Asp	Val	Thr	Val	Ile	Glu	Phe
		115					120					125			
Met	Asp	Arg	Val	Leu	Pro	Asn	Glu	Asp	Ala	Glu	Val	Ser	Lys	Val	Ile
	130					135					140				
Ala	Lys	Ala	Tyr	Lys	Lys	Met	Gly	Val	Lys	Leu	Leu	Pro	Gly	His	Ala
145					150					155					160
Thr	Thr	Ala	Val	Arg	Asp	Asn	Gly	Asp	Phe	Val	Glu	Val	Asp	Tyr	Gln
			165						170					175	
Lys	Lys	Gly	Ser	Asp	Lys	Thr	Glu	Thr	Leu	Thr	Val	Asp	Arg	Val	Met
			180					185					190		
Val	Ser	Val	Gly	Phe	Arg	Pro	Arg	Val	Glu	Gly	Phe	Gly	Leu	Glu	Asn
		195					200					205			
Thr	Gly	Val	Lys	Leu	Thr	Glu	Arg	Gly	Ala	Ile	Glu	Ile	Asp	Asp	Tyr
	210					215					220				
Met	Arg	Thr	Asn	Val	Asp	Gly	Ile	Tyr	Ala	Ile	Gly	Asp	Val	Thr	Ala
225					230					235					240
Lys	Leu	Gln	Leu	Ala	His	Val	Ala	Glu	Ala	Gln	Gly	Ile	Val	Ala	Ala
			245						250					255	
Glu	Thr	Ile	Ala	Gly	Ala	Glu	Thr	Gln	Thr	Leu	Gly	Asp	Tyr	Met	Met
		260						265					270		
Met	Pro	Arg	Ala	Thr	Phe	Cys	Asn	Pro	Gln	Val	Ser	Ser	Phe	Gly	Tyr
		275					280					285			
Thr	Glu	Glu	Gln	Ala	Lys	Glu	Lys	Trp	Pro	Asp	Arg	Glu	Ile	Lys	Val

290	295	300
Ala Ser Phe Pro Phe Ser Ala Asn Gly Lys Ala Val Gly Leu Ala Glu		
305	310	315 320
Thr Asp Gly Phe Ala Lys Ile Val Ala Asp Ala Glu Phe Gly Glu Leu		
	325	330 335
Leu Gly Ala His Leu Val Gly Ala Asn Ala Ser Glu Leu Ile Asn Glu		
	340	345 350
Leu Val Leu Ala Gln Asn Trp Asp Leu Thr Thr Glu Glu Ile Ser Arg		
	355	360 365
Ser Val His Ile His Pro Thr Leu Ser Glu Ala Val Lys Glu Ala Ala		
	370	375 380
His Gly Ile Ser Gly His Met Ile Asn Phe		
385	390	

<210> 183
 <211> 294
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(271)
 <223> RXS01261

<400> 183
 gtgggtgttt ttcattttct tccactctaa aattaagtat ggaaaaccaa ccgcacccgg 60
 atgcacgaca atgaccact aaacacgtat ccttgaatgc gtg act gaa cat tat 115
 Val Thr Glu His Tyr
 1 5
 gac gta gta gta ctc gga gcc ggc ccc ggt ggc tat gtc tcc gcc atc 163
 Asp Val Val Val Leu Gly Ala Gly Pro Gly Gly Tyr Val Ser Ala Ile
 10 15 20
 cgt gca gcg cag ctt ggc aag aag gtt gct gta att gag aag cag tac 211
 Arg Ala Ala Gln Leu Gly Lys Lys Val Ala Val Ile Glu Lys Gln Tyr
 25 30 35
 tgg ggt ggt gtt tgc cta aac gtg ggc tgc att cct tcc aaa gtc tct 259
 Trp Gly Gly Val Cys Leu Asn Val Gly Cys Ile Pro Ser Lys Val Ser
 40 45 50
 gat caa aaa cgc tgaagttgcc cataccttta ccc 294
 Asp Gln Lys Arg
 55

<210> 184
 <211> 57
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 184

Val Thr Glu His Tyr Asp Val Val Val Leu Gly Ala Gly Pro Gly Gly
 1 5 10 15
 Tyr Val Ser Ala Ile Arg Ala Ala Gln Leu Gly Lys Lys Val Ala Val
 20 25 30
 Ile Glu Lys Gln Tyr Trp Gly Gly Val Cys Leu Asn Val Gly Cys Ile
 35 40 45
 Pro Ser Lys Val Ser Asp Gln Lys Arg
 50 55

<210> 185

<211> 1650

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1627)

<223> RXA02640

<400> 185

accaacgacg acgccgtgt agcagatgta ttggagtggg ggttctaata ggtgggtgta 60
 aaacactgct tagtggccca atacgtgcaa aaataaggcc atg aga atc tca aag 115
 Met Arg Ile Ser Lys
 1 5
 gcc aat gcg tat gtt gca gcg att gac caa ggc acc act tcc act cgg 163
 Ala Asn Ala Tyr Val Ala Ala Ile Asp Gln Gly Thr Thr Ser Thr Arg
 10 15 20
 tgc atc ttc att gat gcc caa gga aaa gtg gtg tct tct gct tcc aag 211
 Cys Ile Phe Ile Asp Ala Gln Gly Lys Val Val Ser Ser Ala Ser Lys
 25 30 35
 gag cac cgc caa atc ttc cca caa cag ggc tgg gta gag cac gat cct 259
 Glu His Arg Gln Ile Phe Pro Gln Gln Gly Trp Val Glu His Asp Pro
 40 45 50
 gaa gaa att tgg gac aac att cga tct gtc gtc agc cag gcg atg gtc 307
 Glu Glu Ile Trp Asp Asn Ile Arg Ser Val Val Ser Gln Ala Met Val
 55 60 65
 tcc att gac atc acc cca cac gag gtt gca tcg ctg gga gtc acc aac 355
 Ser Ile Asp Ile Thr Pro His Glu Val Ala Ser Leu Gly Val Thr Asn
 70 75 80 85
 cag cgc gaa acc acc gtg gtg tgg gac aag cac acc ggc gaa cct gtc 403
 Gln Arg Glu Thr Thr Val Val Trp Asp Lys His Thr Gly Glu Pro Val
 90 95 100
 tac aac gca atc gtg tgg caa gac acc cgc acc tct gac att tgc cta 451
 Tyr Asn Ala Ile Val Trp Gln Asp Thr Arg Thr Ser Asp Ile Cys Leu
 105 110 115
 gag atc gcg ggc gaa gaa ggc cag gaa aag tgg ctt gac cgc acc ggc 499
 Glu Ile Ala Gly Glu Glu Gly Gln Glu Lys Trp Leu Asp Arg Thr Gly
 120 125 130

ctg ctg atc aac tcc tac cca tcg ggg ccc aaa atc aag tgg att ctc	547
Leu Leu Ile Asn Ser Tyr Pro Ser Gly Pro Lys Ile Lys Trp Ile Leu	
135 140 145	
gac aac gtt gag gga gct cgc gaa cgc gcc gaa aag ggc gac ctt ttg	595
Asp Asn Val Glu Gly Ala Arg Glu Arg Ala Glu Lys Gly Asp Leu Leu	
150 155 160 165	
ttt ggc acc atg gat acc tgg gtg ctg tgg aac ctg acc ggc ggt gtc	643
Phe Gly Thr Met Asp Thr Trp Val Leu Trp Asn Leu Thr Gly Gly Val	
170 175 180	
cgc ggc gac gac ggt gat gat gcc atc cac gtc acc gat gtc acc aac	691
Arg Gly Asp Asp Gly Asp Asp Ala Ile His Val Thr Asp Val Thr Asn	
185 190 195	
gca tcc cgc aca cta ttg atg gat ctc cgc acg caa cag tgg gat cca	739
Ala Ser Arg Thr Leu Leu Met Asp Leu Arg Thr Gln Gln Trp Asp Pro	
200 205 210	
gaa cta tgc gaa gcc cta gac att ccg atg tcc atg ctc cct gag att	787
Glu Leu Cys Glu Ala Leu Asp Ile Pro Met Ser Met Leu Pro Glu Ile	
215 220 225	
cgt ccc tcc gtc gga gaa ttc cgc tcc gtg cgc cac cgc gga acc cta	835
Arg Pro Ser Val Gly Glu Phe Arg Ser Val Arg His Arg Gly Thr Leu	
230 235 240 245	
gcc gac gtc ccg att act ggc gtg ctc ggc gac cag caa gcg gcc ctt	883
Ala Asp Val Pro Ile Thr Gly Val Leu Gly Asp Gln Gln Ala Ala Leu	
250 255 260	
ttt ggt cag ggc gga ttc cac gaa ggt gct gct aaa aat acc tac ggc	931
Phe Gly Gln Gly Gly Phe His Glu Gly Ala Ala Lys Asn Thr Tyr Gly	
265 270 275	
acc ggc ctc ttc ctg ctg atg aac acc ggc acc tcg ttg aag att tcc	979
Thr Gly Leu Phe Leu Leu Met Asn Thr Gly Thr Ser Leu Lys Ile Ser	
280 285 290	
gag cac ggc ctg ctg tcc acc atc gcc tat caa cgg gaa gga tcc gct	1027
Glu His Gly Leu Leu Ser Thr Ile Ala Tyr Gln Arg Glu Gly Ser Ala	
295 300 305	
ccg gtc tac gcg ctg gaa ggt tcc gta tcc atg ggc ggt tcc ttg gtg	1075
Pro Val Tyr Ala Leu Glu Gly Ser Val Ser Met Gly Gly Ser Leu Val	
310 315 320 325	
cag tgg ctg cgc gac aac cta cag cta atc ccc aac gca cca gcg att	1123
Gln Trp Leu Arg Asp Asn Leu Gln Leu Ile Pro Asn Ala Pro Ala Ile	
330 335 340	
gaa aac ctc gcc cga gaa gtc gaa gac aac ggt ggc gtt cat gtt gtc	1171
Glu Asn Leu Ala Arg Glu Val Glu Asp Asn Gly Gly Val His Val Val	
345 350 355	
cca gca ttc acc gga ctg ttc gca cca cgt tgg cgc ccc gat gct cgt	1219
Pro Ala Phe Thr Gly Leu Phe Ala Pro Arg Trp Arg Pro Asp Ala Arg	
360 365 370	

ggc gtc att aca ggc ctc acc cgt ttt gcc aac cgc aaa cac atc gcc 1267
 Gly Val Ile Thr Gly Leu Thr Arg Phe Ala Asn Arg Lys His Ile Ala
 375 380 385

cgc gca gtc ctt gaa gcc aac gcc ttc caa acc cgc gaa gtt gtg gac 1315
 Arg Ala Val Leu Glu Ala Asn Ala Phe Gln Thr Arg Glu Val Val Asp
 390 395 400 405

gcc atg gcc aaa gac gca ggc aaa gcc ctc gaa tcc ctc cgc gtc gac 1363
 Ala Met Ala Lys Asp Ala Gly Lys Ala Leu Glu Ser Leu Arg Val Asp
 410 415 420

ggt gcg atg gtg gaa aat gac ctc ctc atg caa atg caa gcc gac ttc 1411
 Gly Ala Met Val Glu Asn Asp Leu Leu Met Gln Met Gln Ala Asp Phe
 425 430 435

ctc ggc atc gac gtc caa cgt ctc gag gac gta gaa acc acc gcc gtc 1459
 Leu Gly Ile Asp Val Gln Arg Leu Glu Asp Val Glu Thr Thr Ala Val
 440 445 450

ggc gtc gca ttc gct gca ggt ctc ggc tct gga ttc ttc aaa aca act 1507
 Gly Val Ala Phe Ala Ala Gly Leu Gly Ser Gly Phe Phe Lys Thr Thr
 455 460 465

gac gag atc gaa aaa ctt att gca gtg aag aaa gtc tgg aac cct gac 1555
 Asp Glu Ile Glu Lys Leu Ile Ala Val Lys Lys Val Trp Asn Pro Asp
 470 475 480 485

atg agc gaa gaa gag cgc gaa cgt cgc tat gcc gaa tgg aat agg gca 1603
 Met Ser Glu Glu Glu Arg Glu Arg Arg Tyr Ala Glu Trp Asn Arg Ala
 490 495 500

gtg gag cat tct tat gac cag gcc tagctgattt gggtcggcct tta 1650
 Val Glu His Ser Tyr Asp Gln Ala
 505

<210> 186

<211> 509

<212> PRT

<213> Corynebacterium glutamicum

<400> 186

Met Arg Ile Ser Lys Ala Asn Ala Tyr Val Ala Ala Ile Asp Gln Gly
1 5 10 15

Thr Thr Ser Thr Arg Cys Ile Phe Ile Asp Ala Gln Gly Lys Val Val
20 25 30

Ser Ser Ala Ser Lys Glu His Arg Gln Ile Phe Pro Gln Gln Gly Trp
35 40 45

Val Glu His Asp Pro Glu Glu Ile Trp Asp Asn Ile Arg Ser Val Val
50 55 60

Ser Gln Ala Met Val Ser Ile Asp Ile Thr Pro His Glu Val Ala Ser
65 70 75 80

Leu Gly Val Thr Asn Gln Arg Glu Thr Thr Val Val Trp Asp Lys His
85 90 95

Thr Gly Glu Pro Val Tyr Asn Ala Ile Val Trp Gln Asp Thr Arg Thr
 100 105 110
 Ser Asp Ile Cys Leu Glu Ile Ala Gly Glu Glu Gly Gln Glu Lys Trp
 115 120 125
 Leu Asp Arg Thr Gly Leu Leu Ile Asn Ser Tyr Pro Ser Gly Pro Lys
 130 135 140
 Ile Lys Trp Ile Leu Asp Asn Val Glu Gly Ala Arg Glu Arg Ala Glu
 145 150 155 160
 Lys Gly Asp Leu Leu Phe Gly Thr Met Asp Thr Trp Val Leu Trp Asn
 165 170 175
 Leu Thr Gly Gly Val Arg Gly Asp Asp Gly Asp Asp Ala Ile His Val
 180 185 190
 Thr Asp Val Thr Asn Ala Ser Arg Thr Leu Leu Met Asp Leu Arg Thr
 195 200 205
 Gln Gln Trp Asp Pro Glu Leu Cys Glu Ala Leu Asp Ile Pro Met Ser
 210 215 220
 Met Leu Pro Glu Ile Arg Pro Ser Val Gly Glu Phe Arg Ser Val Arg
 225 230 235 240
 His Arg Gly Thr Leu Ala Asp Val Pro Ile Thr Gly Val Leu Gly Asp
 245 250 255
 Gln Gln Ala Ala Leu Phe Gly Gln Gly Gly Phe His Glu Gly Ala Ala
 260 265 270
 Lys Asn Thr Tyr Gly Thr Gly Leu Phe Leu Leu Met Asn Thr Gly Thr
 275 280 285
 Ser Leu Lys Ile Ser Glu His Gly Leu Leu Ser Thr Ile Ala Tyr Gln
 290 295 300
 Arg Glu Gly Ser Ala Pro Val Tyr Ala Leu Glu Gly Ser Val Ser Met
 305 310 315 320
 Gly Gly Ser Leu Val Gln Trp Leu Arg Asp Asn Leu Gln Leu Ile Pro
 325 330 335
 Asn Ala Pro Ala Ile Glu Asn Leu Ala Arg Glu Val Glu Asp Asn Gly
 340 345 350
 Gly Val His Val Val Pro Ala Phe Thr Gly Leu Phe Ala Pro Arg Trp
 355 360 365
 Arg Pro Asp Ala Arg Gly Val Ile Thr Gly Leu Thr Arg Phe Ala Asn
 370 375 380
 Arg Lys His Ile Ala Arg Ala Val Leu Glu Ala Asn Ala Phe Gln Thr
 385 390 395 400
 Arg Glu Val Val Asp Ala Met Ala Lys Asp Ala Gly Lys Ala Leu Glu
 405 410 415
 Ser Leu Arg Val Asp Gly Ala Met Val Glu Asn Asp Leu Leu Met Gln

420	425	430
Met Gln Ala Asp Phe Leu Gly Ile Asp Val Gln Arg Leu Glu Asp Val		
435	440	445
Glu Thr Thr Ala Val Gly Val Ala Phe Ala Ala Gly Leu Gly Ser Gly		
450	455	460
Phe Phe Lys Thr Thr Asp Glu Ile Glu Lys Leu Ile Ala Val Lys Lys		
465	470	475
Val Trp Asn Pro Asp Met Ser Glu Glu Glu Arg Glu Arg Arg Tyr Ala		
485	490	495
Glu Trp Asn Arg Ala Val Glu His Ser Tyr Asp Gln Ala		
500	505	

<210> 187
 <211> 1119
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1096)
 <223> RXN01025

<400> 187
 gggcagcagc ggcaggtttc caggaggttt ccatgctgggt ggcttgggac atgggctaac 60
 ctgagacggt taaatatcgt ttctgaaagg tgggtttcgc gtg gtt tct gta agc 115
 Val Val Ser Val Ser
 1 5
 gtg atg ggt gca ggt tcc tgg gga acc acg ttg gcc aag gtc ttc tct 163
 Val Met Gly Ala Gly Ser Trp Gly Thr Thr Leu Ala Lys Val Phe Ser
 10 15 20
 gat gct ggc aac gct gtg acg ttg tgg gcg agg cgg gaa gag ttg gca 211
 Asp Ala Gly Asn Ala Val Thr Leu Trp Ala Arg Arg Glu Glu Leu Ala
 25 30 35
 agc acc atc cgt gac agc cat gaa aac cgt gat tac ctt ccg ggg att 259
 Ser Thr Ile Arg Asp Ser His Glu Asn Arg Asp Tyr Leu Pro Gly Ile
 40 45 50
 acg ttg ccg gag tcg ctg cag gtc aca tca tcg gca acg gag gct tta 307
 Thr Leu Pro Glu Ser Leu Gln Val Thr Ser Ser Ala Thr Glu Ala Leu
 55 60 65
 gag ggc gca gcc att gtg gtg ttg gcg att cct tcg cag gcg ttg cgt 355
 Glu Gly Ala Ala Ile Val Val Leu Ala Ile Pro Ser Gln Ala Leu Arg
 70 75 80 85
 ggc aat ttg gcg gag tgg aaa gag acg atc ccg cag gat gcg acc ttg 403
 Gly Asn Leu Ala Glu Trp Lys Glu Thr Ile Pro Gln Asp Ala Thr Leu
 90 95 100
 gtg tcc ttg gct aaa ggt att gaa aag ggc acg cac ctg cgg atg agt 451
 Val Ser Leu Ala Lys Gly Ile Glu Lys Gly Thr His Leu Arg Met Ser

105						110						115						
gaa	gtg	atc	gcg	gag	gtg	acg	gaa	gcg	gat	cct	tca	cgc	atc	gcg	gtg	499		
Glu	Val	Ile	Ala	Glu	Val	Thr	Glu	Ala	Asp	Pro	Ser	Arg	Ile	Ala	Val			
120						125						130						
ttg	tcg	ggg	cca	aac	ctt	gct	cgt	gag	atc	gcg	gag	ggg	cag	cct	gca	547		
Leu	Ser	Gly	Pro	Asn	Leu	Ala	Arg	Glu	Ile	Ala	Glu	Gly	Gln	Pro	Ala			
135						140						145						
gct	acg	gtg	att	gct	tgc	cct	gat	gaa	aac	cga	gcg	aaa	ctt	gtg	cag	595		
Ala	Thr	Val	Ile	Ala	Cys	Pro	Asp	Glu	Asn	Arg	Ala	Lys	Leu	Val	Gln			
150						155						160						165
gct	gca	gtg	gct	gcg	ccg	tat	ttc	cgc	ccg	tac	acc	aac	act	gat	gtg	643		
Ala	Ala	Val	Ala	Ala	Pro	Tyr	Phe	Arg	Pro	Tyr	Thr	Asn	Thr	Asp	Val			
170						175						180						
gtg	ggc	act	gaa	atc	ggg	ggg	gcg	tgt	aag	aac	gtc	atc	gcg	ctg	gcc	691		
Val	Gly	Thr	Glu	Ile	Gly	Gly	Ala	Cys	Lys	Asn	Val	Ile	Ala	Leu	Ala			
185						190						195						
tgt	ggg	att	tcc	cat	ggg	tac	ggc	ctg	ggg	gag	aac	acc	aat	gca	tcg	739		
Cys	Gly	Ile	Ser	His	Gly	Tyr	Gly	Leu	Gly	Glu	Asn	Thr	Asn	Ala	Ser			
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ttg	att	act	cgt	ggc	ctt	gca	gag	atc	gca	cgc	ctc	ggg	gcc	aca	ttg	787		
Leu	Ile	Thr	Arg	Gly	Leu	Ala	Glu	Ile	Ala	Arg	Leu	Gly	Ala	Thr	Leu			
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ggg	gcg	gat	gcg	aag	act	ttt	tct	ggc	ctt	gcg	gga	atg	ggc	gac	ttg	835		
Gly	Ala	Asp	Ala	Lys	Thr	Phe	Ser	Gly	Leu	Ala	Gly	Met	Gly	Asp	Leu			
230						235						240						245
gtg	gct	acg	tgt	tca	tca	ccg	ctg	tcg	cgt	aac	cgc	agc	ttc	ggg	gag	883		
Val	Ala	Thr	Cys	Ser	Ser	Pro	Leu	Ser	Arg	Asn	Arg	Ser	Phe	Gly	Glu			
250						255						260						
cgt	ttg	ggg	cag	ggg	gaa	tcc	cta	gag	aag	gct	cgc	gag	gca	acc	aat	931		
Arg	Leu	Gly	Gln	Gly	Glu	Ser	Leu	Glu	Lys	Ala	Arg	Glu	Ala	Thr	Asn			
265						270						275						
ggg	cag	ggt	gcg	gag	ggg	ggt	att	tcc	tcg	cag	tcg	att	ttt	gat	ctt	979		
Gly	Gln	Val	Ala	Glu	Gly	Val	Ile	Ser	Ser	Gln	Ser	Ile	Phe	Asp	Leu			
280						285						290						
gcc	acc	aag	ctt	ggg	gtg	gag	atg	ccg	atc	acc	cag	gct	gtc	tac	ggg	1027		
Ala	Thr	Lys	Leu	Gly	Val	Glu	Met	Pro	Ile	Thr	Gln	Ala	Val	Tyr	Gly			
295						300						305						
gtg	tgc	cac	cga	gat	atg	aaa	gta	act	gac	atg	att	gtg	gct	ctc	atg	1075		
Val	Cys	His	Arg	Asp	Met	Lys	Val	Thr	Asp	Met	Ile	Val	Ala	Leu	Met			
310						315						320						325
ggg	agg	tct	aag	aag	gct	gag	tagtcttagg	ttgtaagctt	caa							1119		
Gly	Arg	Ser	Lys	Lys	Ala	Glu												
330																		

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<211> 332

<212> PRT

<213> Corynebacterium glutamicum

<400> 188

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 20 25 30
 Arg Glu Glu Leu Ala Ser Thr Ile Arg Asp Ser His Glu Asn Arg Asp
 35 40 45
 Tyr Leu Pro Gly Ile Thr Leu Pro Glu Ser Leu Gln Val Thr Ser Ser
 50 55 60
 Ala Thr Glu Ala Leu Glu Gly Ala Ala Ile Val Val Leu Ala Ile Pro
 65 70 75 80
 Ser Gln Ala Leu Arg Gly Asn Leu Ala Glu Trp Lys Glu Thr Ile Pro
 85 90 95
 Gln Asp Ala Thr Leu Val Ser Leu Ala Lys Gly Ile Glu Lys Gly Thr
 100 105 110
 His Leu Arg Met Ser Glu Val Ile Ala Glu Val Thr Glu Ala Asp Pro
 115 120 125
 Ser Arg Ile Ala Val Leu Ser Gly Pro Asn Leu Ala Arg Glu Ile Ala
 130 135 140
 Glu Gly Gln Pro Ala Ala Thr Val Ile Ala Cys Pro Asp Glu Asn Arg
 145 150 155 160
 Ala Lys Leu Val Gln Ala Ala Val Ala Ala Pro Tyr Phe Arg Pro Tyr
 165 170 175
 Thr Asn Thr Asp Val Val Gly Thr Glu Ile Gly Gly Ala Cys Lys Asn
 180 185 190
 Val Ile Ala Leu Ala Cys Gly Ile Ser His Gly Tyr Gly Leu Gly Glu
 195 200 205
 Asn Thr Asn Ala Ser Leu Ile Thr Arg Gly Leu Ala Glu Ile Ala Arg
 210 215 220
 Leu Gly Ala Thr Leu Gly Ala Asp Ala Lys Thr Phe Ser Gly Leu Ala
 225 230 235 240
 Gly Met Gly Asp Leu Val Ala Thr Cys Ser Ser Pro Leu Ser Arg Asn
 245 250 255
 Arg Ser Phe Gly Glu Arg Leu Gly Gln Gly Glu Ser Leu Glu Lys Ala
 260 265 270
 Arg Glu Ala Thr Asn Gly Gln Val Ala Glu Gly Val Ile Ser Ser Gln
 275 280 285
 Ser Ile Phe Asp Leu Ala Thr Lys Leu Gly Val Glu Met Pro Ile Thr
 290 295 300

Gln Ala Val Tyr Gly Val Cys His Arg Asp Met Lys Val Thr Asp Met
305 310 315 320

Ile Val Ala Leu Met Gly Arg Ser Lys Lys Ala Glu
325 330

<210> 189

<211> 1015

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1015)

<223> FRXA01025

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Val Val Ser Val Ser
1 5

gtg atg ggt gca ggt tcc tgg gga acc acg ttg gcc aag gtc ttc tct 163
Val Met Gly Ala Gly Ser Trp Gly Thr Thr Leu Ala Lys Val Phe Ser
10 15 20

gat gct ggc aac gct gtg acg ttg tgg gcg agg cgg gaa gag ttg gca 211
Asp Ala Gly Asn Ala Val Thr Leu Trp Ala Arg Arg Glu Glu Leu Ala
25 30 35

agc acc atc cgt gac agc cat gaa aac cgt gat tac ctt ccg ggg att 259
Ser Thr Ile Arg Asp Ser His Glu Asn Arg Asp Tyr Leu Pro Gly Ile
40 45 50

acg ttg ccg gag tcg ctg cag gtc aca tca tcg gca acg gag gct tta 307
Thr Leu Pro Glu Ser Leu Gln Val Thr Ser Ser Ala Thr Glu Ala Leu
55 60 65

gag ggc gca gcc att gtg gtg ttg gcg att cct tcg cag gcg ttg cgt 355
Glu Gly Ala Ala Ile Val Val Leu Ala Ile Pro Ser Gln Ala Leu Arg
70 75 80 85

ggc aat ttg gcg gag tgg aaa gag acg atc ccg cag gat gcg acc ttg 403
Gly Asn Leu Ala Glu Trp Lys Glu Thr Ile Pro Gln Asp Ala Thr Leu
90 95 100

gtg tcc ttg gct aaa ggt att gaa aag ggc acg cac ctg cgg atg agt 451
Val Ser Leu Ala Lys Gly Ile Glu Lys Gly Thr His Leu Arg Met Ser
105 110 115

gaa gtg atc gcg gag gtg acg gaa gcg gat cct tca cgc atc gcg gtg 499
Glu Val Ile Ala Glu Val Thr Glu Ala Asp Pro Ser Arg Ile Ala Val
120 125 130

ttg tcg ggg cca aac ctt gct cgt gag atc gcg gag ggg cag cct gca 547
Leu Ser Gly Pro Asn Leu Ala Arg Glu Ile Ala Glu Gly Gln Pro Ala
135 140 145

gct acg gtg att gct tgc cct gat gaa aac cga gcg aaa ctt gtg cag 595

Ala Thr Val Ile Ala Cys Pro Asp Glu Asn Arg Ala Lys Leu Val Gln
 150 155 160 165

gct gca gtg gct gcg ccg tat ttc cgc ccg tac acc aac act gat gtg 643
 Ala Ala Val Ala Ala Pro Tyr Phe Arg Pro Tyr Thr Asn Thr Asp Val
 170 175 180

gtg ggc act gaa atc ggt ggt gcg tgt aag aac gtc atc gcg ctg gcc 691
 Val Gly Thr Glu Ile Gly Gly Ala Cys Lys Asn Val Ile Ala Leu Ala
 185 190 195

tgt ggt att tcc cat ggt tac ggc ctg ggt gag aac acc aat gca tcg 739
 Cys Gly Ile Ser His Gly Tyr Gly Leu Gly Glu Asn Thr Asn Ala Ser
 200 205 210

ttg att act cgt ggc ctt gca gag atc gca cgc ctc ggt gcc aca ttg 787
 Leu Ile Thr Arg Gly Leu Ala Glu Ile Ala Arg Leu Gly Ala Thr Leu
 215 220 225

ggt gcg gat gcg aag act ttt tct ggc ctt gcg gga atg ggc gac ttg 835
 Gly Ala Asp Ala Lys Thr Phe Ser Gly Leu Ala Gly Met Gly Asp Leu
 230 235 240 245

gtg gct acg tgt tca tca ccg ctg tcg cgt aac cgc agc ttc ggt gag 883
 Val Ala Thr Cys Ser Ser Pro Leu Ser Arg Asn Arg Ser Phe Gly Glu
 250 255 260

cgt ttg ggt cag ggt gaa tcc cta gag aag gct cgc gag gca acc aat 931
 Arg Leu Gly Gln Gly Glu Ser Leu Glu Lys Ala Arg Glu Ala Thr Asn
 265 270 275

ggt cag gtt gcg gag ggt gtt att tcc tcg cag tcg att ttt gat ctt 979
 Gly Gln Val Ala Glu Gly Val Ile Ser Ser Gln Ser Ile Phe Asp Leu
 280 285 290

gcc acc aag ctt ggt gtg gag atg ccg atc acc cag 1015
 Ala Thr Lys Leu Gly Val Glu Met Pro Ile Thr Gln
 295 300 305

<210> 190

<211> 305

<212> PRT

<213> Corynebacterium glutamicum

<400> 190

Val Val Ser Val Ser Val Met Gly Ala Gly Ser Trp Gly Thr Thr Leu
 1 5 10 15

Ala Lys Val Phe Ser Asp Ala Gly Asn Ala Val Thr Leu Trp Ala Arg
 20 25 30

Arg Glu Glu Leu Ala Ser Thr Ile Arg Asp Ser His Glu Asn Arg Asp
 35 40 45

Tyr Leu Pro Gly Ile Thr Leu Pro Glu Ser Leu Gln Val Thr Ser Ser
 50 55 60

Ala Thr Glu Ala Leu Glu Gly Ala Ala Ile Val Val Leu Ala Ile Pro
 65 70 75 80

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<211> 1809
<212> DNA
<213> Corynebacterium glutamicum
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<222> (101)..(1786)  
<223> RXA01851
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Met Thr Ser Ala His
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ttt gaa tcc cgc cgg att ggc cct ccg ctt cgc gat aat tat gac gtc																	163
Phe Glu Ser Arg Arg Ile Gly Pro Pro Leu Arg Asp Asn Tyr Asp Val																	
										10		15		20			
att gtg att ggc ggt ggt atc tca ggt gta cag att gcg cga cat gct																	211
Ile Val Ile Gly Gly Gly Ile Ser Gly Val Gln Ile Ala Arg His Ala																	
										25		30		35			
caa ggc cgc ggt tta cgc act gtg atg ttt gag gcc aga gat tat tct																	259
Gln Gly Arg Gly Leu Arg Thr Val Met Phe Glu Ala Arg Asp Tyr Ser																	
										40		45		50			
tct gga aca tca tcg aca acc tcc aag atg att cat ggt ggt ttg cgc																	307
Ser Gly Thr Ser Ser Thr Thr Ser Lys Met Ile His Gly Gly Leu Arg																	
										55		60		65			
tat ttg gag cag tac gat ttc ggc gtg gtc cag gaa gcc gtg aag gaa																	355
Tyr Leu Glu Gln Tyr Asp Phe Gly Val Val Gln Glu Ala Val Lys Glu																	
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cgc cgg tac cta ggt atc gcc gct ccg cat ttg gtg gct cca cgc agt																	403
Arg Arg Tyr Leu Gly Ile Ala Ala Pro His Leu Val Ala Pro Arg Ser																	
										90		95		100			
ttc atg ctc acg gcg ttt gat tgg tca gag ccg aaa gcc cct atg ttg																	451
Phe Met Leu Thr Ala Phe Asp Trp Ser Glu Pro Lys Ala Pro Met Leu																	
										105		110		115			
ggt gct ggt gtg gcg ttg tat gaa acg atg gcg tgg cag cgt aac cag																	499
Gly Ala Gly Val Ala Leu Tyr Glu Thr Met Ala Trp Gln Arg Asn Gln																	
										120		125		130			
ggg caa tcg aag gaa aac cac tcg ccg cgt ttc cgg tgg att cct aaa																	547
Gly Gln Ser Lys Glu Asn His Ser Pro Arg Phe Arg Trp Ile Pro Lys																	
										135		140		145			
aat gca ctg ctc aag gaa gtc ccg tgg ctt gac ccg gag ggc ttg aag																	595
Asn Ala Leu Leu Lys Glu Val Pro Trp Leu Asp Pro Glu Gly Leu Lys																	
										150		155		160		165	
gga gcg tgg cgc cac gat gat acg ttg aat ctc cat gca gaa cga ctc																	643
Gly Ala Trp Arg His Asp Asp Thr Leu Asn Leu His Ala Glu Arg Leu																	
										170		175		180			
ctc ctc gcg gtg att aaa gct ttt gcg gca gat ggc gga acg gcg atc																	691
Leu Leu Ala Val Ile Lys Ala Phe Ala Ala Asp Gly Gly Thr Ala Ile																	
										185		190		195			
aac cac gcc aaa gtc act cgc att ctc cgg aac gtg gaa gaa ggc cgc																	739
Asn His Ala Lys Val Thr Arg Ile Leu Arg Asn Val Glu Glu Gly Arg																	
										200		205		210			
gtc aag ggt gta gaa gtg act gat cag gtc acc aac acc acg cat gag																	787
Val Lys Gly Val Glu Val Thr Asp Gln Val Thr Asn Thr Thr His Glu																	
										215		220		225			
gtg aat gcc cct gtg gtg atc aac gct gcg ggt ccg tgg gtt gcg cag																	835
Val Asn Ala Pro Val Val Ile Asn Ala Ala Gly Pro Trp Val Ala Gln																	
										230		235		240		245	

gcg ttg ggt gat ttg gcg gag gta acc aag ttg aag gtg cgc caa tcc 883
 Ala Leu Gly Asp Leu Ala Glu Val Thr Lys Leu Lys Val Arg Gln Ser
 250 255 260

aag gga gtg cat ttg ctc act ggt gat ttg ggc agc cag agt ggc gtg 931
 Lys Gly Val His Leu Leu Thr Gly Asp Leu Gly Ser Gln Ser Gly Val
 265 270 275

ttt gtg cgt ggc aaa aac ggc aag cat gtg atc gtg aat ccg tgg atg 979
 Phe Val Arg Gly Lys Asn Gly Lys His Val Ile Val Asn Pro Trp Met
 280 285 290

ggg cgc acc ctt att ggt cca acc gac acc atg att gac ggt gac gct 1027
 Gly Arg Thr Leu Ile Gly Pro Thr Asp Thr Met Ile Asp Gly Asp Ala
 295 300 305

gat gat gcg gct gca gat gaa agc gat atc gat ttg ctg ctt gag acc 1075
 Asp Asp Ala Ala Ala Asp Glu Ser Asp Ile Asp Leu Leu Leu Glu Thr
 310 315 320 325

atc gat tcg gta cgc gct aca ccg ctt gat cgc aaa gag atc atc tcc 1123
 Ile Asp Ser Val Arg Ala Thr Pro Leu Asp Arg Lys Glu Ile Ile Ser
 330 335 340

acg ctg gtg ggt gtg cgc ccg ctt gtt gat gac ggc acc gac acc tac 1171
 Thr Leu Val Gly Val Arg Pro Leu Val Asp Asp Gly Thr Asp Thr Tyr
 345 350 355

acg tcc tct cgc cgt ttc gat att tcc gat cac gcc aac gtc ggc att 1219
 Thr Ser Ser Arg Arg Phe Asp Ile Ser Asp His Ala Asn Val Gly Ile
 360 365 370

gat ggt ttg gtg tct gtc tct ggc ggc aag tgg acc act tcc cgc gtg 1267
 Asp Gly Leu Val Ser Val Ser Gly Gly Lys Trp Thr Thr Ser Arg Val
 375 380 385

atg ggg tac aag gtg att gag cat gtg gtg gag cac caa gct gcg gtg 1315
 Met Gly Tyr Lys Val Ile Glu His Val Val Glu His Gln Ala Ala Val
 390 395 400 405

tta cct ccg ctg cgc cac ttt gac tcc agg cag atg ccg ttg agt act 1363
 Leu Pro Pro Leu Arg His Phe Asp Ser Arg Gln Met Pro Leu Ser Thr
 410 415 420

tct ttt ggc gcg tat gag tcc gtg gct gat tcc ttt gag tca gcg ctt 1411
 Ser Phe Gly Ala Tyr Glu Ser Val Ala Asp Ser Phe Glu Ser Ala Leu
 425 430 435

cgc agc cac ccc gag ctg gat gtg gat gat gaa atc cgc gtg cat ctg 1459
 Arg Ser His Pro Glu Leu Asp Val Asp Asp Glu Ile Arg Val His Leu
 440 445 450

gcc aga ctg tat gga act gag cat gaa aaa gtg ctg gat ctc gtc gca 1507
 Ala Arg Leu Tyr Gly Thr Glu His Glu Lys Val Leu Asp Leu Val Ala
 455 460 465

aag caa ccc gac ctg ggg cgc cga ctt gac cca gac aac ctt gat atc 1555
 Lys Gln Pro Asp Leu Gly Arg Arg Leu Asp Pro Asp Asn Leu Asp Ile
 470 475 480 485

gcg gcg cag gcc gtt ttt gct gtc gcc gag gag gcg gcc gtc gac ctg 1603
 Ala Ala Gln Ala Val Phe Ala Val Ala Glu Glu Ala Ala Val Asp Leu
 490 495 500

gcg gac gtg ctg gat cgt cgc atc gtg ctc ggc acg ctg ggt tat gtg 1651
 Ala Asp Val Leu Asp Arg Arg Ile Val Leu Gly Thr Leu Gly Tyr Val
 505 510 515

caa ccg gct gcc gtg cgt gcg acg gcc gaa gca atg gcg cag gtc acc 1699
 Gln Pro Ala Ala Val Arg Ala Thr Ala Glu Ala Met Ala Gln Val Thr
 520 525 530

ggg tgg tca gct gag ctt atc gac gcc cag tgc cag tcc tac ctc gcc 1747
 Gly Trp Ser Ala Glu Leu Ile Asp Ala Gln Cys Gln Ser Tyr Leu Ala
 535 540 545

aag caa gac aaa atc caa gcc gtg tta aag ccg tac cgc taacactccg 1796
 Lys Gln Asp Lys Ile Gln Ala Val Leu Lys Pro Tyr Arg
 550 555 560

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<210> 192
 <211> 562
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 192
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 20 25 30

Ile Ala Arg His Ala Gln Gly Arg Gly Leu Arg Thr Val Met Phe Glu
 35 40 45

Ala Arg Asp Tyr Ser Ser Gly Thr Ser Ser Thr Thr Ser Lys Met Ile
 50 55 60

His Gly Gly Leu Arg Tyr Leu Glu Gln Tyr Asp Phe Gly Val Val Gln
 65 70 75 80

Glu Ala Val Lys Glu Arg Arg Tyr Leu Gly Ile Ala Ala Pro His Leu
 85 90 95

Val Ala Pro Arg Ser Phe Met Leu Thr Ala Phe Asp Trp Ser Glu Pro
 100 105 110

Lys Ala Pro Met Leu Gly Ala Gly Val Ala Leu Tyr Glu Thr Met Ala
 115 120 125

Trp Gln Arg Asn Gln Gly Gln Ser Lys Glu Asn His Ser Pro Arg Phe
 130 135 140

Arg Trp Ile Pro Lys Asn Ala Leu Leu Lys Glu Val Pro Trp Leu Asp
 145 150 155 160

Pro Glu Gly Leu Lys Gly Ala Trp Arg His Asp Asp Thr Leu Asn Leu
 165 170 175

His Ala Glu Arg Leu Leu Leu Ala Val Ile Lys Ala Phe Ala Ala Asp
 180 185 190
 Gly Gly Thr Ala Ile Asn His Ala Lys Val Thr Arg Ile Leu Arg Asn
 195 200 205
 Val Glu Glu Gly Arg Val Lys Gly Val Glu Val Thr Asp Gln Val Thr
 210 215 220
 Asn Thr Thr His Glu Val Asn Ala Pro Val Val Ile Asn Ala Ala Gly
 225 230 235 240
 Pro Trp Val Ala Gln Ala Leu Gly Asp Leu Ala Glu Val Thr Lys Leu
 245 250 255
 Lys Val Arg Gln Ser Lys Gly Val His Leu Leu Thr Gly Asp Leu Gly
 260 265 270
 Ser Gln Ser Gly Val Phe Val Arg Gly Lys Asn Gly Lys His Val Ile
 275 280 285
 Val Asn Pro Trp Met Gly Arg Thr Leu Ile Gly Pro Thr Asp Thr Met
 290 295 300
 Ile Asp Gly Asp Ala Asp Asp Ala Ala Ala Asp Glu Ser Asp Ile Asp
 305 310 315 320
 Leu Leu Leu Glu Thr Ile Asp Ser Val Arg Ala Thr Pro Leu Asp Arg
 325 330 335
 Lys Glu Ile Ile Ser Thr Leu Val Gly Val Arg Pro Leu Val Asp Asp
 340 345 350
 Gly Thr Asp Thr Tyr Thr Ser Ser Arg Arg Phe Asp Ile Ser Asp His
 355 360 365
 Ala Asn Val Gly Ile Asp Gly Leu Val Ser Val Ser Gly Gly Lys Trp
 370 375 380
 Thr Thr Ser Arg Val Met Gly Tyr Lys Val Ile Glu His Val Val Glu
 385 390 395 400
 His Gln Ala Ala Val Leu Pro Pro Leu Arg His Phe Asp Ser Arg Gln
 405 410 415
 Met Pro Leu Ser Thr Ser Phe Gly Ala Tyr Glu Ser Val Ala Asp Ser
 420 425 430
 Phe Glu Ser Ala Leu Arg Ser His Pro Glu Leu Asp Val Asp Asp Glu
 435 440 445
 Ile Arg Val His Leu Ala Arg Leu Tyr Gly Thr Glu His Glu Lys Val
 450 455 460
 Leu Asp Leu Val Ala Lys Gln Pro Asp Leu Gly Arg Arg Leu Asp Pro
 465 470 475 480
 Asp Asn Leu Asp Ile Ala Ala Gln Ala Val Phe Ala Val Ala Glu Glu
 485 490 495

Ala Ala Val Asp Leu Ala Asp Val Leu Asp Arg Arg Ile Val Leu Gly
 500 505 510

Thr Leu Gly Tyr Val Gln Pro Ala Ala Val Arg Ala Thr Ala Glu Ala
 515 520 525

Met Ala Gln Val Thr Gly Trp Ser Ala Glu Leu Ile Asp Ala Gln Cys
 530 535 540

Gln Ser Tyr Leu Ala Lys Gln Asp Lys Ile Gln Ala Val Leu Lys Pro
 545 550 555 560

Tyr Arg

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<211> 900

<212> DNA

<213> Corynebacterium glutamicum

<220>

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<222> (101)..(877)

<223> RXA01242

<400> 193

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 Met Tyr Ala Glu Glu
 1 5

cgc cgt cga cag att gcc tca tta acg gca gtt gag gga cgt gta aat 163
 Arg Arg Arg Gln Ile Ala Ser Leu Thr Ala Val Glu Gly Arg Val Asn
 10 15 20

gtc aca gaa tta gcg ggc cga ttc gat gtc act gca gag acg att cga 211
 Val Thr Glu Leu Ala Gly Arg Phe Asp Val Thr Ala Glu Thr Ile Arg
 25 30 35

cga gac ctt gcg gtg cta gac cgc gag gga att gtt cac cgc gtt cac 259
 Arg Asp Leu Ala Val Leu Asp Arg Glu Gly Ile Val His Arg Val His
 40 45 50

ggt ggc gca gta gcc acc caa tct ttc caa acc aca gag ttg agc ttg 307
 Gly Gly Ala Val Ala Thr Gln Ser Phe Gln Thr Thr Glu Leu Ser Leu
 55 60 65

gat act cgt ttc agg tct gca tcg tca gca aag tac tcc att gcc aag 355
 Asp Thr Arg Phe Arg Ser Ala Ser Ser Ala Lys Tyr Ser Ile Ala Lys
 70 75 80 85

gca gcg atg cag ttc ctg ccc gct gag cat ggc gga ctg ttc ctc gat 403
 Ala Ala Met Gln Phe Leu Pro Ala Glu His Gly Gly Leu Phe Leu Asp
 90 95 100

gcg gga act act gtt act gct ttg gcc gat ctc att tct gag cat cct 451
 Ala Gly Thr Thr Val Thr Ala Leu Ala Asp Leu Ile Ser Glu His Pro
 105 110 115

agc tcc aag cag tgg tcg atc gtg acc aac tgc ctc ccc atc gca ctt 499
 Ser Ser Lys Gln Trp Ser Ile Val Thr Asn Cys Leu Pro Ile Ala Leu
 120 125 130

aat ctg gcc aac gcc ggg ctt gat gat gtc cag ctg ctt gga gga agc 547
 Asn Leu Ala Asn Ala Gly Leu Asp Asp Val Gln Leu Leu Gly Gly Ser
 135 140 145

gtt cgc gcg atc acc cag gct gtt gtg ggt gac act gcg ctt cgt act 595
 Val Arg Ala Ile Thr Gln Ala Val Val Gly Asp Thr Ala Leu Arg Thr
 150 155 160 165

ctc gcg ctg atg cgt gcg gat gta gtg ttc atc ggc acc aac gcg ttg 643
 Leu Ala Leu Met Arg Ala Asp Val Val Phe Ile Gly Thr Asn Ala Leu
 170 175 180

acg ttg gat cac gga ttg tct acg gcc gat tcc caa gag gct gcc atg 691
 Thr Leu Asp His Gly Leu Ser Thr Ala Asp Ser Gln Glu Ala Ala Met
 185 190 195

aaa tct gcg atg atc acc aac gcc cac aag gtg gtg gtg ttg tgt gac 739
 Lys Ser Ala Met Ile Thr Asn Ala His Lys Val Val Val Leu Cys Asp
 200 205 210

tcc acc aag atg ggc acc gac tac ctc gtg agc ttt ggc gca atc agc 787
 Ser Thr Lys Met Gly Thr Asp Tyr Leu Val Ser Phe Gly Ala Ile Ser
 215 220 225

gat atc gat gtg gtg gtc acc gat gcg ggt gca cca gca agt ttc gtt 835
 Asp Ile Asp Val Val Val Thr Asp Ala Gly Ala Pro Ala Ser Phe Val
 230 235 240 245

gag cag ttg cga gaa cgc gat gta gaa gtt gtg att gca gaa 877
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<210> 194

<211> 259

<212> PRT

<213> Corynebacterium glutamicum

<400> 194

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 20 25 30

Ala Glu Thr Ile Arg Arg Asp Leu Ala Val Leu Asp Arg Glu Gly Ile
 35 40 45

Val His Arg Val His Gly Gly Ala Val Ala Thr Gln Ser Phe Gln Thr
 50 55 60

Thr Glu Leu Ser Leu Asp Thr Arg Phe Arg Ser Ala Ser Ser Ala Lys
 65 70 75 80

Tyr Ser Ile Ala Lys Ala Ala Met Gln Phe Leu Pro Ala Glu His Gly

85					90					95					
Gly	Leu	Phe	Leu	Asp	Ala	Gly	Thr	Thr	Val	Thr	Ala	Leu	Ala	Asp	Leu
			100					105					110		
Ile	Ser	Glu	His	Pro	Ser	Ser	Lys	Gln	Trp	Ser	Ile	Val	Thr	Asn	Cys
		115					120					125			
Leu	Pro	Ile	Ala	Leu	Asn	Leu	Ala	Asn	Ala	Gly	Leu	Asp	Asp	Val	Gln
	130					135					140				
Leu	Leu	Gly	Gly	Ser	Val	Arg	Ala	Ile	Thr	Gln	Ala	Val	Val	Gly	Asp
145					150					155					160
Thr	Ala	Leu	Arg	Thr	Leu	Ala	Leu	Met	Arg	Ala	Asp	Val	Val	Phe	Ile
				165					170					175	
Gly	Thr	Asn	Ala	Leu	Thr	Leu	Asp	His	Gly	Leu	Ser	Thr	Ala	Asp	Ser
			180					185						190	
Gln	Glu	Ala	Ala	Met	Lys	Ser	Ala	Met	Ile	Thr	Asn	Ala	His	Lys	Val
		195					200					205			
Val	Val	Leu	Cys	Asp	Ser	Thr	Lys	Met	Gly	Thr	Asp	Tyr	Leu	Val	Ser
	210					215					220				
Phe	Gly	Ala	Ile	Ser	Asp	Ile	Asp	Val	Val	Val	Thr	Asp	Ala	Gly	Ala
225					230					235					240
Pro	Ala	Ser	Phe	Val	Glu	Gln	Leu	Arg	Glu	Arg	Asp	Val	Glu	Val	Val
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Ile Ala Glu

<210> 195
 <211> 969
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
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 <222> (101)..(946)
 <223> RXA02288

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 Met Ser Gln Val Ile
 1 5
 ccc gcc agc tca caa gaa aag cgt cgt gag cgc atc gtt tct tat gtc 163
 Pro Ala Ser Ser Gln Glu Lys Arg Arg Glu Arg Ile Val Ser Tyr Val
 10 15 20
 acc cgt cat gga ttc gct cgt gtt gaa gca tta gct gag ctt ttt gag 211
 Thr Arg His Gly Phe Ala Arg Val Glu Ala Leu Ala Glu Leu Phe Glu
 25 30 35

gtc	agc	gca	atg	acc	att	cac	cgt	gat	ttg	gag	gcg	ctg	gct	gca	gac	259
Val	Ser	Ala	Met	Thr	Ile	His	Arg	Asp	Leu	Glu	Ala	Leu	Ala	Ala	Asp	
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Asn	Leu	Val	Glu	Arg	Ile	Arg	Gly	Gly	Ala	Arg	Ser	Val	Ser	Pro	Ser	
	55					60					65					
atg	agt	gag	ttg	gca	gtg	gag	cag	cgt	cgg	cat	ttg	cat	cgc	act	gtt	355
Met	Ser	Glu	Leu	Ala	Val	Glu	Gln	Arg	Arg	His	Leu	His	Arg	Thr	Val	
	70				75					80					85	
aaa	gag	gcg	ttg	tgt	act	gca	gca	gca	cgg	ttg	att	ccg	gag	ggc	gct	403
Lys	Glu	Ala	Leu	Cys	Thr	Ala	Ala	Ala	Arg	Leu	Ile	Pro	Glu	Gly	Ala	
				90					95					100		
gtg	gtg	gcg	att	gat	gat	tcc	acc	acg	ttg	gag	tct	ttg	gtt	gag	aag	451
Val	Val	Ala	Ile	Asp	Asp	Ser	Thr	Thr	Leu	Glu	Ser	Leu	Val	Glu	Lys	
			105					110					115			
ttg	ccg	cag	cgg	tca	cca	tcg	gcg	ttg	att	acg	cat	tct	ttg	aag	aca	499
Leu	Pro	Gln	Arg	Ser	Pro	Ser	Ala	Leu	Ile	Thr	His	Ser	Leu	Lys	Thr	
		120					125					130				
atg	gcg	gat	cat	cgt	gtg	cgc	gcc	ggg	atg	agc	gat	atc	cgt	ttg	att	547
Met	Ala	Asp	His	Arg	Val	Arg	Ala	Gly	Met	Ser	Asp	Ile	Arg	Leu	Ile	
	135					140					145					
gcg	tgt	gcg	gga	ttg	tat	ttc	gcg	gag	act	gat	tct	ttc	ttg	ggc	aag	595
Ala	Cys	Ala	Gly	Leu	Tyr	Phe	Ala	Glu	Thr	Asp	Ser	Phe	Leu	Gly	Lys	
	150				155					160					165	
gca	act	tca	gcg	cag	ttg	aat	gag	ctg	tcg	gcg	gat	att	tct	ttt	gtt	643
Ala	Thr	Ser	Ala	Gln	Leu	Asn	Glu	Leu	Ser	Ala	Asp	Ile	Ser	Phe	Val	
				170					175					180		
tct	acg	act	gcg	gtg	cgc	gct	acg	ggg	gag	gtt	ccg	gcg	ctg	ttt	cat	691
Ser	Thr	Thr	Ala	Val	Arg	Ala	Thr	Gly	Glu	Val	Pro	Ala	Leu	Phe	His	
			185					190					195			
cct	gat	atg	gag	gct	gct	gat	acg	aag	cgg	gcg	ttg	att	ggg	att	ggt	739
Pro	Asp	Met	Glu	Ala	Ala	Asp	Thr	Lys	Arg	Ala	Leu	Ile	Gly	Ile	Gly	
		200					205					210				
agc	gtg	cgt	gtg	ttg	gtg	gtg	gat	tct	agt	aaa	ttt	ggt	tcg	gct	ggt	787
Ser	Val	Arg	Val	Leu	Val	Val	Asp	Ser	Ser	Lys	Phe	Gly	Ser	Ala	Gly	
	215					220					225					
gtg	ttc	aag	gtt	gct	tcg	att	gag	gag	ttt	gac	cac	atc	atc	att	gat	835
Val	Phe	Lys	Val	Ala	Ser	Ile	Glu	Glu	Phe	Asp	His	Ile	Ile	Ile	Asp	
	230					235				240					245	
cag	cag	tgc	acc	cgt	gag	cag	cgg	gat	ctt	ttg	cgt	aat	tcg	cgc	gcg	883
Gln	Gln	Cys	Thr	Arg	Glu	Gln	Arg	Asp	Leu	Leu	Arg	Asn	Ser	Arg	Ala	
				250					255					260		
cag	atc	cat	gtg	att	gac	cac	aat	ggt	gat	gaa	att	ttg	gat	acc	cca	931
Gln	Ile	His	Val	Ile	Asp	His	Asn	Gly	Asp	Glu	Ile	Leu	Asp	Thr	Pro	
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<210> 196
<211> 282
<212> PRT
<213> Corynebacterium glutamicum
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Ala	Glu	Leu	Phe	Glu	Val	Ser	Ala	Met	Thr	Ile	His	Arg	Asp	Leu	Glu	
		35					40					45				
Ala	Leu	Ala	Ala	Asp	Asn	Leu	Val	Glu	Arg	Ile	Arg	Gly	Gly	Ala	Arg	
	50					55					60					
Ser	Val	Ser	Pro	Ser	Met	Ser	Glu	Leu	Ala	Val	Glu	Gln	Arg	Arg	His	
65					70					75					80	
Leu	His	Arg	Thr	Val	Lys	Glu	Ala	Leu	Cys	Thr	Ala	Ala	Ala	Arg	Leu	
				85					90					95		
Ile	Pro	Glu	Gly	Ala	Val	Val	Ala	Ile	Asp	Asp	Ser	Thr	Thr	Leu	Glu	
			100					105					110			
Ser	Leu	Val	Glu	Lys	Leu	Pro	Gln	Arg	Ser	Pro	Ser	Ala	Leu	Ile	Thr	
		115					120					125				
His	Ser	Leu	Lys	Thr	Met	Ala	Asp	His	Arg	Val	Arg	Ala	Gly	Met	Ser	
	130					135					140					
Asp	Ile	Arg	Leu	Ile	Ala	Cys	Ala	Gly	Leu	Tyr	Phe	Ala	Glu	Thr	Asp	
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Ser	Phe	Leu	Gly	Lys	Ala	Thr	Ser	Ala	Gln	Leu	Asn	Glu	Leu	Ser	Ala	
				165					170					175		
Asp	Ile	Ser	Phe	Val	Ser	Thr	Thr	Ala	Val	Arg	Ala	Thr	Gly	Glu	Val	
			180					185					190			
Pro	Ala	Leu	Phe	His	Pro	Asp	Met	Glu	Ala	Ala	Asp	Thr	Lys	Arg	Ala	
		195					200					205				
Leu	Ile	Gly	Ile	Gly	Ser	Val	Arg	Val	Leu	Val	Val	Asp	Ser	Ser	Lys	
	210					215					220					
Phe	Gly	Ser	Ala	Gly	Val	Phe	Lys	Val	Ala	Ser	Ile	Glu	Glu	Phe	Asp	
225					230					235					240	
His	Ile	Ile	Ile	Asp	Gln	Gln	Cys	Thr	Arg	Glu	Gln	Arg	Asp	Leu	Leu	
				245					250					255		
Arg	Asn	Ser	Arg	Ala	Gln	Ile	His	Val	Ile	Asp	His	Asn	Gly	Asp	Glu	
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Ile Leu Asp Thr Pro Thr Glu Glu Asp Phe
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<210> 197

<211> 887

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(864)

<223> RXN01891

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tac aac aag gat ctg tgg gct aag gct ggc ctg gaa gat cgt ggc cca	96
Tyr Asn Lys Asp Leu Trp Ala Lys Ala Gly Leu Glu Asp Arg Gly Pro	
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gag tca tgg gaa gag ttc tcc gag tgg ggt cca aag ctg cag gaa gcg	144
Glu Ser Trp Glu Glu Phe Ser Glu Trp Gly Pro Lys Leu Gln Glu Ala	
35 40 45	
atg gac agt ggt ttc gca cac ggt tgg gga gat gca acc aac tac ctt	192
Met Asp Ser Gly Phe Ala His Gly Trp Gly Asp Ala Thr Asn Tyr Leu	
50 55 60	
tct tgg act ttc gaa ggc cca atg tgg tcc ctc ggc ggc aac tac tct	240
Ser Trp Thr Phe Glu Gly Pro Met Trp Ser Leu Gly Gly Asn Tyr Ser	
65 70 75 80	
gaa ggt tgg gag tcc cgt ctg act acc cca gag acc atc cgt gca gtt	288
Glu Gly Trp Glu Ser Arg Leu Thr Thr Pro Glu Thr Ile Arg Ala Val	
85 90 95	
gag tgg ctc aag tcc acc gtt gat gaa ggt ttc gca acc gtc tcc acc	336
Glu Trp Leu Lys Ser Thr Val Asp Glu Gly Phe Ala Thr Val Ser Thr	
100 105 110	
gac gtc acc aac gag ttc gca acc ggc ctg atc ggt tca tgc atc cag	384
Asp Val Thr Asn Glu Phe Ala Thr Gly Leu Ile Gly Ser Cys Ile Gln	
115 120 125	
tcc acc ggt gat ctg tct tcg gtt gcc ggc gct gca agc ttc gac tgg	432
Ser Thr Gly Asp Leu Ser Ser Val Ala Gly Ala Ala Ser Phe Asp Trp	
130 135 140	
ggc gta gca gca ctt cct aac cca acc ggc gag ggc gct tgc cca acc	480
Gly Val Ala Ala Leu Pro Asn Pro Thr Gly Glu Gly Ala Cys Pro Thr	
145 150 155 160	
ggt ggc gca ggc ctg gga atc cca tct ggc atc tct gag cag cgt cag	528
Gly Gly Ala Gly Leu Gly Ile Pro Ser Gly Ile Ser Glu Gln Arg Gln	
165 170 175	
gac aac gcc ctg aag ttc atc gac ttc ctc acc aac gcc gcg aac act	576
Asp Asn Ala Leu Lys Phe Ile Asp Phe Leu Thr Asn Ala Ala Asn Thr	

180										185					190					
ggc	tac	tgg	tcc	cgc	gag	acc	ggg	tat	gtt	cca	gtt	cgt	aag	gat	gct	624				
Gly	Tyr	Trp	Ser	Arg	Glu	Thr	Gly	Tyr	Val	Pro	Val	Arg	Lys	Asp	Ala					
		195						200				205								
gca	tct	gat	cca	gat	cac	gca	gca	ttc	ctc	gag	gag	aac	cct	gca	tac	672				
Ala	Ser	Asp	Pro	Asp	His	Ala	Ala	Phe	Leu	Glu	Glu	Asn	Pro	Ala	Tyr					
	210					215					220									
aac	gtt	gca	gtg	gag	cag	ctt	cct	gat	acc	cgt	tcc	cag	gac	aac	ttc	720				
Asn	Val	Ala	Val	Glu	Gln	Leu	Pro	Asp	Thr	Arg	Ser	Gln	Asp	Asn	Phe					
225					230					235					240					
cgc	gtg	ctg	ctg	cca	aac	ggg	gac	cgc	acc	atc	ggg	gac	gca	ctg	gag	768				
Arg	Val	Leu	Leu	Pro	Asn	Gly	Asp	Arg	Thr	Ile	Gly	Asp	Ala	Leu	Glu					
				245					250					255						
aag	atc	tgc	ctg	act	ggg	gca	gac	atc	gat	gtc	acc	ctg	gct	gag	gtt	816				
Lys	Ile	Cys	Leu	Thr	Gly	Ala	Asp	Ile	Asp	Val	Thr	Leu	Ala	Glu	Val					
			260					265					270							
gag	acc	aag	ctg	aac	acc	atc	tac	acc	cgc	gac	atc	gaa	cca	ctt	att	864				
Glu	Thr	Lys	Leu	Asn	Thr	Ile	Tyr	Thr	Arg	Asp	Ile	Glu	Pro	Leu	Ile					
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<211> 288

<212> PRT

<213> Corynebacterium glutamicum

<400> 198

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			20					25					30		

Glu	Ser	Trp	Glu	Glu	Phe	Ser	Glu	Trp	Gly	Pro	Lys	Leu	Gln	Glu	Ala
		35					40					45			

Met	Asp	Ser	Gly	Phe	Ala	His	Gly	Trp	Gly	Asp	Ala	Thr	Asn	Tyr	Leu
	50					55					60				

Ser	Trp	Thr	Phe	Glu	Gly	Pro	Met	Trp	Ser	Leu	Gly	Gly	Asn	Tyr	Ser
	65				70					75				80	

Glu	Gly	Trp	Glu	Ser	Arg	Leu	Thr	Thr	Pro	Glu	Thr	Ile	Arg	Ala	Val
			85						90					95	

Glu	Trp	Leu	Lys	Ser	Thr	Val	Asp	Glu	Gly	Phe	Ala	Thr	Val	Ser	Thr
		100						105					110		

Asp	Val	Thr	Asn	Glu	Phe	Ala	Thr	Gly	Leu	Ile	Gly	Ser	Cys	Ile	Gln
	115						120					125			

Ser	Thr	Gly	Asp	Leu	Ser	Ser	Val	Ala	Gly	Ala	Ala	Ser	Phe	Asp	Trp
	130					135					140				

Gly Val Ala Ala Leu Pro Asn Pro Thr Gly Glu Gly Ala Cys Pro Thr
 145 150 155 160
 Gly Gly Ala Gly Leu Gly Ile Pro Ser Gly Ile Ser Glu Gln Arg Gln
 165 170 175
 Asp Asn Ala Leu Lys Phe Ile Asp Phe Leu Thr Asn Ala Ala Asn Thr
 180 185 190
 Gly Tyr Trp Ser Arg Glu Thr Gly Tyr Val Pro Val Arg Lys Asp Ala
 195 200 205
 Ala Ser Asp Pro Asp His Ala Ala Phe Leu Glu Glu Asn Pro Ala Tyr
 210 215 220
 Asn Val Ala Val Glu Gln Leu Pro Asp Thr Arg Ser Gln Asp Asn Phe
 225 230 235 240
 Arg Val Leu Leu Pro Asn Gly Asp Arg Thr Ile Gly Asp Ala Leu Glu
 245 250 255
 Lys Ile Cys Leu Thr Gly Ala Asp Ile Asp Val Thr Leu Ala Glu Val
 260 265 270
 Glu Thr Lys Leu Asn Thr Ile Tyr Thr Arg Asp Ile Glu Pro Leu Ile
 275 280 285

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 <212> DNA
 <213> *Corynebacterium glutamicum*

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 <222> (1)..(819)
 <223> FRXA01891

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 cca gag tca tgg gaa gag ttc tcc gag tgg ggt cca aag ctg cag gaa 96
 Pro Glu Ser Trp Glu Glu Phe Ser Glu Trp Gly Pro Lys Leu Gln Glu
 20 25 30
 gcg atg gac agt ggt ttc gca cac ggt tgg gga gat gca acc aac tac 144
 Ala Met Asp Ser Gly Phe Ala His Gly Trp Gly Asp Ala Thr Asn Tyr
 35 40 45
 ctt tct tgg act ttc gaa ggc cca atg tgg tcc ctc ggc ggc aac tac 192
 Leu Ser Trp Thr Phe Glu Gly Pro Met Trp Ser Leu Gly Gly Asn Tyr
 50 55 60
 tct gaa ggt tgg gag tcc cgt ctg act acc cca gag acc atc cgt gca 240
 Ser Glu Gly Trp Glu Ser Arg Leu Thr Thr Pro Glu Thr Ile Arg Ala

65	70	75	80	
ggt gag tgg ctc aag tcc acc gtt gat gaa ggt ttc gca acc gtc tcc				288
Val Glu Trp Leu Lys Ser Thr Val Asp Glu Gly Phe Ala Thr Val Ser				
	85	90	95	
acc gac gtc acc aac gag ttc gca acc ggc ctg atc ggt tca tgc atc				336
Thr Asp Val Thr Asn Glu Phe Ala Thr Gly Leu Ile Gly Ser Cys Ile				
	100	105	110	
cag tcc acc ggt gat ctg tct tcg gtt gcc ggc gct gca agc ttc gac				384
Gln Ser Thr Gly Asp Leu Ser Ser Val Ala Gly Ala Ala Ser Phe Asp				
	115	120	125	
tgg ggc gta gca gca ctt cct aac cca acc ggc gag ggc gct tgc cca				432
Trp Gly Val Ala Ala Leu Pro Asn Pro Thr Gly Glu Gly Ala Cys Pro				
	130	135	140	
acc ggt ggc gca ggc ctg gga atc cca tct ggc atc tct gag cag cgt				480
Thr Gly Gly Ala Gly Leu Gly Ile Pro Ser Gly Ile Ser Glu Gln Arg				
	145	150	155	160
cag gac aac gcc ctg aag ttc atc gac ttc ctc acc aac gcc gcg aac				528
Gln Asp Asn Ala Leu Lys Phe Ile Asp Phe Leu Thr Asn Ala Ala Asn				
	165	170	175	
act ggc tac tgg tcc cgc gag acc ggt tat gtt cca gtt cgt aag gat				576
Thr Gly Tyr Trp Ser Arg Glu Thr Gly Tyr Val Pro Val Arg Lys Asp				
	180	185	190	
gct gca tct gat cca gat cac gca gca ttc ctc gag gag aac cct gca				624
Ala Ala Ser Asp Pro Asp His Ala Ala Phe Leu Glu Glu Asn Pro Ala				
	195	200	205	
tac aac gtt gca gtg gag cag ctt cct gat acc cgt tcc cag gac aac				672
Tyr Asn Val Ala Val Glu Gln Leu Pro Asp Thr Arg Ser Gln Asp Asn				
	210	215	220	
ttc cgc gtg ctg ctg cca aac ggt gac cgc acc atc ggt gac gca ctg				720
Phe Arg Val Leu Leu Pro Asn Gly Asp Arg Thr Ile Gly Asp Ala Leu				
	225	230	235	240
gag aag atc tgc ctg act ggt gca gac atc gat gtc acc ctg gct gag				768
Glu Lys Ile Cys Leu Thr Gly Ala Asp Ile Asp Val Thr Leu Ala Glu				
	245	250	255	
ggt gag acc aag ctg aac acc atc tac acc cgc gac atc gaa cca ctt				816
Val Glu Thr Lys Leu Asn Thr Ile Tyr Thr Arg Asp Ile Glu Pro Leu				
	260	265	270	
att taatccgagc acttcagcta cac				842
Ile				

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<211> 273

<212> PRT

<213> Corynebacterium glutamicum

<400> 200

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 35 40 45
 Leu Ser Trp Thr Phe Glu Gly Pro Met Trp Ser Leu Gly Gly Asn Tyr
 50 55 60
 Ser Glu Gly Trp Glu Ser Arg Leu Thr Thr Pro Glu Thr Ile Arg Ala
 65 70 75 80
 Val Glu Trp Leu Lys Ser Thr Val Asp Glu Gly Phe Ala Thr Val Ser
 85 90 95
 Thr Asp Val Thr Asn Glu Phe Ala Thr Gly Leu Ile Gly Ser Cys Ile
 100 105 110
 Gln Ser Thr Gly Asp Leu Ser Ser Val Ala Gly Ala Ala Ser Phe Asp
 115 120 125
 Trp Gly Val Ala Ala Leu Pro Asn Pro Thr Gly Glu Gly Ala Cys Pro
 130 135 140
 Thr Gly Gly Ala Gly Leu Gly Ile Pro Ser Gly Ile Ser Glu Gln Arg
 145 150 155 160
 Gln Asp Asn Ala Leu Lys Phe Ile Asp Phe Leu Thr Asn Ala Ala Asn
 165 170 175
 Thr Gly Tyr Trp Ser Arg Glu Thr Gly Tyr Val Pro Val Arg Lys Asp
 180 185 190
 Ala Ala Ser Asp Pro Asp His Ala Ala Phe Leu Glu Glu Asn Pro Ala
 195 200 205
 Tyr Asn Val Ala Val Glu Gln Leu Pro Asp Thr Arg Ser Gln Asp Asn
 210 215 220
 Phe Arg Val Leu Leu Pro Asn Gly Asp Arg Thr Ile Gly Asp Ala Leu
 225 230 235 240
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 Val Glu Thr Lys Leu Asn Thr Ile Tyr Thr Arg Asp Ile Glu Pro Leu
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Ile

<210> 201

<211> 776

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (7)..(753)

<223> RXA02414

<400> 201

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Gly Ala Phe Gln Pro Ala Gly Gly Pro Val Lys Pro Trp Asn Lys Pro
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gat gcc agc ctg aat cag cag ctg aaa aac aaa tcc cgt gtg cgc aca 147
Asp Ala Ser Leu Asn Gln Gln Leu Lys Asn Lys Ser Arg Val Arg Thr
          35             40             45

ggt ctt acc atc gcc atc ggt tat gta gtg gtg att tgg gcg gtg cat 195
Gly Leu Thr Ile Ala Ile Gly Tyr Val Val Val Ile Trp Ala Val His
          50             55             60

ttg gca tcc atc gtc att gcg ctg ctc act ggc ttc aac ctg acc aac 243
Leu Ala Ser Ile Val Ile Ala Leu Leu Thr Gly Phe Asn Leu Thr Asn
          65             70             75

ttt ggt att cat ccg ctg gat acc agt gca ctg tgg ggt att ttc acc 291
Phe Gly Ile His Pro Leu Asp Thr Ser Ala Leu Trp Gly Ile Phe Thr
          80             85             90             95

tca ccg ctg ttg cat gga agc ttc agc cac ctc att gga aat acc gtt 339
Ser Pro Leu Leu His Gly Ser Phe Ser His Leu Ile Gly Asn Thr Val
          100             105             110

cca ggc ttt ata ttc agt ttc ctc atc ggt atg agt ggc aag cgc gtg 387
Pro Gly Phe Ile Phe Ser Phe Leu Ile Gly Met Ser Gly Lys Arg Val
          115             120             125

ttc tgg gaa gtc acg att atc gca ggt ctc atc ggc ggt ctt ggt aca 435
Phe Trp Glu Val Thr Ile Ile Ala Gly Leu Ile Gly Gly Leu Gly Thr
          130             135             140

tgg att ttc ggt gga atc ggc acc aac cac atc ggt gcg tcc ggc ctg 483
Trp Ile Phe Gly Gly Ile Gly Thr Asn His Ile Gly Ala Ser Gly Leu
          145             150             155

att tat ggc tgg ctt ggc tac ctg atc gtg cgt gga att ttc aac aag 531
Ile Tyr Gly Trp Leu Gly Tyr Leu Ile Val Arg Gly Ile Phe Asn Lys
          160             165             170             175

gat att aaa cag ttc ctg ctt ggc ata gtt ttg gcg ttc att tac tcc 579
Asp Ile Lys Gln Phe Leu Leu Gly Ile Val Leu Ala Phe Ile Tyr Ser
          180             185             190

ggt ttg ttc tgg ggt ctg cta cct act caa atc ggt gtg tcc tgg cag 627
Gly Leu Phe Trp Gly Leu Leu Pro Thr Gln Ile Gly Val Ser Trp Gln
          195             200             205

ggc cac ctt ttc ggt gca ctt ggt gga atc ggt gcg ggt gct ttt atc 675
Gly His Leu Phe Gly Ala Leu Gly Gly Ile Gly Ala Gly Ala Phe Ile
          210             215             220

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gcc tcg gat gac ccg gca gcg ttg aaa gcg aag aag caa cag aag aaa 723
 Ala Ser Asp Asp Pro Ala Ala Leu Lys Ala Lys Lys Gln Gln Lys Lys
 225 230 235

tta gaa aag caa caa cgc caa aga ggc tta tagttttcac ctacgcgacta 773
 Leu Glu Lys Gln Gln Arg Gln Arg Gly Leu
 240 245

cac 776

<210> 202

<211> 249

<212> PRT

<213> Corynebacterium glutamicum

<400> 202

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 20 25 30

Ala Ser Leu Asn Gln Gln Leu Lys Asn Lys Ser Arg Val Arg Thr Gly
 35 40 45

Leu Thr Ile Ala Ile Gly Tyr Val Val Val Ile Trp Ala Val His Leu
 50 55 60

Ala Ser Ile Val Ile Ala Leu Leu Thr Gly Phe Asn Leu Thr Asn Phe
 65 70 75 80

Gly Ile His Pro Leu Asp Thr Ser Ala Leu Trp Gly Ile Phe Thr Ser
 85 90 95

Pro Leu Leu His Gly Ser Phe Ser His Leu Ile Gly Asn Thr Val Pro
 100 105 110

Gly Phe Ile Phe Ser Phe Leu Ile Gly Met Ser Gly Lys Arg Val Phe
 115 120 125

Trp Glu Val Thr Ile Ile Ala Gly Leu Ile Gly Gly Leu Gly Thr Trp
 130 135 140

Ile Phe Gly Gly Ile Gly Thr Asn His Ile Gly Ala Ser Gly Leu Ile
 145 150 155 160

Tyr Gly Trp Leu Gly Tyr Leu Ile Val Arg Gly Ile Phe Asn Lys Asp
 165 170 175

Ile Lys Gln Phe Leu Leu Gly Ile Val Leu Ala Phe Ile Tyr Ser Gly
 180 185 190

Leu Phe Trp Gly Leu Leu Pro Thr Gln Ile Gly Val Ser Trp Gln Gly
 195 200 205

His Leu Phe Gly Ala Leu Gly Gly Ile Gly Ala Gly Ala Phe Ile Ala
 210 215 220

Ser Asp Asp Pro Ala Ala Leu Lys Ala Lys Lys Gln Gln Lys Lys Leu
 225 230 235 240

Glu Lys Gln Gln Arg Gln Arg Gly Leu
245

<210> 203

<211> 840

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(817)

<223> RXN01580

<400> 203

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Met Tyr Lys Asn Met
1 5

cac att gtt gcc cat cgc ggt gcg gaa gat ctg cac ctc gaa aac acc 163
His Ile Val Ala His Arg Gly Ala Glu Asp Leu His Leu Glu Asn Thr
10 15 20

atg acc gct ttc cag gct gcc gcg ccc gct gac gct ttt gag ctg gat 211
Met Thr Ala Phe Gln Ala Ala Ala Pro Ala Asp Ala Phe Glu Leu Asp
25 30 35

atc cac gcc acc gct gac aat cag gtc gtc gtt atc cac gac cgc acc 259
Ile His Ala Thr Ala Asp Asn Gln Val Val Val Ile His Asp Arg Thr
40 45 50

gca gcg cgt gtt gcc gcg cca gat tcc ctg cac cgc gac acc ccg gtt 307
Ala Ala Arg Val Ala Ala Pro Asp Ser Leu His Arg Asp Thr Pro Val
55 60 65

gcg cgc tta agc gcc gcg caa atc aag gag ata acg ctt atc gac gga 355
Ala Arg Leu Ser Ala Ala Gln Ile Lys Glu Ile Thr Leu Ile Asp Gly
70 75 80 85

tcc ccc gta cca acc ctg gag gaa gtt cta ctc cag acg agc ctg ccg 403
Ser Pro Val Pro Thr Leu Glu Glu Val Leu Leu Gln Thr Ser Leu Pro
90 95 100

atc caa gtg gaa atc aaa tct gcc ggt gca gtt cca gca gcc gca gca 451
Ile Gln Val Glu Ile Lys Ser Ala Gly Ala Val Pro Ala Ala Ala Ala
105 110 115

tta ttg cag aaa tac cca gag cac ctg gag cgc ctg ctg ttc atc agt 499
Leu Leu Gln Lys Tyr Pro Glu His Leu Glu Arg Leu Leu Phe Ile Ser
120 125 130

ttc atc gat gca gca ctg gtg gaa atc gtg gat cga ctg cca gaa gct 547
Phe Ile Asp Ala Ala Leu Val Glu Ile Val Asp Arg Leu Pro Glu Ala
135 140 145

cgc gtg gga atc ttg cgc gat gcg tcc atg gat gat ctg cgc att ctt 595
Arg Val Gly Ile Leu Arg Asp Ala Ser Met Asp Asp Leu Arg Ile Leu
150 155 160 165

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165	170	175
Leu Pro Ser Trp Lys Ala Leu Asn Val Ala Ser Ile Ala Asp Leu His		
180	185	190
Thr Lys Gly Ile Lys Val Gly Cys Trp Thr Ile Arg Asp Glu Asn Ala		
195	200	205
Phe Gly Ile Ala Gln Gln Ala Gly Val Asp Tyr Ala Thr Val Ser Asp		
210	215	220
Pro Ser Arg Phe Leu Ala Pro Ser Pro Ala Gly Glu Leu His Trp		
225	230	235

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 <223> RXA01436

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 Met Ala Leu Ala Leu
 1 5
 gtt ttg aac tcc ggt tca tct tcc atc aaa ttc cag ctg gtc aac ccc 163
 Val Leu Asn Ser Gly Ser Ser Ser Ile Lys Phe Gln Leu Val Asn Pro
 10 15 20
 gaa aac tct gcc atc gac gag cca tat gtt tct ggt ctt gtg gag cag 211
 Glu Asn Ser Ala Ile Asp Glu Pro Tyr Val Ser Gly Leu Val Glu Gln
 25 30 35
 att ggt gag cca aac ggc cgc atc gta ctc aaa ata gag ggt gaa aaa 259
 Ile Gly Glu Pro Asn Gly Arg Ile Val Leu Lys Ile Glu Gly Glu Lys
 40 45 50
 tat acc cta gag aca ccc atc gca gat cac tcc gaa ggc cta aac ctg 307
 Tyr Thr Leu Glu Thr Pro Ile Ala Asp His Ser Glu Gly Leu Asn Leu
 55 60 65
 gcg ttc gat ctc atg gac cag cac aac tgt ggt cct tcc caa ctg gaa 355
 Ala Phe Asp Leu Met Asp Gln His Asn Cys Gly Pro Ser Gln Leu Glu
 70 75 80 85
 atc acc gca gtt gga cac cgc gtg gtc cac ggc gga atc ttg ttc tcc 403
 Ile Thr Ala Val Gly His Arg Val Val His Gly Gly Ile Leu Phe Ser
 90 95 100
 gca ccg gaa ctt atc act gat gaa atc gtg gaa atg atc cgc gat ctc 451
 Ala Pro Glu Leu Ile Thr Asp Glu Ile Val Glu Met Ile Arg Asp Leu
 105 110 115
 att cca ctc gca cca ctg cac aac cct gca aac gtt gac ggc att gat 499

gat tac atc ccg cta aaa aat gtg ggc gcg atc ttg ccc tcg tgg aaa 643
 Asp Tyr Ile Pro Leu Lys Asn Val Gly Ala Ile Leu Pro Ser Trp Lys
 170 175 180

 gca cta aac gtg gcg tca att gct gat cta cat acc aag gga atc aag 691
 Ala Leu Asn Val Ala Ser Ile Ala Asp Leu His Thr Lys Gly Ile Lys
 185 190 195

 gtt ggc tgc tgg aca att cgg gat gaa aat gcg ttt ggg atc gca caa 739
 Val Gly Cys Trp Thr Ile Arg Asp Glu Asn Ala Phe Gly Ile Ala Gln
 200 205 210

 caa gct ggc gtt gat tac gcc act gtt agc gat ccc tct cgt ttc ctc 787
 Gln Ala Gly Val Asp Tyr Ala Thr Val Ser Asp Pro Ser Arg Phe Leu
 215 220 225

 gcg ccc tcc cct gct ggg gag ttg cac tgg taaataatct agtgaccaga 837
 Ala Pro Ser Pro Ala Gly Glu Leu His Trp
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 ctg 840

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 <211> 239
 <212> PRT
 <213> *Corynebacterium glutamicum*

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 20 25 30

 Ala Phe Glu Leu Asp Ile His Ala Thr Ala Asp Asn Gln Val Val Val
 35 40 45

 Ile His Asp Arg Thr Ala Ala Arg Val Ala Ala Pro Asp Ser Leu His
 50 55 60

 Arg Asp Thr Pro Val Ala Arg Leu Ser Ala Ala Gln Ile Lys Glu Ile
 65 70 75 80

 Thr Leu Ile Asp Gly Ser Pro Val Pro Thr Leu Glu Glu Val Leu Leu
 85 90 95

 Gln Thr Ser Leu Pro Ile Gln Val Glu Ile Lys Ser Ala Gly Ala Val
 100 105 110

 Pro Ala Ala Ala Ala Leu Leu Gln Lys Tyr Pro Glu His Leu Glu Arg
 115 120 125

 Leu Leu Phe Ile Ser Phe Ile Asp Ala Ala Leu Val Glu Ile Val Asp
 130 135 140

 Arg Leu Pro Glu Ala Arg Val Gly Ile Leu Arg Asp Ala Ser Met Asp
 145 150 155 160

 Asp Leu Arg Ile Leu Asp Tyr Ile Pro Leu Lys Asn Val Gly Ala Ile

Ile	Pro	Leu	Ala	Pro	Leu	His	Asn	Pro	Ala	Asn	Val	Asp	Gly	Ile	Asp		
		120					125					130					
gtt	gct	cga	aaa	att	ctc	ccc	gat	gtc	cca	cac	gta	gct	gtc	ttt	gac	547	
Val	Ala	Arg	Lys	Ile	Leu	Pro	Asp	Val	Pro	His	Val	Ala	Val	Phe	Asp		
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acc	ggt	ttc	ttc	cac	tca	ctt	cca	cca	gca	gct	gcg	ctg	tat	gcc	atc	595	
Thr	Gly	Phe	Phe	His	Ser	Leu	Pro	Pro	Ala	Ala	Ala	Leu	Tyr	Ala	Ile		
		150			155				160					165			
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Asn	Lys	Asp	Val	Ala	Ala	Glu	His	Gly	Ile	Arg	Arg	Tyr	Gly	Phe	His		
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ggc	acc	tcc	cat	gaa	ttt	gtg	tcc	aag	cgc	gtg	gtg	gaa	att	ctg	gaa	691	
Gly	Thr	Ser	His	Glu	Phe	Val	Ser	Lys	Arg	Val	Val	Glu	Ile	Leu	Glu		
			185					190					195				
aag	ccc	acc	gaa	gac	atc	aac	acc	atc	acc	ttc	cac	ctg	ggc	aac	ggc	739	
Lys	Pro	Thr	Glu	Asp	Ile	Asn	Thr	Ile	Thr	Phe	His	Leu	Gly	Asn	Gly		
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gca	tcc	atg	gct	gct	gtt	caa	ggg	ggc	cgt	gcg	gta	gat	act	tcc	atg	787	
Ala	Ser	Met	Ala	Ala	Val	Gln	Gly	Gly	Arg	Ala	Val	Asp	Thr	Ser	Met		
		215				220					225						
ggg	atg	aca	cct	ctc	gcg	ggc	ctt	gtc	atg	ggg	acc	cga	agc	ggg	gac	835	
Gly	Met	Thr	Pro	Leu	Ala	Gly	Leu	Val	Met	Gly	Thr	Arg	Ser	Gly	Asp		
		230			235				240					245			
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Ile	Asp	Pro	Gly	Ile	Val	Phe	His	Leu	Ser	Arg	Thr	Ala	Gly	Met	Ser		
				250					255					260			
atc	gat	gag	atc	gat	aat	ctg	ctg	aac	aaa	aag	tcg	ggg	gta	aag	gga	931	
Ile	Asp	Glu	Ile	Asp	Asn	Leu	Leu	Asn	Lys	Lys	Ser	Gly	Val	Lys	Gly		
			265					270					275				
ctt	tcc	ggg	gtt	aat	gat	ttc	cgt	gaa	ctg	cgg	gaa	atg	atc	gac	aac	979	
Leu	Ser	Gly	Val	Asn	Asp	Phe	Arg	Glu	Leu	Arg	Glu	Met	Ile	Asp	Asn		
		280					285					290					
aat	gat	caa	gat	gcc	tgg	tcc	gcg	tac	aac	att	tac	ata	cac	caa	ctc	1027	
Asn	Asp	Gln	Asp	Ala	Trp	Ser	Ala	Tyr	Asn	Ile	Tyr	Ile	His	Gln	Leu		
		295				300					305						
cgc	cgc	tac	ctc	ggg	tcc	tac	atg	gtg	gca	ctg	gga	cgg	gta	gac	acc	1075	
Arg	Arg	Tyr	Leu	Gly	Ser	Tyr	Met	Val	Ala	Leu	Gly	Arg	Val	Asp	Thr		
		310			315					320				325			
atc	gtg	ttc	acc	gcc	ggg	gtc	ggg	gaa	aat	gcc	cag	ttt	gtc	cgt	gag	1123	
Ile	Val	Phe	Thr	Ala	Gly	Val	Gly	Glu	Asn	Ala	Gln	Phe	Val	Arg	Glu		
				330				335					340				
gat	gcc	ttg	gca	ggg	ttg	gaa	atg	tac	gga	att	gag	atc	gat	cca	gag	1171	
Asp	Ala	Leu	Ala	Gly	Leu	Glu	Met	Tyr	Gly	Ile	Glu	Ile	Asp	Pro	Glu		
			345					350				355					
cgt	aac	gca	ttg	cca	aac	gat	ggg	cct	cga	ttg	att	tcc	acc	gat	gcc	1219	
Arg	Asn	Ala	Leu	Pro	Asn	Asp	Gly	Pro	Arg	Leu	Ile	Ser	Thr	Asp	Ala		

360 365 370
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 Ser Lys Val Lys Val Phe Val Ile Pro Thr Asn Glu Glu Leu Ala Ile
 375 380 385

gct agg tac gcg gtg aag ttc gct tagctctcct ggtaggatac cac 1314
 Ala Arg Tyr Ala Val Lys Phe Ala
 390 395

<210> 206

<211> 397

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 206

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 20 25 30

Gly Leu Val Glu Gln Ile Gly Glu Pro Asn Gly Arg Ile Val Leu Lys
 35 40 45

Ile Glu Gly Glu Lys Tyr Thr Leu Glu Thr Pro Ile Ala Asp His Ser
 50 55 60

Glu Gly Leu Asn Leu Ala Phe Asp Leu Met Asp Gln His Asn Cys Gly
 65 70 75 80

Pro Ser Gln Leu Glu Ile Thr Ala Val Gly His Arg Val Val His Gly
 85 90 95

Gly Ile Leu Phe Ser Ala Pro Glu Leu Ile Thr Asp Glu Ile Val Glu
 100 105 110

Met Ile Arg Asp Leu Ile Pro Leu Ala Pro Leu His Asn Pro Ala Asn
 115 120 125

Val Asp Gly Ile Asp Val Ala Arg Lys Ile Leu Pro Asp Val Pro His
 130 135 140

Val Ala Val Phe Asp Thr Gly Phe Phe His Ser Leu Pro Pro Ala Ala
 145 150 155 160

Ala Leu Tyr Ala Ile Asn Lys Asp Val Ala Ala Glu His Gly Ile Arg
 165 170 175

Arg Tyr Gly Phe His Gly Thr Ser His Glu Phe Val Ser Lys Arg Val
 180 185 190

Val Glu Ile Leu Glu Lys Pro Thr Glu Asp Ile Asn Thr Ile Thr Phe
 195 200 205

His Leu Gly Asn Gly Ala Ser Met Ala Ala Val Gln Gly Gly Arg Ala
 210 215 220

Val Asp Thr Ser Met Gly Met Thr Pro Leu Ala Gly Leu Val Met Gly
 225 230 235 240

Thr Arg Ser Gly Asp Ile Asp Pro Gly Ile Val Phe His Leu Ser Arg
 245 250 255
 Thr Ala Gly Met Ser Ile Asp Glu Ile Asp Asn Leu Leu Asn Lys Lys
 260 265 270
 Ser Gly Val Lys Gly Leu Ser Gly Val Asn Asp Phe Arg Glu Leu Arg
 275 280 285
 Glu Met Ile Asp Asn Asn Asp Gln Asp Ala Trp Ser Ala Tyr Asn Ile
 290 295 300
 Tyr Ile His Gln Leu Arg Arg Tyr Leu Gly Ser Tyr Met Val Ala Leu
 305 310 315 320
 Gly Arg Val Asp Thr Ile Val Phe Thr Ala Gly Val Gly Glu Asn Ala
 325 330 335
 Gln Phe Val Arg Glu Asp Ala Leu Ala Gly Leu Glu Met Tyr Gly Ile
 340 345 350
 Glu Ile Asp Pro Glu Arg Asn Ala Leu Pro Asn Asp Gly Pro Arg Leu
 355 360 365
 Ile Ser Thr Asp Ala Ser Lys Val Lys Val Phe Val Ile Pro Thr Asn
 370 375 380
 Glu Glu Leu Ala Ile Ala Arg Tyr Ala Val Lys Phe Ala
 385 390 395

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 <211> 927
 <212> DNA
 <213> *Corynebacterium glutamicum*

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 <222> (101)..(904)
 <223> RXA00686

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 Met Ala Gly Gly Asn
 1 5
 cgc gaa cct gga cgt aca gtc acc tcc aag gtg atc gcc gta ctg gga 163
 Arg Glu Pro Gly Arg Thr Val Thr Ser Lys Val Ile Ala Val Leu Gly
 10 15 20
 gct ttt gaa cac acc atg cgt cca ctt ggt gtc act gaa atc gct gag 211
 Ala Phe Glu His Thr Met Arg Pro Leu Gly Val Thr Glu Ile Ala Glu
 25 30 35
 ctg gca gac ctc cca cca agt acc acc cac cgt ctc gtt tct gaa tta 259
 Leu Ala Asp Leu Pro Pro Ser Thr Thr His Arg Leu Val Ser Glu Leu
 40 45 50

acc gaa ggc gga cta ctc agc aag aaa tct gat ggg cgc tac caa ttg 307
 Thr Glu Gly Gly Leu Leu Ser Lys Lys Ser Asp Gly Arg Tyr Gln Leu
 55 60 65

ggc tta cgt atc tgg gaa ctc gcc caa aat aca gga cgg cag tta cgc 355
 Gly Leu Arg Ile Trp Glu Leu Ala Gln Asn Thr Gly Arg Gln Leu Arg
 70 75 80 85

gac act gca cgc ccg ttc atc caa gag ctc tac tca ctt act tcc gag 403
 Asp Thr Ala Arg Pro Phe Ile Gln Glu Leu Tyr Ser Leu Thr Ser Glu
 90 95 100

act gcg cag cta gtg gtc cgc gat aaa gat gaa gca ctt ttg att gac 451
 Thr Ala Gln Leu Val Val Arg Asp Lys Asp Glu Ala Leu Leu Ile Asp
 105 110 115

cga gcc tac ggc acg aag aaa att cca cgc tcg gct cga gtc ggt ggt 499
 Arg Ala Tyr Gly Thr Lys Lys Ile Pro Arg Ser Ala Arg Val Gly Gly
 120 125 130

cga cta cct ctg aac tcc act gcg gtt ggc aag att ctc ctt gcg ttt 547
 Arg Leu Pro Leu Asn Ser Thr Ala Val Gly Lys Ile Leu Leu Ala Phe
 135 140 145

gat gag cca tgg gta aaa cag tcc tat ctc aag ctg cca ctc aac gcc 595
 Asp Glu Pro Trp Val Lys Gln Ser Tyr Leu Lys Leu Pro Leu Asn Ala
 150 155 160 165

tcc acc cca aag aca att gtg aat ccc gac gtc ttg gct gcg cag ctg 643
 Ser Thr Pro Lys Thr Ile Val Asn Pro Asp Val Leu Ala Ala Gln Leu
 170 175 180

aaa caa att cac tcg caa ggc ttt gcc atc aca cat gac gag caa cga 691
 Lys Gln Ile His Ser Gln Gly Phe Ala Ile Thr His Asp Glu Gln Arg
 185 190 195

atc ggc ggc gca tcg atc gcc gta ccg gtc tgg cat aca gga aaa ctg 739
 Ile Gly Gly Ala Ser Ile Ala Val Pro Val Trp His Thr Gly Lys Leu
 200 205 210

gga gca gca ctg ggg ttg gtg gtt ccc acc gca cag gct gca aat ctt 787
 Gly Ala Ala Leu Gly Leu Val Val Pro Thr Ala Gln Ala Ala Asn Leu
 215 220 225

gag cgc tat ctc ccg atc ctt cag gcg aca agt cag aga att aca aaa 835
 Glu Arg Tyr Leu Pro Ile Leu Gln Ala Thr Ser Gln Arg Ile Thr Lys
 230 235 240 245

gca acc gcg ctc att cct ttg gac aca ctt ttg gct tca cac aaa aat 883
 Ala Thr Ala Leu Ile Pro Leu Asp Thr Leu Leu Ala Ser His Lys Asn
 250 255 260

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<210> 208

<211> 268

<212> PRT

<213> Corynebacterium glutamicum

<400> 208

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Thr Glu Ile Ala Glu Leu Ala Asp Leu Pro Pro Ser Thr Thr His Arg
      35           40           45

Leu Val Ser Glu Leu Thr Glu Gly Gly Leu Leu Ser Lys Lys Ser Asp
      50           55           60

Gly Arg Tyr Gln Leu Gly Leu Arg Ile Trp Glu Leu Ala Gln Asn Thr
      65           70           75           80

Gly Arg Gln Leu Arg Asp Thr Ala Arg Pro Phe Ile Gln Glu Leu Tyr
      85           90           95

Ser Leu Thr Ser Glu Thr Ala Gln Leu Val Val Arg Asp Lys Asp Glu
      100           105           110

Ala Leu Leu Ile Asp Arg Ala Tyr Gly Thr Lys Lys Ile Pro Arg Ser
      115           120           125

Ala Arg Val Gly Gly Arg Leu Pro Leu Asn Ser Thr Ala Val Gly Lys
      130           135           140

Ile Leu Leu Ala Phe Asp Glu Pro Trp Val Lys Gln Ser Tyr Leu Lys
      145           150           155           160

Leu Pro Leu Asn Ala Ser Thr Pro Lys Thr Ile Val Asn Pro Asp Val
      165           170           175

Leu Ala Ala Gln Leu Lys Gln Ile His Ser Gln Gly Phe Ala Ile Thr
      180           185           190

His Asp Glu Gln Arg Ile Gly Gly Ala Ser Ile Ala Val Pro Val Trp
      195           200           205

His Thr Gly Lys Leu Gly Ala Ala Leu Gly Leu Val Val Pro Thr Ala
      210           215           220

Gln Ala Ala Asn Leu Glu Arg Tyr Leu Pro Ile Leu Gln Ala Thr Ser
      225           230           235           240

Gln Arg Ile Thr Lys Ala Thr Ala Leu Ile Pro Leu Asp Thr Leu Leu
      245           250           255

Ala Ser His Lys Asn Ala Glu Arg Lys Gly Asp Thr
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<211> 1158

<212> DNA

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<220>

<221> CDS

<222> (101)..(1135)

<223> RXA00246

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                                   Met Thr Thr Ala Ala
                                   1 5

ccc caa gaa ttt acc gct gct gtt gtt gaa aaa ttc ggt cat gac gtg 163
Pro Gln Glu Phe Thr Ala Ala Val Val Glu Lys Phe Gly His Asp Val
                                   10 15 20

acc gtg aag gat att gac ctt cca aag cca ggg cca cac cag gca ttg 211
Thr Val Lys Asp Ile Asp Leu Pro Lys Pro Gly Pro His Gln Ala Leu
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gtg aag gta ctc acc tcc ggc atc tgc cac acc gac ctc cac gcc ttg 259
Val Lys Val Leu Thr Ser Gly Ile Cys His Thr Asp Leu His Ala Leu
                                   40 45 50

gag ggc gat tgg cca gta aag ccg gaa cca cca ttc gta cca gga cac 307
Glu Gly Asp Trp Pro Val Lys Pro Glu Pro Pro Phe Val Pro Gly His
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gaa ggt gta ggt gaa gtt gtt gag ctc gga cca ggt gaa cac gat gtg 355
Glu Gly Val Gly Glu Val Val Glu Leu Gly Pro Gly Glu His Asp Val
                                   70 75 80 85

aag gtc ggc gat att gtc ggc aat gcg tgg ctc tgg tca gcg tgt ggc 403
Lys Val Gly Asp Ile Val Gly Asn Ala Trp Leu Trp Ser Ala Cys Gly
                                   90 95 100

acc tgc gaa tac tgc atc acc ggc agg gaa act cag tgc aac gaa gct 451
Thr Cys Glu Tyr Cys Ile Thr Gly Arg Glu Thr Gln Cys Asn Glu Ala
                                   105 110 115

gag tat ggt ggc tac acc caa aat gga tcc ttc ggc cag tac atg ctg 499
Glu Tyr Gly Gly Tyr Thr Gln Asn Gly Ser Phe Gly Gln Tyr Met Leu
                                   120 125 130

gtg gat acc cgt tac gcc gct cgc atc cca gac ggc gtg gac tac ctc 547
Val Asp Thr Arg Tyr Ala Ala Arg Ile Pro Asp Gly Val Asp Tyr Leu
                                   135 140 145

gaa gca gca cca att ctg tgt gca ggc gtg act gtc tac aag gca ctc 595
Glu Ala Ala Pro Ile Leu Cys Ala Gly Val Thr Val Tyr Lys Ala Leu
                                   150 155 160 165

aaa gtc tct gaa acc cgc ccg ggc caa ttc atg gtg atc tcc ggt gtc 643
Lys Val Ser Glu Thr Arg Pro Gly Gln Phe Met Val Ile Ser Gly Val
                                   170 175 180

ggc gga ctt ggc cac atc gca gtc caa tac gca gcg gcg atg ggc atg 691
Gly Gly Leu Gly His Ile Ala Val Gln Tyr Ala Ala Ala Met Gly Met
                                   185 190 195

cgt gtc att gcg gta gat att gcc gat gac aag ctg gaa ctt gcc cgt 739
Arg Val Ile Ala Val Asp Ile Ala Asp Asp Lys Leu Glu Leu Ala Arg
                                   200 205 210

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aag cac ggt gcg gaa ttt acc gtg aat gcg cgt aat gaa gat tca ggc 787
 Lys His Gly Ala Glu Phe Thr Val Asn Ala Arg Asn Glu Asp Ser Gly
 215 220 225

 gaa gct gta cag aag tac acc aac ggt ggc gca cac ggc gtg ctt gtg 835
 Glu Ala Val Gln Lys Tyr Thr Asn Gly Gly Ala His Gly Val Leu Val
 230 235 240 245

 act gca gtt cac gag gca gca ttc ggc cag gca ctg gat atg gct cga 883
 Thr Ala Val His Glu Ala Ala Phe Gly Gln Ala Leu Asp Met Ala Arg
 250 255 260

 cgt gca gga aca att gtg ttc aac ggt ctg cca ccg gga gag ttc cca 931
 Arg Ala Gly Thr Ile Val Phe Asn Gly Leu Pro Pro Gly Glu Phe Pro
 265 270 275

 gca tcc gtg ttc aac atc gta ttc aag ggc ctg acc atc cgt gga tcc 979
 Ala Ser Val Phe Asn Ile Val Phe Lys Gly Leu Thr Ile Arg Gly Ser
 280 285 290

 ctc gtg gga acc cgc caa gac ttg gcc gaa gcg ctc gat ttc ttt gca 1027
 Leu Val Gly Thr Arg Gln Asp Leu Ala Glu Ala Leu Asp Phe Phe Ala
 295 300 305

 cgc gga cta atc aag cca acc gtg agt gag tgc tcc ctc gat gag gtc 1075
 Arg Gly Leu Ile Lys Pro Thr Val Ser Glu Cys Ser Leu Asp Glu Val
 310 315 320 325

 aat ggt gtg ctt gac cgc atg cga aac ggc aag atc gat ggt cgt gtg 1123
 Asn Gly Val Leu Asp Arg Met Arg Asn Gly Lys Ile Asp Gly Arg Val
 330 335 340

 gcg att cgt ttc taacggattg tgttgaaact gct 1158
 Ala Ile Arg Phe
 345

<210> 210

<211> 345

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 210

Met Thr Thr Ala Ala Pro Gln Glu Phe Thr Ala Ala Val Val Glu Lys
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 Phe Gly His Asp Val Thr Val Lys Asp Ile Asp Leu Pro Lys Pro Gly
 20 25 30

 Pro His Gln Ala Leu Val Lys Val Leu Thr Ser Gly Ile Cys His Thr
 35 40 45

 Asp Leu His Ala Leu Glu Gly Asp Trp Pro Val Lys Pro Glu Pro Pro
 50 55 60

 Phe Val Pro Gly His Glu Gly Val Gly Glu Val Val Glu Leu Gly Pro
 65 70 75 80

 Gly Glu His Asp Val Lys Val Gly Asp Ile Val Gly Asn Ala Trp Leu
 85 90 95

Trp Ser Ala Cys Gly Thr Cys Glu Tyr Cys Ile Thr Gly Arg Glu Thr
 100 105 110
 Gln Cys Asn Glu Ala Glu Tyr Gly Gly Tyr Thr Gln Asn Gly Ser Phe
 115 120 125
 Gly Gln Tyr Met Leu Val Asp Thr Arg Tyr Ala Ala Arg Ile Pro Asp
 130 135 140
 Gly Val Asp Tyr Leu Glu Ala Ala Pro Ile Leu Cys Ala Gly Val Thr
 145 150 155 160
 Val Tyr Lys Ala Leu Lys Val Ser Glu Thr Arg Pro Gly Gln Phe Met
 165 170 175
 Val Ile Ser Gly Val Gly Gly Leu Gly His Ile Ala Val Gln Tyr Ala
 180 185 190
 Ala Ala Met Gly Met Arg Val Ile Ala Val Asp Ile Ala Asp Asp Lys
 195 200 205
 Leu Glu Leu Ala Arg Lys His Gly Ala Glu Phe Thr Val Asn Ala Arg
 210 215 220
 Asn Glu Asp Ser Gly Glu Ala Val Gln Lys Tyr Thr Asn Gly Gly Ala
 225 230 235 240
 His Gly Val Leu Val Thr Ala Val His Glu Ala Ala Phe Gly Gln Ala
 245 250 255
 Leu Asp Met Ala Arg Arg Ala Gly Thr Ile Val Phe Asn Gly Leu Pro
 260 265 270
 Pro Gly Glu Phe Pro Ala Ser Val Phe Asn Ile Val Phe Lys Gly Leu
 275 280 285
 Thr Ile Arg Gly Ser Leu Val Gly Thr Arg Gln Asp Leu Ala Glu Ala
 290 295 300
 Leu Asp Phe Phe Ala Arg Gly Leu Ile Lys Pro Thr Val Ser Glu Cys
 305 310 315 320
 Ser Leu Asp Glu Val Asn Gly Val Leu Asp Arg Met Arg Asn Gly Lys
 325 330 335
 Ile Asp Gly Arg Val Ala Ile Arg Phe
 340 345

<210> 211
 <211> 723
 <212> DNA
 <213> *Corynebacterium glutamicum*

<220>
 <221> CDS
 <222> (101)..(700)
 <223> RXA01571

<400> 211

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cgctcgtagg cgcttttgat ttttcggtag gctaactggg gtg agt atc tca gta 115
                                   Val Ser Ile Ser Val
                                   1 5

aaa gca cta caa aag tcc ggc cca gaa gca cct ttc gag gtc aag atc 163
Lys Ala Leu Gln Lys Ser Gly Pro Glu Ala Pro Phe Glu Val Lys Ile
                                   10 15 20

att gaa cgc cgt gac cca cgc gca gat gat gtg gtt att gat atc aaa 211
Ile Glu Arg Arg Asp Pro Arg Ala Asp Asp Val Val Ile Asp Ile Lys
                                   25 30 35

gct gcg ggc atc tgc cac agc gat atc cac acc atc cgc aac gaa tgg 259
Ala Ala Gly Ile Cys His Ser Asp Ile His Thr Ile Arg Asn Glu Trp
                                   40 45 50

ggc gag gcg cac ttc ccg ctc acc gtc ggc cac gaa atc gca ggc gtt 307
Gly Glu Ala His Phe Pro Leu Thr Val Gly His Glu Ile Ala Gly Val
                                   55 60 65

gtc tct gcg gtt gga tcc gat gta acc aaa tgg aaa gtc ggc gac cgc 355
Val Ser Ala Val Gly Ser Asp Val Thr Lys Trp Lys Val Gly Asp Arg
                                   70 75 80 85

gtg ggc gtc ggc tgc ctc gtt aac tcc tgc ggc gaa tgc gaa cag tgc 403
Val Gly Val Gly Cys Leu Val Asn Ser Cys Gly Glu Cys Glu Gln Cys
                                   90 95 100

gtc gca gga ttt gaa aac aac tgc ctt cgc gga aac gtc gga acc tac 451
Val Ala Gly Phe Glu Asn Asn Cys Leu Arg Gly Asn Val Gly Thr Tyr
                                   105 110 115

aac tct aac gac gtc gac ggc acc atc acc caa ggc ggc tac gct gaa 499
Asn Ser Asn Asp Val Asp Gly Thr Ile Thr Gln Gly Gly Tyr Ala Glu
                                   120 125 130

aag gta gtg gtc aac gaa cgt ttc ctg tgc agc atc cca gag gaa ctt 547
Lys Val Val Val Asn Glu Arg Phe Leu Cys Ser Ile Pro Glu Glu Leu
                                   135 140 145

aac ttc gat gtc gca gca cca ctg ctg tgc gca ggc atc acc acc tac 595
Asn Phe Asp Val Ala Ala Pro Leu Leu Cys Ala Gly Ile Thr Thr Tyr
                                   150 155 160 165

tcc cca atc gct cgc tgg aac gtt aaa gaa ggc gac aaa gta gca gtc 643
Ser Pro Ile Ala Arg Trp Asn Val Lys Glu Gly Asp Lys Val Ala Val
                                   170 175 180

atg ggc ctc ggc ggg act cgg aca cat ggg tgt cca gat cgc tgc agc 691
Met Gly Leu Gly Gly Thr Arg Thr His Gly Cys Pro Asp Arg Cys Ser
                                   185 190 195

caa ggg tgc tgaggttacc gttctgtccc gtt 723
Gln Gly Cys
                                   200

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<210> 212

<211> 200

<212> PRT

<213> Corynebacterium glutamicum

<400> 212

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Val Ser Ile Ser Val Lys Ala Leu Gln Lys Ser Gly Pro Glu Ala Pro
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Phe Glu Val Lys Ile Ile Glu Arg Arg Asp Pro Arg Ala Asp Asp Val
      20           25           30
Val Ile Asp Ile Lys Ala Ala Gly Ile Cys His Ser Asp Ile His Thr
      35           40           45
Ile Arg Asn Glu Trp Gly Glu Ala His Phe Pro Leu Thr Val Gly His
      50           55           60
Glu Ile Ala Gly Val Val Ser Ala Val Gly Ser Asp Val Thr Lys Trp
      65           70           75           80
Lys Val Gly Asp Arg Val Gly Val Gly Cys Leu Val Asn Ser Cys Gly
      85           90           95
Glu Cys Glu Gln Cys Val Ala Gly Phe Glu Asn Asn Cys Leu Arg Gly
      100          105          110
Asn Val Gly Thr Tyr Asn Ser Asn Asp Val Asp Gly Thr Ile Thr Gln
      115          120          125
Gly Gly Tyr Ala Glu Lys Val Val Val Asn Glu Arg Phe Leu Cys Ser
      130          135          140
Ile Pro Glu Glu Leu Asn Phe Asp Val Ala Ala Pro Leu Leu Cys Ala
      145          150          155          160
Gly Ile Thr Thr Tyr Ser Pro Ile Ala Arg Trp Asn Val Lys Glu Gly
      165          170          175
Asp Lys Val Ala Val Met Gly Leu Gly Gly Thr Arg Thr His Gly Cys
      180          185          190
Pro Asp Arg Cys Ser Gln Gly Cys
      195          200

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<210> 213

<211> 615

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(592)

<223> RXA01572

<400> 213

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gacaaagtag cagtcattggg cctcggcggg actcggacac atg ggt gtc cag atc 115
              Met Gly Val Gln Ile
              1           5

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gct gca gcc aag ggt gct gag gtt acc gtt ctg tcc cgt tcc ctg cgc 163
 Ala Ala Ala Lys Gly Ala Glu Val Thr Val Leu Ser Arg Ser Leu Arg
 10 15 20

 aag gca gaa ctt gcc aag gaa ctc ggc gca gct cgc acg ctt gcg act 211
 Lys Ala Glu Leu Ala Lys Glu Leu Gly Ala Ala Arg Thr Leu Ala Thr
 25 30 35

 tct gat gag gat ttc ttc acc gaa cac gcc ggt gaa ttc gac ttc atc 259
 Ser Asp Glu Asp Phe Phe Thr Glu His Ala Gly Glu Phe Asp Phe Ile
 40 45 50

 ctc aac acc att agc gca tcc atc cca gtc gac aag tac ctg agc ctt 307
 Leu Asn Thr Ile Ser Ala Ser Ile Pro Val Asp Lys Tyr Leu Ser Leu
 55 60 65

 ctc aag cca cac ggt gtc atg gct gtt gtc ggt ctg cca cca gag aag 355
 Leu Lys Pro His Gly Val Met Ala Val Val Gly Leu Pro Pro Glu Lys
 70 75 80 85

 cag cca ctg agc ttc ggt gcg ctc atc ggc ggc gga aaa gtc ctc acc 403
 Gln Pro Leu Ser Phe Gly Ala Leu Ile Gly Gly Gly Lys Val Leu Thr
 90 95 100

 gga tcc aac att ggc ggc atc cct gaa acc cag gaa atg ctc gac ttc 451
 Gly Ser Asn Ile Gly Gly Ile Pro Glu Thr Gln Glu Met Leu Asp Phe
 105 110 115

 tgt gca aaa cac ggc ctc ggt gcg atg atc gaa act gtc ggc gtc aac 499
 Cys Ala Lys His Gly Leu Gly Ala Met Ile Glu Thr Val Gly Val Asn
 120 125 130

 gat gtt gat gca gcc tac gac cgt gtt gtt gcc ggc gac gtt cag ttc 547
 Asp Val Asp Ala Ala Tyr Asp Arg Val Val Ala Gly Asp Val Gln Phe
 135 140 145

 cgc gtt gtc att gat act gct tcg ttt gct gag gtt gag gcg gtt 592
 Arg Val Val Ile Asp Thr Ala Ser Phe Ala Glu Val Glu Ala Val
 150 155 160

 taggtttact gaagttcaga ctt 615

<210> 214

<211> 164

<212> PRT

<213> Corynebacterium glutamicum

<400> 214

Met Gly Val Gln Ile Ala Ala Ala Lys Gly Ala Glu Val Thr Val Leu
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 Ser Arg Ser Leu Arg Lys Ala Glu Leu Ala Lys Glu Leu Gly Ala Ala
 20 25 30

 Arg Thr Leu Ala Thr Ser Asp Glu Asp Phe Phe Thr Glu His Ala Gly
 35 40 45

 Glu Phe Asp Phe Ile Leu Asn Thr Ile Ser Ala Ser Ile Pro Val Asp
 50 55 60

Lys Tyr Leu Ser Leu Leu Lys Pro His Gly Val Met Ala Val Val Gly
 65 70 75 80
 Leu Pro Pro Glu Lys Gln Pro Leu Ser Phe Gly Ala Leu Ile Gly Gly
 85 90 95
 Gly Lys Val Leu Thr Gly Ser Asn Ile Gly Gly Ile Pro Glu Thr Gln
 100 105 110
 Glu Met Leu Asp Phe Cys Ala Lys His Gly Leu Gly Ala Met Ile Glu
 115 120 125
 Thr Val Gly Val Asn Asp Val Asp Ala Ala Tyr Asp Arg Val Val Ala
 130 135 140
 Gly Asp Val Gln Phe Arg Val Val Ile Asp Thr Ala Ser Phe Ala Glu
 145 150 155 160
 Val Glu Ala Val

<210> 215
 <211> 1140
 <212> DNA
 <213> *Corynebacterium glutamicum*

<220>
 <221> CDS
 <222> (101)..(1117)
 <223> RXA01758

<400> 215
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 gatagcgcgc tcagaagttc tttagtga aa gcagaaccaa atg ccc aaa tac att 115
 Met Pro Lys Tyr Ile
 1 5
 gcc atg cag gta tcc gaa tcc ggt gca ccg tta gcc gcg aat ctc gtg 163
 Ala Met Gln Val Ser Glu Ser Gly Ala Pro Leu Ala Ala Asn Leu Val
 10 15 20
 caa cct gct ccg ttg aaa tcg agg gaa gtc cgc gtg gaa atc gct gct 211
 Gln Pro Ala Pro Leu Lys Ser Arg Glu Val Arg Val Glu Ile Ala Ala
 25 30 35
 agt ggt gtg tgc cat gca gat att ggc acg gca gca gca tcg ggg aag 259
 Ser Gly Val Cys His Ala Asp Ile Gly Thr Ala Ala Ala Ser Gly Lys
 40 45 50
 cac act gtt ttt cct gtt acc cct ggt cat gag att gca gga acc atc 307
 His Thr Val Phe Pro Val Thr Pro Gly His Glu Ile Ala Gly Thr Ile
 55 60 65
 gcg gaa att ggt gaa aac gta tct cgg tgg acg gtt ggt gat cgc gtt 355
 Ala Glu Ile Gly Glu Asn Val Ser Arg Trp Thr Val Gly Asp Arg Val
 70 75 80 85
 gca atc ggt tgg ttt ggt ggc aat tgc ggt gac tgc gct ttt tgt cgt 403
 Ala Ile Gly Trp Phe Gly Gly Asn Cys Gly Asp Cys Ala Phe Cys Arg

90								95				100				
gca	ggt	gat	cct	gtg	cat	tgc	aga	gag	cgg	aag	att	cct	ggc	ggt	tct	451
Ala	Gly	Asp	Pro	Val	His	Cys	Arg	Glu	Arg	Lys	Ile	Pro	Gly	Val	Ser	
			105					110					115			
tat	gcg	ggt	ggt	tgg	gca	cag	aat	att	ggt	ggt	cca	gcg	gag	gct	ctt	499
Tyr	Ala	Gly	Gly	Trp	Ala	Gln	Asn	Ile	Val	Val	Pro	Ala	Glu	Ala	Leu	
		120					125					130				
gct	gcg	att	cca	gat	ggc	atg	gac	ttt	tac	gag	ccc	gcc	ccg	atg	ggc	547
Ala	Ala	Ile	Pro	Asp	Gly	Met	Asp	Phe	Tyr	Glu	Pro	Ala	Pro	Met	Gly	
		135				140					145					
tgc	gca	ggt	gtg	aca	aca	ttc	aat	gcg	ttg	cga	aac	ctg	aag	ctg	gat	595
Cys	Ala	Gly	Val	Thr	Thr	Phe	Asn	Ala	Leu	Arg	Asn	Leu	Lys	Leu	Asp	
150					155					160					165	
ccc	ggt	gcg	gct	gtc	gcg	gtc	ttt	gga	atc	ggc	ggt	tta	gtg	cgc	cta	643
Pro	Gly	Ala	Ala	Val	Ala	Val	Phe	Gly	Ile	Gly	Gly	Leu	Val	Arg	Leu	
				170					175					180		
gct	att	cag	ttt	gct	gcg	aaa	atg	ggt	tat	cga	acc	atc	acc	atc	gcc	691
Ala	Ile	Gln	Phe	Ala	Ala	Lys	Met	Gly	Tyr	Arg	Thr	Ile	Thr	Ile	Ala	
			185					190					195			
cgc	ggt	tta	gag	cgt	gag	gag	cta	gct	agg	caa	ctt	ggc	gcc	aac	cac	739
Arg	Gly	Leu	Glu	Arg	Glu	Glu	Leu	Ala	Arg	Gln	Leu	Gly	Ala	Asn	His	
		200					205					210				
tac	atc	gat	agc	aat	gat	ctg	cac	cct	ggc	cag	gcg	tta	ttt	gaa	ctt	787
Tyr	Ile	Asp	Ser	Asn	Asp	Leu	His	Pro	Gly	Gln	Ala	Leu	Phe	Glu	Leu	
		215				220					225					
ggc	ggg	gct	gac	ttg	atc	ttg	tct	act	gcg	tcc	acc	acg	gag	cct	ctt	835
Gly	Gly	Ala	Asp	Leu	Ile	Leu	Ser	Thr	Ala	Ser	Thr	Thr	Glu	Pro	Leu	
230					235					240					245	
tcg	gag	ttg	tct	acc	ggt	ctt	tct	att	ggc	ggg	cag	cta	acc	att	atc	883
Ser	Glu	Leu	Ser	Thr	Gly	Leu	Ser	Ile	Gly	Gly	Gln	Leu	Thr	Ile	Ile	
				250					255					260		
gga	ggt	gat	ggg	gga	gat	atc	acc	ggt	tcg	gca	gcc	caa	ttg	atg	atg	931
Gly	Val	Asp	Gly	Gly	Asp	Ile	Thr	Val	Ser	Ala	Ala	Gln	Leu	Met	Met	
			265					270					275			
aac	cgt	cag	atc	atc	aca	ggt	cac	ctc	act	gga	agt	gcg	aat	gac	acg	979
Asn	Arg	Gln	Ile	Ile	Thr	Gly	His	Leu	Thr	Gly	Ser	Ala	Asn	Asp	Thr	
		280					285					290				
gaa	cag	act	atg	aaa	ttt	gct	cat	ctc	cat	ggc	gtg	aaa	ccg	ctt	att	1027
Glu	Gln	Thr	Met	Lys	Phe											

taatgccaac agcaagccca att

1140

<210> 216

<211> 339

<212> PRT

<213> Corynebacterium glutamicum

<400> 216

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Ala	Ala	Asn	Leu	Val	Gln	Pro	Ala	Pro	Leu	Lys	Ser	Arg	Glu	Val	Arg	20	25	30	
Val	Glu	Ile	Ala	Ala	Ser	Gly	Val	Cys	His	Ala	Asp	Ile	Gly	Thr	Ala	35	40	45	
Ala	Ala	Ser	Gly	Lys	His	Thr	Val	Phe	Pro	Val	Thr	Pro	Gly	His	Glu	50	55	60	
Ile	Ala	Gly	Thr	Ile	Ala	Glu	Ile	Gly	Glu	Asn	Val	Ser	Arg	Trp	Thr	65	70	75	80
Val	Gly	Asp	Arg	Val	Ala	Ile	Gly	Trp	Phe	Gly	Gly	Asn	Cys	Gly	Asp	85	90	95	
Cys	Ala	Phe	Cys	Arg	Ala	Gly	Asp	Pro	Val	His	Cys	Arg	Glu	Arg	Lys	100	105	110	
Ile	Pro	Gly	Val	Ser	Tyr	Ala	Gly	Gly	Trp	Ala	Gln	Asn	Ile	Val	Val	115	120	125	
Pro	Ala	Glu	Ala	Leu	Ala	Ala	Ile	Pro	Asp	Gly	Met	Asp	Phe	Tyr	Glu	130	135	140	
Pro	Ala	Pro	Met	Gly	Cys	Ala	Gly	Val	Thr	Thr	Phe	Asn	Ala	Leu	Arg	145	150	155	160
Asn	Leu	Lys	Leu	Asp	Pro	Gly	Ala	Ala	Val	Ala	Val	Phe	Gly	Ile	Gly	165	170	175	
Gly	Leu	Val	Arg	Leu	Ala	Ile	Gln	Phe	Ala	Ala	Lys	Met	Gly	Tyr	Arg	180	185	190	
Thr	Ile	Thr	Ile	Ala	Arg	Gly	Leu	Glu	Arg	Glu	Glu	Leu	Ala	Arg	Gln	195	200	205	
Leu	Gly	Ala	Asn	His	Tyr	Ile	Asp	Ser	Asn	Asp	Leu	His	Pro	Gly	Gln	210	215	220	
Ala	Leu	Phe	Glu	Leu	Gly	Gly	Ala	Asp	Leu	Ile	Leu	Ser	Thr	Ala	Ser	225	230	235	240
Thr	Thr	Glu	Pro	Leu	Ser	Glu	Leu	Ser	Thr	Gly	Leu	Ser	Ile	Gly	Gly	245	250	255	
Gln	Leu	Thr	Ile	Ile	Gly	Val	Asp	Gly	Gly	Asp	Ile	Thr	Val	Ser	Ala	260	265	270	

Ala Gln Leu Met Met Asn Arg Gln Ile Ile Thr Gly His Leu Thr Gly
 275 280 285

Ser Ala Asn Asp Thr Glu Gln Thr Met Lys Phe Ala His Leu His Gly
 290 295 300

Val Lys Pro Leu Ile Glu Arg Met Pro Leu Asp Gln Ala Asn Glu Ala
 305 310 315 320

Ile Ala Arg Ile Ser Ala Gly Lys Pro Arg Phe Arg Ile Val Leu Glu
 325 330 335

Pro Asn Ser

<210> 217
 <211> 1641
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1618)
 <223> RXA02539

<400> 217
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acaggtagtg ctcagggtgga ggtggcccaa aggagaccca atg act gtc tac gca 115
 Met Thr Val Tyr Ala
 1 5

aat cca gga acc gaa ggc tcg atc gtt aac tat gaa aag cgc tac gag 163
 Asn Pro Gly Thr Glu Gly Ser Ile Val Asn Tyr Glu Lys Arg Tyr Glu
 10 15 20

aac tac att ggt ggc aag tgg gtt cca ccg gta gag ggc cag tac ctt 211
 Asn Tyr Ile Gly Gly Lys Trp Val Pro Pro Val Glu Gly Gln Tyr Leu
 25 30 35

gag aac att tca cct gtc act ggt gaa gtt ttc tgt gag gtc gca cgt 259
 Glu Asn Ile Ser Pro Val Thr Gly Glu Val Phe Cys Glu Val Ala Arg
 40 45 50

ggc acc gca gcg gac gtg gag ctt gca ctg gat gct gca cat gca gcc 307
 Gly Thr Ala Ala Asp Val Glu Leu Ala Leu Asp Ala Ala His Ala Ala
 55 60 65

gct gat gcg tgg ggc aag act tct gtc gct gaa cgt gct ctg atc ctg 355
 Ala Asp Ala Trp Gly Lys Thr Ser Val Ala Glu Arg Ala Leu Ile Leu
 70 75 80 85

cac cgc att gcg gac cgc atg gaa gag cac ctg gaa gaa atc gca gtt 403
 His Arg Ile Ala Asp Arg Met Glu Glu His Leu Glu Glu Ile Ala Val
 90 95 100

gca gaa acc tgg gag aac ggc aag gca gtc cgt gag act ctt gct gca 451
 Ala Glu Thr Trp Glu Asn Gly Lys Ala Val Arg Glu Thr Leu Ala Ala
 105 110 115

gat atc cca ctg gca atc gac cac ttc cgc tac ttt gct ggc gcg atc	499
Asp Ile Pro Leu Ala Ile Asp His Phe Arg Tyr Phe Ala Gly Ala Ile	
120 125 130	
cgt gct cag gaa gat cgt tcc tca cag atc gac cac aac act gtt gct	547
Arg Ala Gln Glu Asp Arg Ser Ser Gln Ile Asp His Asn Thr Val Ala	
135 140 145	
tac cac ttc aac gag cca atc ggt gtt gtt ggt cag atc att cct tgg	595
Tyr His Phe Asn Glu Pro Ile Gly Val Val Gly Gln Ile Ile Pro Trp	
150 155 160 165	
aac ttc cca atc ctc atg gct acc tgg aag ctc gca ccg gca ctt gct	643
Asn Phe Pro Ile Leu Met Ala Thr Trp Lys Leu Ala Pro Ala Leu Ala	
170 175 180	
gca ggt aac gcg atc gtc atg aag cca gct gag cag acc cca gca tcc	691
Ala Gly Asn Ala Ile Val Met Lys Pro Ala Glu Gln Thr Pro Ala Ser	
185 190 195	
att ttg tat ctg att aac atc atc ggc gat ctc atc cca gag ggc gtc	739
Ile Leu Tyr Leu Ile Asn Ile Ile Gly Asp Leu Ile Pro Glu Gly Val	
200 205 210	
ctc aac atc gtc aac gga ctc ggc ggt gaa gca ggc gct gca ctg tcc	787
Leu Asn Ile Val Asn Gly Leu Gly Gly Glu Ala Gly Ala Ala Leu Ser	
215 220 225	
ggc tct aat cgg att ggc aag att gct ttc acc ggt tcc acc gag gtc	835
Gly Ser Asn Arg Ile Gly Lys Ile Ala Phe Thr Gly Ser Thr Glu Val	
230 235 240 245	
ggc aag ctg atc aac cgc gct gca tcc gac aag atc att cct gtc acc	883
Gly Lys Leu Ile Asn Arg Ala Ala Ser Asp Lys Ile Ile Pro Val Thr	
250 255 260	
ctg gag ctc ggc ggt aag tcc cca tcc atc ttc ttc tcc gat gtt ctg	931
Leu Glu Leu Gly Lys Ser Pro Ser Ile Phe Phe Ser Asp Val Leu	
265 270 275	
tca cag gat gac gcc ttc gca gag aag gca gtt gaa ggc ttc gcg atg	979
Ser Gln Asp Asp Ala Phe Ala Glu Lys Ala Val Glu Gly Phe Ala Met	
280 285 290	
ttc gcc ctc aat cag ggt gaa gtt tgt acc tgt cct tcc cgt gca ctt	1027
Phe Ala Leu Asn Gln Gly Glu Val Cys Thr Cys Pro Ser Arg Ala Leu	
295 300 305	
gtt cat gag tcc atc gct gat gaa ttc ctc gag ctt ggc gtg aag cga	1075
Val His Glu Ser Ile Ala Asp Glu Phe Leu Glu Leu Gly Val Lys Arg	
310 315 320 325	
gtt cag aac atc aag ctg ggt aac cca ctt gat act gaa acc atg atg	1123
Val Gln Asn Ile Lys Leu Gly Asn Pro Leu Asp Thr Glu Thr Met Met	
330 335 340	
ggc gct cag gcg tcc cag gag cag atg gac aag atc tcc tcc tac ctg	1171
Gly Ala Gln Ala Ser Gln Glu Gln Met Asp Lys Ile Ser Ser Tyr Leu	
345 350 355	
aag atc ggc cca gaa gaa ggc gct caa acc ctc act ggt ggc aag gtc	1219

Lys Ile Gly Pro Glu Glu Gly Ala Gln Thr Leu Thr Gly Gly Lys Val
 360 365 370
 aac aag gtt gat ggc atg gag aac ggt tac tac att gag cca acc gtt 1267
 Asn Lys Val Asp Gly Met Glu Asn Gly Tyr Tyr Ile Glu Pro Thr Val
 375 380 385
 ttc cgc ggc acc aac gac atg agg atc ttc cgc gag gaa atc ttc gga 1315
 Phe Arg Gly Thr Asn Asp Met Arg Ile Phe Arg Glu Glu Ile Phe Gly
 390 395 400 405
 cca gtc ctt tct gtt gct acc ttc agc gac ttc gat gag gcc atc cgt 1363
 Pro Val Leu Ser Val Ala Thr Phe Ser Asp Phe Asp Glu Ala Ile Arg
 410 415 420
 att gca aac gac acc aac tac ggc ctc ggc gct ggt gtc tgg agc cgt 1411
 Ile Ala Asn Asp Thr Asn Tyr Gly Leu Gly Ala Gly Val Trp Ser Arg
 425 430 435
 gac caa aac acc att tat cgt gca ggt cgc gca atc cag gct ggt cga 1459
 Asp Gln Asn Thr Ile Tyr Arg Ala Gly Arg Ala Ile Gln Ala Gly Arg
 440 445 450
 gtt tgg gtc aac cag tac cac aac tac cca gcg cac tcc gct ttc ggt 1507
 Val Trp Val Asn Gln Tyr His Asn Tyr Pro Ala His Ser Ala Phe Gly
 455 460 465
 gga tac aag gag tcc ggc atc ggc cgt gag aac cac ctc atg atg ctg 1555
 Gly Tyr Lys Glu Ser Gly Ile Gly Arg Glu Asn His Leu Met Met Leu
 470 475 480 485
 aac cac tac cag cag acc aag aac ctg ttg gtc tcc tac gat cca aac 1603
 Asn His Tyr Gln Gln Thr Lys Asn Leu Leu Val Ser Tyr Asp Pro Asn
 490 495 500
 cca acc gga ctg ttc tgatctaagc gttaagtcct aga 1641
 Pro Thr Gly Leu Phe
 505

<210> 218

<211> 506

<212> PRT

<213> Corynebacterium glutamicum

<400> 218

Met Thr Val Tyr Ala Asn Pro Gly Thr Glu Gly Ser Ile Val Asn Tyr
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 Glu Lys Arg Tyr Glu Asn Tyr Ile Gly Gly Lys Trp Val Pro Pro Val
 20 25 30
 Glu Gly Gln Tyr Leu Glu Asn Ile Ser Pro Val Thr Gly Glu Val Phe
 35 40 45
 Cys Glu Val Ala Arg Gly Thr Ala Ala Asp Val Glu Leu Ala Leu Asp
 50 55 60
 Ala Ala His Ala Ala Ala Asp Ala Trp Gly Lys Thr Ser Val Ala Glu
 65 70 75 80

Arg Ala Leu Ile Leu His Arg Ile Ala Asp Arg Met Glu Glu His Leu
 85 90 95
 Glu Glu Ile Ala Val Ala Glu Thr Trp Glu Asn Gly Lys Ala Val Arg
 100 105 110
 Glu Thr Leu Ala Ala Asp Ile Pro Leu Ala Ile Asp His Phe Arg Tyr
 115 120 125
 Phe Ala Gly Ala Ile Arg Ala Gln Glu Asp Arg Ser Ser Gln Ile Asp
 130 135 140
 His Asn Thr Val Ala Tyr His Phe Asn Glu Pro Ile Gly Val Val Gly
 145 150 155 160
 Gln Ile Ile Pro Trp Asn Phe Pro Ile Leu Met Ala Thr Trp Lys Leu
 165 170 175
 Ala Pro Ala Leu Ala Ala Gly Asn Ala Ile Val Met Lys Pro Ala Glu
 180 185 190
 Gln Thr Pro Ala Ser Ile Leu Tyr Leu Ile Asn Ile Ile Gly Asp Leu
 195 200 205
 Ile Pro Glu Gly Val Leu Asn Ile Val Asn Gly Leu Gly Gly Glu Ala
 210 215 220
 Gly Ala Ala Leu Ser Gly Ser Asn Arg Ile Gly Lys Ile Ala Phe Thr
 225 230 235 240
 Gly Ser Thr Glu Val Gly Lys Leu Ile Asn Arg Ala Ala Ser Asp Lys
 245 250 255
 Ile Ile Pro Val Thr Leu Glu Leu Gly Gly Lys Ser Pro Ser Ile Phe
 260 265 270
 Phe Ser Asp Val Leu Ser Gln Asp Asp Ala Phe Ala Glu Lys Ala Val
 275 280 285
 Glu Gly Phe Ala Met Phe Ala Leu Asn Gln Gly Glu Val Cys Thr Cys
 290 295 300
 Pro Ser Arg Ala Leu Val His Glu Ser Ile Ala Asp Glu Phe Leu Glu
 305 310 315 320
 Leu Gly Val Lys Arg Val Gln Asn Ile Lys Leu Gly Asn Pro Leu Asp
 325 330 335
 Thr Glu Thr Met Met Gly Ala Gln Ala Ser Gln Glu Gln Met Asp Lys
 340 345 350
 Ile Ser Ser Tyr Leu Lys Ile Gly Pro Glu Glu Gly Ala Gln Thr Leu
 355 360 365
 Thr Gly Gly Lys Val Asn Lys Val Asp Gly Met Glu Asn Gly Tyr Tyr
 370 375 380
 Ile Glu Pro Thr Val Phe Arg Gly Thr Asn Asp Met Arg Ile Phe Arg
 385 390 395 400
 Glu Glu Ile Phe Gly Pro Val Leu Ser Val Ala Thr Phe Ser Asp Phe

405	410	415
Asp Glu Ala Ile Arg Ile Ala Asn Asp Thr Asn Tyr Gly Leu Gly Ala 420 425 430		
Gly Val Trp Ser Arg Asp Gln Asn Thr Ile Tyr Arg Ala Gly Arg Ala 435 440 445		
Ile Gln Ala Gly Arg Val Trp Val Asn Gln Tyr His Asn Tyr Pro Ala 450 455 460		
His Ser Ala Phe Gly Gly Tyr Lys Glu Ser Gly Ile Gly Arg Glu Asn 465 470 475 480		
His Leu Met Met Leu Asn His Tyr Gln Gln Thr Lys Asn Leu Leu Val 485 490 495		
Ser Tyr Asp Pro Asn Pro Thr Gly Leu Phe 500 505		
<210> 219		
<211> 430		
<212> DNA		
<213> Corynebacterium glutamicum		
<220>		
<221> CDS		
<222> (101)..(430)		
<223> RXN03061		
<400> 219		
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gccctagagc gcgaaaccgc gcaccagaag gtgggctaaa gtg tct ttg acc ttc	115	
	Val Ser Leu Thr Phe	
	1 5	
cca gta atc aac ccc agc gat ggc tcc acc atc acc gag cta gaa aac	163	
Pro Val Ile Asn Pro Ser Asp Gly Ser Thr Ile Thr Glu Leu Glu Asn		
	10 15 20	
cac gat tcc acc cag tgg atg tcc gcg ctc tct gat gca gtt gca gct	211	
His Asp Ser Thr Gln Trp Met Ser Ala Leu Ser Asp Ala Val Ala Ala		
	25 30 35	
ggg cct tca tgg gct gcg aaa act ccc cgc gaa aga tcc gtg gta ctc	259	
Gly Pro Ser Trp Ala Ala Lys Thr Pro Arg Glu Arg Ser Val Val Leu		
	40 45 50	
acc gca atc ttc gaa gca ctg acc gaa cgc gcc caa gaa ctt gca gag	307	
Thr Ala Ile Phe Glu Ala Leu Thr Glu Arg Ala Gln Glu Leu Ala Glu		
	55 60 65	
atc atc cac ctg gaa gct gga aaa tcc gat gca gaa gct ctt ggt gaa	355	
Ile Ile His Leu Glu Ala Gly Lys Ser Asp Ala Glu Ala Leu Gly Glu		
	70 75 80 85	
gtc gct tat ggt gca gaa tac ttc cgt tgg ttt gcg gaa gaa gca gtg	403	
Val Ala Tyr Gly Ala Glu Tyr Phe Arg Trp Phe Ala Glu Glu Ala Val		
	90 95 100	

40	45	50	
cag atc gga ccg atg gcg act gcc cgg cag cgt gag cgc gtg gaa tcc			307
Gln Ile Gly Pro Met Ala Thr Ala Arg Gln Arg Glu Arg Val Glu Ser			
55	60	65	
tac att tcc caa ggc aaa aat gct gga gcc cgc atc act gtc ggt ggc			355
Tyr Ile Ser Gln Gly Lys Asn Ala Gly Ala Arg Ile Thr Val Gly Gly			
70	75	80	85
agc cgt cca cga gat ctt gac gcc gga ttc ttc gtt gag cca aca gtg			403
Ser Arg Pro Arg Asp Leu Asp Ala Gly Phe Phe Val Glu Pro Thr Val			
90	95	100	
ttc gcc gat gta gac aat cgc gca gcc att gcc caa gat gaa atc ttc			451
Phe Ala Asp Val Asp Asn Arg Ala Ala Ile Ala Gln Asp Glu Ile Phe			
105	110	115	
gga ccg gtg ccc tct gtt gtt tcc tac caa gac gat gaa cac gcc atc			499
Gly Pro Val Pro Ser Val Val Ser Tyr Gln Asp Asp Glu His Ala Ile			
120	125	130	
caa cta gcc aac gat tcc gaa ttc ggt ctc ggc gga act gtc tgg acg			547
Gln Leu Ala Asn Asp Ser Glu Phe Gly Leu Gly Gly Thr Val Trp Thr			
135	140	145	
agc gat ccc gag cgc ggc gct gca ttg gcc cgc cga gtt cac aca gga			595
Ser Asp Pro Glu Arg Gly Ala Ala Leu Ala Arg Arg Val His Thr Gly			
150	155	160	165
acc att ggc atc aac cgc tat atc cct gat ccc gcc gca cca ttt gga			643
Thr Ile Gly Ile Asn Arg Tyr Ile Pro Asp Pro Ala Ala Pro Phe Gly			
170	175	180	
ggt gtg aaa aac agt ggc ctt ggc aga gaa ctc ggc ccc gaa ggt ctt			691
Gly Val Lys Asn Ser Gly Leu Gly Arg Glu Leu Gly Pro Glu Gly Leu			
185	190	195	
gct tcc tac caa gaa acc caa acc att tat ctc taatccaaac tgcacctata			744
Ala Ser Tyr Gln Glu Thr Gln Thr Ile Tyr Leu			
200	205		
tat			747
<210> 222			
<211> 208			
<212> PRT			
<213> Corynebacterium glutamicum			
<400> 222			
Val Glu Ala Gln Phe Thr Ser Pro Leu Leu Asn Asn Gly Gln Thr Cys			
1	5	10	15
Phe Leu Gly Thr Arg Ile Leu Ala Pro Lys Ser Arg Tyr Ala Glu Val			
20	25	30	
Val Asp Ala Phe Thr Ala Phe Ala Gly Ser Leu Gln Val Gly Val Thr			
35	40	45	
Ser Ser Pro Asp Thr Gln Ile Gly Pro Met Ala Thr Ala Arg Gln Arg			

50 55 60
 Glu Arg Val Glu Ser Tyr Ile Ser Gln Gly Lys Asn Ala Gly Ala Arg
 65 70 75 80
 Ile Thr Val Gly Gly Ser Arg Pro Arg Asp Leu Asp Ala Gly Phe Phe
 85 90
 Val Glu Pro Thr Val Phe Ala Asp Val Asp Asn Arg Ala Ala Ile Ala
 100 105 110
 Gln Asp Glu Ile Phe Gly Pro Val Pro Ser Val Val Ser Tyr Gln Asp
 115 120 125
 Asp Glu His Ala Ile Gln Leu Ala Asn Asp Ser Glu Phe Gly Leu Gly
 130 135 140
 Gly Thr Val Trp Thr Ser Asp Pro Glu Arg Gly Ala Ala Leu Ala Arg
 145 150 155 160
 Arg Val His Thr Gly Thr Ile Gly Ile Asn Arg Tyr Ile Pro Asp Pro
 165 170 175
 Ala Ala Pro Phe Gly Gly Val Lys Asn Ser Gly Leu Gly Arg Glu Leu
 180 185 190
 Gly Pro Glu Gly Leu Ala Ser Tyr Gln Glu Thr Gln Thr Ile Tyr Leu
 195 200 205

<210> 223
 <211> 881
 <212> DNA
 <213> *Corynebacterium glutamicum*

<220>
 <221> CDS
 <222> (1)..(858)
 <223> RXN01340

<400> 223
 aaa gtg ggg gag atc atc gcc tcc gtc ttt gat acc ttt aat atc ccg 48
 Lys Val Gly Glu Ile Ile Ala Ser Val Phe Asp Thr Phe Asn Ile Pro
 1 5 10 15
 cag ggc ttg gtc tca atc atc acc acc act cga gat gca gag cta tcg 96
 Gln Gly Leu Val Ser Ile Ile Thr Thr Thr Arg Asp Ala Glu Leu Ser
 20 25 30
 gca gaa ctc atg gct gat cct cgc ttg gct aaa gtc acc ttc act gga 144
 Ala Glu Leu Met Ala Asp Pro Arg Leu Ala Lys Val Thr Phe Thr Gly
 35 40 45
 tca acc aac gtg gga cgc atc ctg gtc cgc caa tcc gcg gac cga ctg 192
 Ser Thr Asn Val Gly Arg Ile Leu Val Arg Gln Ser Ala Asp Arg Leu
 50 55 60
 ctg cgc acc tcc atg gaa ctc ggc gga aat gca gct ttt gtt atc gac 240

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Leu Arg Thr Ser Met Glu Leu Gly Gly Asn Ala Ala Phe Val Ile Asp
65              70              75              80

gaa gcc gca gac ctc gac gaa gcc gta tcc ggt gcc atc gcc gca aaa 288
Glu Ala Ala Asp Leu Asp Glu Ala Val Ser Gly Ala Ile Ala Ala Lys
85              90              95

ctc cgc aac gcc ggc caa gta tgc atc gca gct aac cgt ttc ttg gtt 336
Leu Arg Asn Ala Gly Gln Val Cys Ile Ala Ala Asn Arg Phe Leu Val
100             105             110

cat gaa tcc cgc gct gcc gaa ttc acc tca aag ctg gcg aca gcc atg 384
His Glu Ser Arg Ala Ala Glu Phe Thr Ser Lys Leu Ala Thr Ala Met
115             120             125

cag aac act ccc att ggg ccg gtg att tct gcc cgc caa cgc gac cgg 432
Gln Asn Thr Pro Ile Gly Pro Val Ile Ser Ala Arg Gln Arg Asp Arg
130             135             140

atc gca gca cta gtg gat gaa gcc atc acc gac ggc gcc cgc ctc atc 480
Ile Ala Ala Leu Val Asp Glu Ala Ile Thr Asp Gly Ala Arg Leu Ile
145             150             155             160

atc ggt ggg gag gtc ccc gac ggc tcc ggc ttc ttc tat cca gcc acc 528
Ile Gly Gly Glu Val Pro Asp Gly Ser Gly Phe Phe Tyr Pro Ala Thr
165             170             175

atc ttg gcc gat gtc cct gca cag tca cgg att gtg cat gag gaa atc 576
Ile Leu Ala Asp Val Pro Ala Gln Ser Arg Ile Val His Glu Glu Ile
180             185             190

ttc gga cct gtg gcc acc att gcc act ttc acc gac ttg gcc gaa ggc 624
Phe Gly Pro Val Ala Thr Ile Ala Thr Phe Thr Asp Leu Ala Glu Gly
195             200             205

gtt gca caa gca aat tcc acc gaa ttc ggc ctc gca gcc tac gga ttc 672
Val Ala Gln Ala Asn Ser Thr Glu Phe Gly Leu Ala Ala Tyr Gly Phe
210             215             220

agc aac aat gtg aaa gca aca cag tac atg gcg gaa cac ttg gaa gcc 720
Ser Asn Asn Val Lys Ala Thr Gln Tyr Met Ala Glu His Leu Glu Ala
225             230             235             240

gga atg gtc gga atc aac aga ggc gcc atc tct gac cca gca gca cct 768
Gly Met Val Gly Ile Asn Arg Gly Ala Ile Ser Asp Pro Ala Ala Pro
245             250             255

ttt ggc ggc atc gga caa tcc ggc ttc ggc aga gaa ggc gga acc gaa 816
Phe Gly Gly Ile Gly Gln Ser Gly Phe Gly Arg Glu Gly Gly Thr Glu
260             265             270

gga atc gaa gaa tat ctc tcc gtg cgt tac ctc gct ttg ccg 858
Gly Ile Glu Glu Tyr Leu Ser Val Arg Tyr Leu Ala Leu Pro
275             280             285

tgacacatga gctgtccggt gaa 881

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<210> 224
 <211> 286
 <212> PRT

<213> Corynebacterium glutamicum

<400> 224

Lys Val Gly Glu Ile Ile Ala Ser Val Phe Asp Thr Phe Asn Ile Pro
 1 5 10 15

Gln Gly Leu Val Ser Ile Ile Thr Thr Thr Arg Asp Ala Glu Leu Ser
 20 25 30

Ala Glu Leu Met Ala Asp Pro Arg Leu Ala Lys Val Thr Phe Thr Gly
 35 40 45

Ser Thr Asn Val Gly Arg Ile Leu Val Arg Gln Ser Ala Asp Arg Leu
 50 55 60

Leu Arg Thr Ser Met Glu Leu Gly Gly Asn Ala Ala Phe Val Ile Asp
 65 70 75 80

Glu Ala Ala Asp Leu Asp Glu Ala Val Ser Gly Ala Ile Ala Ala Lys
 85 90 95

Leu Arg Asn Ala Gly Gln Val Cys Ile Ala Ala Asn Arg Phe Leu Val
 100 105 110

His Glu Ser Arg Ala Ala Glu Phe Thr Ser Lys Leu Ala Thr Ala Met
 115 120 125

Gln Asn Thr Pro Ile Gly Pro Val Ile Ser Ala Arg Gln Arg Asp Arg
 130 135 140

Ile Ala Ala Leu Val Asp Glu Ala Ile Thr Asp Gly Ala Arg Leu Ile
 145 150 155 160

Ile Gly Gly Glu Val Pro Asp Gly Ser Gly Phe Phe Tyr Pro Ala Thr
 165 170 175

Ile Leu Ala Asp Val Pro Ala Gln Ser Arg Ile Val His Glu Glu Ile
 180 185 190

Phe Gly Pro Val Ala Thr Ile Ala Thr Phe Thr Asp Leu Ala Glu Gly
 195 200 205

Val Ala Gln Ala Asn Ser Thr Glu Phe Gly Leu Ala Ala Tyr Gly Phe
 210 215 220

Ser Asn Asn Val Lys Ala Thr Gln Tyr Met Ala Glu His Leu Glu Ala
 225 230 235 240

Gly Met Val Gly Ile Asn Arg Gly Ala Ile Ser Asp Pro Ala Ala Pro
 245 250 255

Phe Gly Gly Ile Gly Gln Ser Gly Phe Gly Arg Glu Gly Gly Thr Glu
 260 265 270

Gly Ile Glu Glu Tyr Leu Ser Val Arg Tyr Leu Ala Leu Pro
 275 280 285

<210> 225

<211> 1686

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1663)

<223> RXN01498

<400> 225

cagtggacaa ctacttggcg ggtcttaaata cagctgtgaa ggattctgca taagctgggc 60

accacacgag catcagaacg cgaaacgaag gtaaaagccc atg atc aaa cgt ctt 115
 Met Ile Lys Arg Leu
 1 5

cct tta ggt ccg ctg cct aaa gaa ctt cat cag act ctg ctt gat ctg 163
 Pro Leu Gly Pro Leu Pro Lys Glu Leu His Gln Thr Leu Leu Asp Leu
 10 15 20

acc gca aat gcc caa gat gcg gcg aaa gtg gag gtt ata gcg cca ttt 211
 Thr Ala Asn Ala Gln Asp Ala Ala Lys Val Glu Val Ile Ala Pro Phe
 25 30 35

act ggc gag acc ctc gga ttt ggt ttt gat ggt gat gag caa gac gtc 259
 Thr Gly Glu Thr Leu Gly Phe Gly Phe Asp Gly Asp Glu Gln Asp Val
 40 45 50

gag cat gct ttt gca ctt tca agg gca gcc cag aaa aag tgg gtg cac 307
 Glu His Ala Phe Ala Leu Ser Arg Ala Ala Gln Lys Lys Trp Val His
 55 60 65

acc acg gca gtg gaa cgg aag aag atc ttc ctg aag gtt cat gat ctg 355
 Thr Thr Ala Val Glu Arg Lys Lys Ile Phe Leu Lys Val His Asp Leu
 70 75 80 85

gta ttg aaa aac cgt gag ctg ctc atg gac atc gtg cag ttg gaa aca 403
 Val Leu Lys Asn Arg Glu Leu Leu Met Asp Ile Val Gln Leu Glu Thr
 90 95 100

ggc aaa aat cga gca tcg gct gcc gat gag gtg ttg gac gtt gcg atc 451
 Gly Lys Asn Arg Ala Ser Ala Ala Asp Glu Val Leu Asp Val Ala Ile
 105 110 115

acc acc cgc ttc tac gca aac aat gca gga aag ttt tta aat gac aag 499
 Thr Thr Arg Phe Tyr Ala Asn Asn Ala Gly Lys Phe Leu Asn Asp Lys
 120 125 130

aaa cgc ccc ggc gcg ctt ccg atc atc acg aaa aac aca caa cag tat 547
 Lys Arg Pro Gly Ala Leu Pro Ile Ile Thr Lys Asn Thr Gln Gln Tyr
 135 140 145

gtg ccc aag gga gtg gtc ggg cag atc acg ccg tgg aat tac cct tta 595
 Val Pro Lys Gly Val Val Gly Gln Ile Thr Pro Trp Asn Tyr Pro Leu
 150 155 160 165

act ttg gga gta tct gat gct gtt ccg gcg ctg ctg gca gga aac gca 643
 Thr Leu Gly Val Ser Asp Ala Val Pro Ala Leu Leu Ala Gly Asn Ala
 170 175 180

gtg gtg gct aaa cct gac ctc gcg aca cct ttc tcc tgc ttg atc atg 691
 Val Val Ala Lys Pro Asp Leu Ala Thr Pro Phe Ser Cys Leu Ile Met
 185 190 195

gtg cac ctg ctc att gaa gcc ggt ctg ccg cgt gat ttg atg cag gtt	739
Val His Leu Leu Ile Glu Ala Gly Leu Pro Arg Asp Leu Met Gln Val	
200 205 210	
gtc acc ggc cct ggc gat att gtt ggc ggt gcg att gca gct cag tgt	787
Val Thr Gly Pro Gly Asp Ile Val Gly Gly Ala Ile Ala Ala Gln Cys	
215 220 225	
gat ttc ctc atg ttc act gga tcc acg gcc acg ggc cgg atc ttg ggt	835
Asp Phe Leu Met Phe Thr Gly Ser Thr Ala Thr Gly Arg Ile Leu Gly	
230 235 240 245	
cgg aca atg ggt gag cgt ttg gtg ggt ttc tct gcg gaa tta ggc gga	883
Arg Thr Met Gly Glu Arg Leu Val Gly Phe Ser Ala Glu Leu Gly Gly	
250 255 260	
aag aac cct ctt att gtg gcc aag gat gca gat ctg gac aag gtg gaa	931
Lys Asn Pro Leu Ile Val Ala Lys Asp Ala Asp Leu Asp Lys Val Glu	
265 270 275	
gct gag ctt ccg cag gcg tgt ttt tcc aac tcg ggg caa ttg tgt gtc	979
Ala Glu Leu Pro Gln Ala Cys Phe Ser Asn Ser Gly Gln Leu Cys Val	
280 285 290	
tcc act gaa cgt att tat gtc gag gaa gac gtg tac gag gag gtg att	1027
Ser Thr Glu Arg Ile Tyr Val Glu Glu Asp Val Tyr Glu Glu Val Ile	
295 300 305	
gca cgg ttt agc aag gcg gcg aaa gcc atg tcc att ggt gcc gga ttt	1075
Ala Arg Phe Ser Lys Ala Ala Lys Ala Met Ser Ile Gly Ala Gly Phe	
310 315 320 325	
gag tgg aaa tat gag atg ggt tcg ttg atc aat cac gcg cag ctg gat	1123
Glu Trp Lys Tyr Glu Met Gly Ser Leu Ile Asn His Ala Gln Leu Asp	
330 335 340	
cgg gtg agc acc ttt gtt gat cag gct aaa gct gcg ggc gcc acg gtg	1171
Arg Val Ser Thr Phe Val Asp Gln Ala Lys Ala Ala Gly Ala Thr Val	
345 350 355	
ctg tgc ggt ggc aag tca cgc cct gat att ggt ccc ttc ttc tat gag	1219
Leu Cys Gly Gly Lys Ser Arg Pro Asp Ile Gly Pro Phe Phe Tyr Glu	
360 365 370	
ccc acg gta ttg gcg gat gtc cca gag ggc acc cca ctg ctc acg gag	1267
Pro Thr Val Leu Ala Asp Val Pro Glu Gly Thr Pro Leu Leu Thr Glu	
375 380 385	
gaa gtc ttc ggg ccg gtg gtg ttc atc gaa aag gta gcc aca ctg gaa	1315
Glu Val Phe Gly Pro Val Val Phe Ile Glu Lys Val Ala Thr Leu Glu	
390 395 400 405	
gaa gcc gtc gat aag gca aat ggc acg ccc tac ggc ctg aat gcg tcc	1363
Glu Ala Val Asp Lys Ala Asn Gly Thr Pro Tyr Gly Leu Asn Ala Ser	
410 415 420	
gtc ttt ggg tcg tcg gaa acc ggc aat ctt gtt gca ggc cag ctg gaa	1411
Val Phe Gly Ser Ser Glu Thr Gly Asn Leu Val Ala Gly Gln Leu Glu	
425 430 435	

gct ggc ggt atc ggt att aat gat ggc tac gcc gcg acg tgg gcg agc 1459
 Ala Gly Gly Ile Gly Ile Asn Asp Gly Tyr Ala Ala Thr Trp Ala Ser
 440 445 450

gtg tcc acg cct ctg ggt ggc atg aag cag tcg ggg ctg ggg cac cgc 1507
 Val Ser Thr Pro Leu Gly Gly Met Lys Gln Ser Gly Leu Gly His Arg
 455 460 465

cat ggt gcg gag gga att aca aaa tat gcg gag atc cga aac atc gcg 1555
 His Gly Ala Glu Gly Ile Thr Lys Tyr Ala Glu Ile Arg Asn Ile Ala
 470 475 480 485

gag cag cgc tgg atg tct atg cgt ggg ccg gcc aaa atg ccg cga aag 1603
 Glu Gln Arg Trp Met Ser Met Arg Gly Pro Ala Lys Met Pro Arg Lys
 490 495 500

gtg tac tca gac acc gtg gcc aca gcg cta aag ctg ggc aaa atc ttt 1651
 Val Tyr Ser Asp Thr Val Ala Thr Ala Leu Lys Leu Gly Lys Ile Phe
 505 510 515

aaa gtt ttg ccg tagcaaaaag ccggaccctt gct 1686
 Lys Val Leu Pro
 520

<210> 226

<211> 521

<212> PRT

<213> Corynebacterium glutamicum

<400> 226

Met Ile Lys Arg Leu Pro Leu Gly Pro Leu Pro Lys Glu Leu His Gln
 1 5 10 15

Thr Leu Leu Asp Leu Thr Ala Asn Ala Gln Asp Ala Ala Lys Val Glu
 20 25 30

Val Ile Ala Pro Phe Thr Gly Glu Thr Leu Gly Phe Gly Phe Asp Gly
 35 40 45

Asp Glu Gln Asp Val Glu His Ala Phe Ala Leu Ser Arg Ala Ala Gln
 50 55 60

Lys Lys Trp Val His Thr Thr Ala Val Glu Arg Lys Lys Ile Phe Leu
 65 70 75 80

Lys Val His Asp Leu Val Leu Lys Asn Arg Glu Leu Leu Met Asp Ile
 85 90 95

Val Gln Leu Glu Thr Gly Lys Asn Arg Ala Ser Ala Ala Asp Glu Val
 100 105 110

Leu Asp Val Ala Ile Thr Thr Arg Phe Tyr Ala Asn Asn Ala Gly Lys
 115 120 125

Phe Leu Asn Asp Lys Lys Arg Pro Gly Ala Leu Pro Ile Ile Thr Lys
 130 135 140

Asn Thr Gln Gln Tyr Val Pro Lys Gly Val Val Gly Gln Ile Thr Pro
 145 150 155 160

Trp Asn Tyr Pro Leu Thr Leu Gly Val Ser Asp Ala Val Pro Ala Leu
 165 170 175
 Leu Ala Gly Asn Ala Val Val Ala Lys Pro Asp Leu Ala Thr Pro Phe
 180 185 190
 Ser Cys Leu Ile Met Val His Leu Leu Ile Glu Ala Gly Leu Pro Arg
 195 200 205
 Asp Leu Met Gln Val Val Thr Gly Pro Gly Asp Ile Val Gly Gly Ala
 210 215 220
 Ile Ala Ala Gln Cys Asp Phe Leu Met Phe Thr Gly Ser Thr Ala Thr
 225 230 235 240
 Gly Arg Ile Leu Gly Arg Thr Met Gly Glu Arg Leu Val Gly Phe Ser
 245 250 255
 Ala Glu Leu Gly Gly Lys Asn Pro Leu Ile Val Ala Lys Asp Ala Asp
 260 265 270
 Leu Asp Lys Val Glu Ala Glu Leu Pro Gln Ala Cys Phe Ser Asn Ser
 275 280 285
 Gly Gln Leu Cys Val Ser Thr Glu Arg Ile Tyr Val Glu Glu Asp Val
 290 295 300
 Tyr Glu Glu Val Ile Ala Arg Phe Ser Lys Ala Ala Lys Ala Met Ser
 305 310 315 320
 Ile Gly Ala Gly Phe Glu Trp Lys Tyr Glu Met Gly Ser Leu Ile Asn
 325 330 335
 His Ala Gln Leu Asp Arg Val Ser Thr Phe Val Asp Gln Ala Lys Ala
 340 345 350
 Ala Gly Ala Thr Val Leu Cys Gly Gly Lys Ser Arg Pro Asp Ile Gly
 355 360 365
 Pro Phe Phe Tyr Glu Pro Thr Val Leu Ala Asp Val Pro Glu Gly Thr
 370 375 380
 Pro Leu Leu Thr Glu Glu Val Phe Gly Pro Val Val Phe Ile Glu Lys
 385 390 395 400
 Val Ala Thr Leu Glu Glu Ala Val Asp Lys Ala Asn Gly Thr Pro Tyr
 405 410 415
 Gly Leu Asn Ala Ser Val Phe Gly Ser Ser Glu Thr Gly Asn Leu Val
 420 425 430
 Ala Gly Gln Leu Glu Ala Gly Gly Ile Gly Ile Asn Asp Gly Tyr Ala
 435 440 445
 Ala Thr Trp Ala Ser Val Ser Thr Pro Leu Gly Gly Met Lys Gln Ser
 450 455 460
 Gly Leu Gly His Arg His Gly Ala Glu Gly Ile Thr Lys Tyr Ala Glu
 465 470 475 480
 Ile Arg Asn Ile Ala Glu Gln Arg Trp Met Ser Met Arg Gly Pro Ala

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                485                490                495
Lys Met Pro Arg Lys Val Tyr Ser Asp Thr Val Ala Thr Ala Leu Lys
                500                505                510

Leu Gly Lys Ile Phe Lys Val Leu Pro
                515                520

<210> 227
<211> 1575
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1552)
<223> RXN02674

<400> 227
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acagttggtg aagtatccac aatcaacttt aggagacctt gtg act gca aca ttt 115
                                   Val Thr Ala Thr Phe
                                   1                               5

gct gga atc gac gcc acc aaa cac ctc atc gga ggt cag tgg gtg gag 163
Ala Gly Ile Asp Ala Thr Lys His Leu Ile Gly Gly Gln Trp Val Glu
                10                15                20

gga aac tcg gat cga att tcc acc aat atc aat cct tac gac gat tcc 211
Gly Asn Ser Asp Arg Ile Ser Thr Asn Ile Asn Pro Tyr Asp Asp Ser
                25                30                35

gta atc gcc gaa agc aaa caa gct tcc att gct gat gtt gat gcc gcg 259
Val Ile Ala Glu Ser Lys Gln Ala Ser Ile Ala Asp Val Asp Ala Ala
                40                45                50

tat gaa gcc gcg aag aag gcc cag gct gag tgg gca gct acg ccc gct 307
Tyr Glu Ala Ala Lys Lys Ala Gln Ala Glu Trp Ala Ala Thr Pro Ala
                55                60                65

gcg gaa cga tct gcc atc atc tac cgt gcg gct gaa ctt ctt gaa gag 355
Ala Glu Arg Ser Ala Ile Ile Tyr Arg Ala Ala Glu Leu Leu Glu Glu
                70                75                80                85

cac cgg gag gaa atc gtg gaa tgg ctg atc aag gaa tcc ggc tcg acg 403
His Arg Glu Glu Ile Val Glu Trp Leu Ile Lys Glu Ser Gly Ser Thr
                90                95                100

cgt tcc aag gct aat ttg gaa atc act ttg gca gga aac atc act aaa 451
Arg Ser Lys Ala Asn Leu Glu Ile Thr Leu Ala Gly Asn Ile Thr Lys
                105                110                115

gaa tcg gct tca ttc cct ggt cgt gtg cat ggt cga att tct cct tcg 499
Glu Ser Ala Ser Phe Pro Gly Arg Val His Gly Arg Ile Ser Pro Ser
                120                125                130

aat act ccg ggc aaa gaa aac cgt gtg tac cgc gta gcc aag ggc gtt 547
Asn Thr Pro Gly Lys Glu Asn Arg Val Tyr Arg Val Ala Lys Gly Val
                135                140                145

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gtc gga gtg att agt cca tgg aat ttc cca ctg aac ctc tcg atc cgc	595
Val Gly Val Ile Ser Pro Trp Asn Phe Pro Leu Asn Leu Ser Ile Arg	
150 155 160 165	
tcg gtt gct ccg gca cta gcc gtg ggc aac gcc gta gtg att aag cct	643
Ser Val Ala Pro Ala Leu Ala Val Gly Asn Ala Val Val Ile Lys Pro	
170 175 180	
gcg agt gat acc cca gtt act ggt ggt gta att cct gca cga atc ttt	691
Ala Ser Asp Thr Pro Val Thr Gly Gly Val Ile Pro Ala Arg Ile Phe	
185 190 195	
gag gag gcc gga gtt cct gca ggc gtg atc agc acg gtt gcg ggc gca	739
Glu Glu Ala Gly Val Pro Ala Gly Val Ile Ser Thr Val Ala Gly Ala	
200 205 210	
gga tct gaa atc ggt gat cac ttt gtc acc cac gcc gtg cca aag ctg	787
Gly Ser Glu Ile Gly Asp His Phe Val Thr His Ala Val Pro Lys Leu	
215 220 225	
att tct ttc acc ggt tca acc cca gtc ggt cgt cgt gtc ggt gag ctg	835
Ile Ser Phe Thr Gly Ser Thr Pro Val Gly Arg Arg Val Gly Glu Leu	
230 235 240 245	
gca att aat ggt gga cca atg aaa act gtt gca cta gag ctc ggt ggc	883
Ala Ile Asn Gly Gly Pro Met Lys Thr Val Ala Leu Glu Leu Gly Gly	
250 255 260	
aac gcg ccg ttc gtt gtg ctt gcc gac gcc gac atc gac gcc gct gcc	931
Asn Ala Pro Phe Val Val Leu Ala Asp Ala Asp Ile Asp Ala Ala Ala	
265 270 275	
cag gct gcc gca gtt ggc gct ttc cta cac cag gga cag att tgt atg	979
Gln Ala Ala Ala Val Gly Ala Phe Leu His Gln Gly Gln Ile Cys Met	
280 285 290	
tca atc aac cga gtc att gtt gat gct gca gtt cat gat gaa ttc cta	1027
Ser Ile Asn Arg Val Ile Val Asp Ala Ala Val His Asp Glu Phe Leu	
295 300 305	
gag aag ttc gtt gaa gca gtg aag aac att cca acc ggc gat cca agc	1075
Glu Lys Phe Val Glu Ala Val Lys Asn Ile Pro Thr Gly Asp Pro Ser	
310 315 320 325	
gca gaa gga acc ctt gtt gga cct gtc att aat gac agt cag ctc agt	1123
Ala Glu Gly Thr Leu Val Gly Pro Val Ile Asn Asp Ser Gln Leu Ser	
330 335 340	
ggt ttg aag gaa aag atc gag ttg gcc aaa aag gaa ggc gca acc gtc	1171
Gly Leu Lys Glu Lys Ile Glu Leu Ala Lys Lys Glu Gly Ala Thr Val	
345 350 355	
cag gtt gaa ggg cca att gaa ggc cga ctg gtt cat ccg cat gtg ttc	1219
Gln Val Glu Gly Pro Ile Glu Gly Arg Leu Val His Pro His Val Phe	
360 365 370	
tct gat gtc acc tct gac atg gaa atc gct cgt gag gaa atc ttc gga	1267
Ser Asp Val Thr Ser Asp Met Glu Ile Ala Arg Glu Glu Ile Phe Gly	
375 380 385	

cct ctc atc agc gtg ctg aag gcc gat gat gag gca cac gca gca gag 1315
 Pro Leu Ile Ser Val Leu Lys Ala Asp Asp Glu Ala His Ala Ala Glu
 390 395 400 405

ctg gcc aat gct tcc gac ttt ggt ttg agc gcg gca gtg tgg tcg aag 1363
 Leu Ala Asn Ala Ser Asp Phe Gly Leu Ser Ala Ala Val Trp Ser Lys
 410 415 420

gat att gat cgt gca gcc cag ttt gct ctg cag att gat tcc ggc atg 1411
 Asp Ile Asp Arg Ala Ala Gln Phe Ala Leu Gln Ile Asp Ser Gly Met
 425 430 435

gtt cac atc aat gac ctc acc gtc aac gat gaa cca cac gtg atg ttc 1459
 Val His Ile Asn Asp Leu Thr Val Asn Asp Glu Pro His Val Met Phe
 440 445 450

ggt ggt tca aag aac tct ggc ctc ggc cgc ttc aac ggc gat tgg gcg 1507
 Gly Gly Ser Lys Asn Ser Gly Leu Gly Arg Phe Asn Gly Asp Trp Ala
 455 460 465

atc gag gag ttc acc aca gat cga tgg atc ggc atc aag cgc agc 1552
 Ile Glu Glu Phe Thr Thr Asp Arg Trp Ile Gly Ile Lys Arg Ser
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taattgtttt tcgacgtaac ccc 1575

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<211> 484

<212> PRT

<213> Corynebacterium glutamicum

<400> 228

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Gly Gln Trp Val Glu Gly Asn Ser Asp Arg Ile Ser Thr Asn Ile Asn
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Pro Tyr Asp Asp Ser Val Ile Ala Glu Ser Lys Gln Ala Ser Ile Ala
 35 40 45

Asp Val Asp Ala Ala Tyr Glu Ala Ala Lys Lys Ala Gln Ala Glu Trp
 50 55 60

Ala Ala Thr Pro Ala Ala Glu Arg Ser Ala Ile Ile Tyr Arg Ala Ala
 65 70 75 80

Glu Leu Leu Glu Glu His Arg Glu Glu Ile Val Glu Trp Leu Ile Lys
 85 90 95

Glu Ser Gly Ser Thr Arg Ser Lys Ala Asn Leu Glu Ile Thr Leu Ala
 100 105 110

Gly Asn Ile Thr Lys Glu Ser Ala Ser Phe Pro Gly Arg Val His Gly
 115 120 125

Arg Ile Ser Pro Ser Asn Thr Pro Gly Lys Glu Asn Arg Val Tyr Arg
 130 135 140

Val Ala Lys Gly Val Val Gly Val Ile Ser Pro Trp Asn Phe Pro Leu

145	150	155	160
Asn Leu Ser Ile Arg Ser Val Ala Pro Ala Leu Ala Val Gly Asn Ala	165	170	175
Val Val Ile Lys Pro Ala Ser Asp Thr Pro Val Thr Gly Gly Val Ile	180	185	190
Pro Ala Arg Ile Phe Glu Glu Ala Gly Val Pro Ala Gly Val Ile Ser	195	200	205
Thr Val Ala Gly Ala Gly Ser Glu Ile Gly Asp His Phe Val Thr His	210	215	220
Ala Val Pro Lys Leu Ile Ser Phe Thr Gly Ser Thr Pro Val Gly Arg	225	230	235
Arg Val Gly Glu Leu Ala Ile Asn Gly Gly Pro Met Lys Thr Val Ala	245	250	255
Leu Glu Leu Gly Gly Asn Ala Pro Phe Val Val Leu Ala Asp Ala Asp	260	265	270
Ile Asp Ala Ala Ala Gln Ala Ala Ala Val Gly Ala Phe Leu His Gln	275	280	285
Gly Gln Ile Cys Met Ser Ile Asn Arg Val Ile Val Asp Ala Ala Val	290	295	300
His Asp Glu Phe Leu Glu Lys Phe Val Glu Ala Val Lys Asn Ile Pro	305	310	315
Thr Gly Asp Pro Ser Ala Glu Gly Thr Leu Val Gly Pro Val Ile Asn	325	330	335
Asp Ser Gln Leu Ser Gly Leu Lys Glu Lys Ile Glu Leu Ala Lys Lys	340	345	350
Glu Gly Ala Thr Val Gln Val Glu Gly Pro Ile Glu Gly Arg Leu Val	355	360	365
His Pro His Val Phe Ser Asp Val Thr Ser Asp Met Glu Ile Ala Arg	370	375	380
Glu Glu Ile Phe Gly Pro Leu Ile Ser Val Leu Lys Ala Asp Asp Glu	385	390	395
Ala His Ala Ala Glu Leu Ala Asn Ala Ser Asp Phe Gly Leu Ser Ala	405	410	415
Ala Val Trp Ser Lys Asp Ile Asp Arg Ala Ala Gln Phe Ala Leu Gln	420	425	430
Ile Asp Ser Gly Met Val His Ile Asn Asp Leu Thr Val Asn Asp Glu	435	440	445
Pro His Val Met Phe Gly Gly Ser Lys Asn Ser Gly Leu Gly Arg Phe	450	455	460
Asn Gly Asp Trp Ala Ile Glu Glu Phe Thr Thr Asp Arg Trp Ile Gly	465	470	475
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Ile Lys Arg Ser

<210> 229

<211> 2034

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(2011)

<223> RXN00868

<400> 229

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                                         Met Ala Glu Thr Lys
                                         1           5

aga atg aca gtt agc cag gca ctg gtt gaa ttc ctt ggt cac cag tgg 163
Arg Met Thr Val Ser Gln Ala Leu Val Glu Phe Leu Gly His Gln Trp
          10          15          20

act gtc gac ggc gat atc cgc gag cgc acc att cca ggc atg ttc gga 211
Thr Val Asp Gly Asp Ile Arg Glu Arg Thr Ile Pro Gly Met Phe Gly
          25          30          35

att ttc gga cac gga aac gtt gct ggc att ggc cag gca ctc aag cag 259
Ile Phe Gly His Gly Asn Val Ala Gly Ile Gly Gln Ala Leu Lys Gln
          40          45          50

tac aac gtt gaa caa cct gag ctc atg ccg tac tac cag gct cgt aat 307
Tyr Asn Val Glu Gln Pro Glu Leu Met Pro Tyr Tyr Gln Ala Arg Asn
          55          60          65

gag cag gcg atg gtg cac cag tct gtt gga tat gca cgc atg cac cgc 355
Glu Gln Ala Met Val His Gln Ser Val Gly Tyr Ala Arg Met His Arg
          70          75          80          85

cgt cgt ggc aca tac gca tct gcc gca tct gtt gga ccc ggc gcg acc 403
Arg Arg Gly Thr Tyr Ala Ser Ala Ala Ser Val Gly Pro Gly Ala Thr
          90          95          100

aac ctg tta acc ggt gcg gct ctt gct acc acc aac cgt ttg cca gcg 451
Asn Leu Leu Thr Gly Ala Ala Leu Ala Thr Thr Asn Arg Leu Pro Ala
          105          110          115

ttg ctg ctg cct agt gat act ttt gcc acc cgc gtg gcg gat cca gtg 499
Leu Leu Leu Pro Ser Asp Thr Phe Ala Thr Arg Val Ala Asp Pro Val
          120          125          130

ttg cag cag ttg gag cag cca tgg gat atc ggg ctg acg gtt aat gat 547
Leu Gln Gln Leu Glu Gln Pro Trp Asp Ile Gly Leu Thr Val Asn Asp
          135          140          145

gct ttc cgc cct gtg tct aag ttc ttt gat cgg gtg cag cgc ccg gag 595
Ala Phe Arg Pro Val Ser Lys Phe Phe Asp Arg Val Gln Arg Pro Glu
          150          155          160          165

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cag ttg ttc tct att gcg ttg gct gcg atg cgt gtg ttg act gat ccc	643
Gln Leu Phe Ser Ile Ala Leu Ala Ala Met Arg Val Leu Thr Asp Pro	
170 175 180	
gca gaa acc ggt gcg gtc acc att gcg ctt cca gaa gat gtg cag gct	691
Ala Glu Thr Gly Ala Val Thr Ile Ala Leu Pro Glu Asp Val Gln Ala	
185 190 195	
gaa atg ctc gat gtg ccg gtg gag ttc ttg cag gat cgt gag tgg cac	739
Glu Met Leu Asp Val Pro Val Glu Phe Leu Gln Asp Arg Glu Trp His	
200 205 210	
att agg cgc cca cgt cca gag cgt gct gcg ttg gct cgt gcg att gaa	787
Ile Arg Arg Pro Arg Pro Glu Arg Ala Ala Leu Ala Arg Ala Ile Glu	
215 220 225	
gtc atc aaa aac gct aag aat ccg atg atc att gct ggt ggc gga gtg	835
Val Ile Lys Asn Ala Lys Asn Pro Met Ile Ile Ala Gly Gly Gly Val	
230 235 240 245	
ttg tac tcc gat gcg gaa acg cag ctg cag gca ctt gtg gag cag act	883
Leu Tyr Ser Asp Ala Glu Thr Gln Leu Gln Ala Leu Val Glu Gln Thr	
250 255 260	
ggc att cca gtg ggt acc tcc caa gct ggt ggt ggc gtg ttg gcg tgg	931
Gly Ile Pro Val Gly Thr Ser Gln Ala Gly Gly Gly Val Leu Ala Trp	
265 270 275	
gat cat gca caa aac tta ggt ggt gtg ggt gcc acc gga acg ttg gct	979
Asp His Ala Gln Asn Leu Gly Gly Val Gly Ala Thr Gly Thr Leu Ala	
280 285 290	
gcc aac cgc att gcg ggt gat gct gat gtg atc atc ggt atc ggt act	1027
Ala Asn Arg Ile Ala Gly Asp Ala Asp Val Ile Ile Gly Ile Gly Thr	
295 300 305	
cgt tac agc gat ttc acc acc gca tct cgc act gcg ttc caa aac cct	1075
Arg Tyr Ser Asp Phe Thr Ala Ser Arg Thr Ala Phe Gln Asn Pro	
310 315 320 325	
gat gtc acc ttc atc aac atc aat gtt gct tcc ttc gat gct tac aag	1123
Asp Val Thr Phe Ile Asn Ile Asn Val Ala Ser Phe Asp Ala Tyr Lys	
330 335 340	
cat ggc act cag ttg cct gtg att gca gat gca cgc gag gca att gtg	1171
His Gly Thr Gln Leu Pro Val Ile Ala Asp Ala Arg Glu Ala Ile Val	
345 350 355	
gag ctt gct gaa gcc ctg cag gga ttc acc gtg gca gag gat tac gcg	1219
Glu Leu Ala Glu Ala Leu Gln Gly Phe Thr Val Ala Glu Asp Tyr Ala	
360 365 370	
cag cgc atc gcg aag gaa aag gct gcg tgg gac gca gaa gta gat aag	1267
Gln Arg Ile Ala Lys Glu Lys Ala Ala Trp Asp Ala Glu Val Asp Lys	
375 380 385	
tct ttt gcc ccc tcc ggt ctt gcg ctg cct gga cag ccg gag atc atc	1315
Ser Phe Ala Pro Ser Gly Leu Ala Leu Pro Gly Gln Pro Glu Ile Ile	
390 395 400 405	

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gcg ctg ggc tac cac gtg gaa tat gcg ttc tcg tgc atg ggc tat gaa Ala Leu Gly Tyr His Val Glu Tyr Ala Phe Ser Cys Met Gly Tyr Glu 440 445 450	1459
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act gtc ggt tcg cag cgt ttt ggt act tgg tac cgc gaa tat gac gct Thr Val Gly Ser Gln Arg Phe Gly Thr Trp Tyr Arg Glu Tyr Asp Ala 520 525 530	1699
gag gcg aaa aac ttc cag ggc gag cag att ctg cct gtt gac ctg gcg Glu Ala Lys Asn Phe Gln Gly Glu Gln Ile Leu Pro Val Asp Leu Ala 535 540 545	1747
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gcg aat gcg atc gag gat ctc aaa gca gcg atg gca acc gcg aag gct Ala Asn Ala Ile Glu Asp Leu Lys Ala Ala Met Ala Thr Ala Lys Ala 570 575 580	1843
tcg gag aaa tcc acc ttc atc cac atc aac agc gat ccg ttg atc tac Ser Glu Lys Ser Thr Phe Ile His Ile Asn Ser Asp Pro Leu Ile Tyr 585 590 595	1891
gca cca gac ggt gct ggt tgg tgg gac gtg ccg gtg tcg gag acg tcc Ala Pro Asp Gly Ala Gly Trp Trp Asp Val Pro Val Ser Glu Thr Ser 600 605 610	1939
act ctg gat agc acc aac gcg gct cgt gaa gat tac ctg aaa aac caa Thr Leu Asp Ser Thr Asn Ala Ala Arg Glu Asp Tyr Leu Lys Asn Gln 615 620 625	1987
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 <212> PRT
 <213> Corynebacterium glutamicum

<400> 230

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 20 25 30

Pro Gly Met Phe Gly Ile Phe Gly His Gly Asn Val Ala Gly Ile Gly
 35 40 45

Gln Ala Leu Lys Gln Tyr Asn Val Glu Gln Pro Glu Leu Met Pro Tyr
 50 55 60

Tyr Gln Ala Arg Asn Glu Gln Ala Met Val His Gln Ser Val Gly Tyr
 65 70 75 80

Ala Arg Met His Arg Arg Arg Gly Thr Tyr Ala Ser Ala Ala Ser Val
 85 90 95

Gly Pro Gly Ala Thr Asn Leu Leu Thr Gly Ala Ala Leu Ala Thr Thr
 100 105 110

Asn Arg Leu Pro Ala Leu Leu Leu Pro Ser Asp Thr Phe Ala Thr Arg
 115 120 125

Val Ala Asp Pro Val Leu Gln Gln Leu Glu Gln Pro Trp Asp Ile Gly
 130 135 140

Leu Thr Val Asn Asp Ala Phe Arg Pro Val Ser Lys Phe Phe Asp Arg
 145 150 155 160

Val Gln Arg Pro Glu Gln Leu Phe Ser Ile Ala Leu Ala Ala Met Arg
 165 170 175

Val Leu Thr Asp Pro Ala Glu Thr Gly Ala Val Thr Ile Ala Leu Pro
 180 185 190

Glu Asp Val Gln Ala Glu Met Leu Asp Val Pro Val Glu Phe Leu Gln
 195 200 205

Asp Arg Glu Trp His Ile Arg Arg Pro Arg Pro Glu Arg Ala Ala Leu
 210 215 220

Ala Arg Ala Ile Glu Val Ile Lys Asn Ala Lys Asn Pro Met Ile Ile
 225 230 235 240

Ala Gly Gly Gly Val Leu Tyr Ser Asp Ala Glu Thr Gln Leu Gln Ala
 245 250 255

Leu Val Glu Gln Thr Gly Ile Pro Val Gly Thr Ser Gln Ala Gly Gly
 260 265 270

Gly Val Leu Ala Trp Asp His Ala Gln Asn Leu Gly Gly Val Gly Ala
 275 280 285

Thr Gly Thr Leu Ala Ala Asn Arg Ile Ala Gly Asp Ala Asp Val Ile

290 295 300
 Ile Gly Ile Gly Thr Arg Tyr Ser Asp Phe Thr Thr Ala Ser Arg Thr
 305 310 315 320
 Ala Phe Gln Asn Pro Asp Val Thr Phe Ile Asn Ile Asn Val Ala Ser
 325 330 335
 Phe Asp Ala Tyr Lys His Gly Thr Gln Leu Pro Val Ile Ala Asp Ala
 340 345 350
 Arg Glu Ala Ile Val Glu Leu Ala Glu Ala Leu Gln Gly Phe Thr Val
 355 360 365
 Ala Glu Asp Tyr Ala Gln Arg Ile Ala Lys Glu Lys Ala Ala Trp Asp
 370 375 380
 Ala Glu Val Asp Lys Ser Phe Ala Pro Ser Gly Leu Ala Leu Pro Gly
 385 390 395 400
 Gln Pro Glu Ile Ile Gly Ala Val Gln Ala Ser Thr Ser Glu Lys Asp
 405 410 415
 Val Ile Val Gln Ala Ala Gly Ser Leu Pro Gly Asp Leu His Lys Leu
 420 425 430
 Trp Arg Val Arg Asp Ala Leu Gly Tyr His Val Glu Tyr Ala Phe Ser
 435 440 445
 Cys Met Gly Tyr Glu Ile Ala Gly Gly Ile Gly Ala Lys Arg Gly Leu
 450 455 460
 Asp Ala Ala Gly Asp Asp Arg Asp Val Val Ile Met Val Gly Asp Gly
 465 470 475 480
 Ser Tyr Leu Met Leu Asn Thr Glu Leu Val Thr Ala Val Ala Glu Gly
 485 490 495
 Ile Lys Val Ile Val Val Leu Ile Gln Asn His Gly Tyr Ala Ser Ile
 500 505 510
 Gly His Leu Ser Glu Thr Val Gly Ser Gln Arg Phe Gly Thr Trp Tyr
 515 520 525
 Arg Glu Tyr Asp Ala Glu Ala Lys Asn Phe Gln Gly Glu Gln Ile Leu
 530 535 540
 Pro Val Asp Leu Ala Met Asn Ala Arg Ser Tyr Gly Met Asp Val Ile
 545 550 555 560
 Glu Val Glu Pro Ser Ala Asn Ala Ile Glu Asp Leu Lys Ala Ala Met
 565 570 575
 Ala Thr Ala Lys Ala Ser Glu Lys Ser Thr Phe Ile His Ile Asn Ser
 580 585 590
 Asp Pro Leu Ile Tyr Ala Pro Asp Gly Ala Gly Trp Trp Asp Val Pro
 595 600 605
 Val Ser Glu Thr Ser Thr Leu Asp Ser Thr Asn Ala Ala Arg Glu Asp
 610 615 620

Tyr Leu Lys Asn Gln Ala Leu Gln Arg Pro Leu Leu Gly
 625 630 635

<210> 231

<211> 1142

<212> DNA

<213> Corynebacterium glutamicum

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<222> (1)..(1119)

<223> RXN01143

<400> 231

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cac gag ctg cac atg ggt atg cca ggc atg cat ggc act gtg tcc gct	96
His Glu Leu His Met Gly Met Pro Gly Met His Gly Thr Val Ser Ala	
20 25 30	
gtt ggt gca ctg cag cgc agc gac ctg ctg att gct atc ggc tcc cgc	144
Val Gly Ala Leu Gln Arg Ser Asp Leu Leu Ile Ala Ile Gly Ser Arg	
35 40 45	
ttt gat gac cgc gtc acc ggt gac gtt gac acc ttc gcg cct gac gcc	192
Phe Asp Asp Arg Val Thr Gly Asp Val Asp Thr Phe Ala Pro Asp Ala	
50 55 60	
aag atc att cac gcc gac att gat cct gcc gaa atc ggc aag atc aag	240
Lys Ile Ile His Ala Asp Ile Asp Pro Ala Glu Ile Gly Lys Ile Lys	
65 70 75 80	
cag gtt gag gtt cca atc gtg ggc gat gcc cgc gaa gtt ctt gct cgt	288
Gln Val Glu Val Pro Ile Val Gly Asp Ala Arg Glu Val Leu Ala Arg	
85 90 95	
ctg ctg gaa acc acc aag gca agc aag gca gag acc gag gac atc tcc	336
Leu Leu Glu Thr Thr Lys Ala Ser Lys Ala Glu Thr Glu Asp Ile Ser	
100 105 110	
gag tgg gtt gac tac ctc aag ggc ctc aag gca cgt ttc ccg cgt ggc	384
Glu Trp Val Asp Tyr Leu Lys Gly Leu Lys Ala Arg Phe Pro Arg Gly	
115 120 125	
tac gac gag cag cca ggc gat ctg ctg gca cca cag ttt gtc att gaa	432
Tyr Asp Glu Gln Pro Gly Asp Leu Leu Ala Pro Gln Phe Val Ile Glu	
130 135 140	
acc ctg tcc aag gaa gtt ggc ccc gac gca att tac tgc gcc ggc gtt	480
Thr Leu Ser Lys Glu Val Gly Pro Asp Ala Ile Tyr Cys Ala Gly Val	
145 150 155 160	
ggc cag cac caa atg tgg gca gct cag ttc gtt gac ttt gaa aag cca	528
Gly Gln His Gln Met Trp Ala Ala Gln Phe Val Asp Phe Glu Lys Pro	
165 170 175	
cgc acc tgg ctc aac tcc ggt gga ctg ggc acc atg ggc tac gca gtt	576

Arg Thr Trp Leu Asn Ser Gly Gly Leu Gly Thr Met Gly Tyr Ala Val	
180 185 190	
cct gcg gcc ctt gga gca aag gct ggc gca cct gac aag gaa gtc tgg	624
Pro Ala Ala Leu Gly Ala Lys Ala Gly Ala Pro Asp Lys Glu Val Trp	
195 200 205	
gct atc gac ggc gac ggc tgt ttc cag atg acc aac cag gaa ctc acc	672
Ala Ile Asp Gly Asp Gly Cys Phe Gln Met Thr Asn Gln Glu Leu Thr	
210 215 220	
acc gcc gca gtt gaa ggt ttc ccc att aag atc gca cta atc aac aac	720
Thr Ala Ala Val Glu Gly Phe Pro Ile Lys Ile Ala Leu Ile Asn Asn	
225 230 235 240	
gga aaa cct ggg gca tgg gtt cgc caa tgg cag acc cta ttc tat gaa	768
Gly Lys Pro Gly Ala Trp Val Arg Gln Trp Gln Thr Leu Phe Tyr Glu	
245 250 255	
gga cgg tac tca aat act aaa ctt cgt aac cag ggc gag tac atg ccc	816
Gly Arg Tyr Ser Asn Thr Lys Leu Arg Asn Gln Gly Glu Tyr Met Pro	
260 265 270	
gac ttt gtt acc ctt tct gag gga ctt ggc tgt gtt gcc atc cgc gtc	864
Asp Phe Val Thr Leu Ser Glu Gly Leu Gly Cys Val Ala Ile Arg Val	
275 280 285	
acc aaa gcg gag gaa gta ctg cca gcc atc caa aag gct cga gag atc	912
Thr Lys Ala Glu Glu Val Leu Pro Ala Ile Gln Lys Ala Arg Glu Ile	
290 295 300	
aac gac cgc cca gta gtc atc gac ttc atc gtc ggt gaa gac gca cag	960
Asn Asp Arg Pro Val Val Ile Asp Phe Ile Val Gly Glu Asp Ala Gln	
305 310 315 320	
gta tgg cca atg gtg tct gct gga tca tcc aac tcc gat atc cag tac	1008
Val Trp Pro Met Val Ser Ala Gly Ser Ser Asn Ser Asp Ile Gln Tyr	
325 330 335	
gca ctc gga ttg cgc cca ttc ttt gat ggt gat gaa tct gca gca gaa	1056
Ala Leu Gly Leu Arg Pro Phe Phe Asp Gly Asp Glu Ser Ala Ala Glu	
340 345 350	
gat cct gcc gac att cac gaa gcc gtc agc gac att gat gcc gcc gtt	1104
Asp Pro Ala Asp Ile His Glu Ala Val Ser Asp Ile Asp Ala Ala Val	
355 360 365	
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<211> 373

<212> PRT

<213> Corynebacterium glutamicum

<400> 232

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 Val Gly Ala Leu Gln Arg Ser Asp Leu Leu Ile Ala Ile Gly Ser Arg
 35 40 45
 Phe Asp Asp Arg Val Thr Gly Asp Val Asp Thr Phe Ala Pro Asp Ala
 50 55 60
 Lys Ile Ile His Ala Asp Ile Asp Pro Ala Glu Ile Gly Lys Ile Lys
 65 70 75 80
 Gln Val Glu Val Pro Ile Val Gly Asp Ala Arg Glu Val Leu Ala Arg
 85 90 95
 Leu Leu Glu Thr Thr Lys Ala Ser Lys Ala Glu Thr Glu Asp Ile Ser
 100 105 110
 Glu Trp Val Asp Tyr Leu Lys Gly Leu Lys Ala Arg Phe Pro Arg Gly
 115 120 125
 Tyr Asp Glu Gln Pro Gly Asp Leu Leu Ala Pro Gln Phe Val Ile Glu
 130 135 140
 Thr Leu Ser Lys Glu Val Gly Pro Asp Ala Ile Tyr Cys Ala Gly Val
 145 150 155 160
 Gly Gln His Gln Met Trp Ala Ala Gln Phe Val Asp Phe Glu Lys Pro
 165 170 175
 Arg Thr Trp Leu Asn Ser Gly Gly Leu Gly Thr Met Gly Tyr Ala Val
 180 185 190
 Pro Ala Ala Leu Gly Ala Lys Ala Gly Ala Pro Asp Lys Glu Val Trp
 195 200 205
 Ala Ile Asp Gly Asp Gly Cys Phe Gln Met Thr Asn Gln Glu Leu Thr
 210 215 220
 Thr Ala Ala Val Glu Gly Phe Pro Ile Lys Ile Ala Leu Ile Asn Asn
 225 230 235 240
 Gly Lys Pro Gly Ala Trp Val Arg Gln Trp Gln Thr Leu Phe Tyr Glu
 245 250 255
 Gly Arg Tyr Ser Asn Thr Lys Leu Arg Asn Gln Gly Glu Tyr Met Pro
 260 265 270
 Asp Phe Val Thr Leu Ser Glu Gly Leu Gly Cys Val Ala Ile Arg Val
 275 280 285
 Thr Lys Ala Glu Glu Val Leu Pro Ala Ile Gln Lys Ala Arg Glu Ile
 290 295 300
 Asn Asp Arg Pro Val Val Ile Asp Phe Ile Val Gly Glu Asp Ala Gln
 305 310 315 320
 Val Trp Pro Met Val Ser Ala Gly Ser Ser Asn Ser Asp Ile Gln Tyr
 325 330 335
 Ala Leu Gly Leu Arg Pro Phe Phe Asp Gly Asp Glu Ser Ala Ala Glu

340 345 350
 Asp Pro Ala Asp Ile His Glu Ala Val Ser Asp Ile Asp Ala Ala Val
 355 360 365
 Glu Ser Thr Glu Ala
 370

 <210> 233
 <211> 793
 <212> DNA
 <213> Corynebacterium glutamicum

 <220>
 <221> CDS
 <222> (101)..(793)
 <223> RXN01146

 <400> 233
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 cacggttgca agccgtggtc gatccgccgc ccctgagcgg atg aca ggt gca aag 115
 Met Thr Gly Ala Lys
 1 5

 gca att gtt cga tcg ctc gag gag ctt aac gcc gac atc gtg ttc ggt 163
 Ala Ile Val Arg Ser Leu Glu Glu Leu Asn Ala Asp Ile Val Phe Gly
 10 15 20

 att cct ggt ggt gcg gtg cta ccg gtg tat gac ccg ctc tat tcc tcc 211
 Ile Pro Gly Gly Ala Val Leu Pro Val Tyr Asp Pro Leu Tyr Ser Ser
 25 30 35

 aca aag gtg cgc cac gtc ttg gtg cgc cac gag cag ggc gca ggc cac 259
 Thr Lys Val Arg His Val Leu Val Arg His Glu Gln Gly Ala Gly His
 40 45 50

 gca gca acc ggc tac gcg cag gtt act gga cgc gtt ggc gtc tgc att 307
 Ala Ala Thr Gly Tyr Ala Gln Val Thr Gly Arg Val Gly Val Cys Ile
 55 60 65

 gca acc tct ggc cca gga gca acc aac ttg gtt acc cca atc gct gat 355
 Ala Thr Ser Gly Pro Gly Ala Thr Asn Leu Val Thr Pro Ile Ala Asp
 70 75 80 85

 gca aac ttg gac tcc gtt ccc atg gtt gcc atc acc ggc cag gtc gga 403
 Ala Asn Leu Asp Ser Val Pro Met Val Ala Ile Thr Gly Gln Val Gly
 90 95 100

 agt ggc ctg ctg ggt acc gac gct ttc cag gaa gcc gat atc cgc ggc 451
 Ser Gly Leu Leu Gly Thr Asp Ala Phe Gln Glu Ala Asp Ile Arg Gly
 105 110 115

 atc acc atg cca gtg acc aag cac aac ttc atg gtc acc aac cct aac 499
 Ile Thr Met Pro Val Thr Lys His Asn Phe Met Val Thr Asn Pro Asn
 120 125 130

 gac att cca cag gca ttg gct gag gca ttc cac ctc gcg att act ggt 547
 Asp Ile Pro Gln Ala Leu Ala Glu Ala Phe His Leu Ala Ile Thr Gly
 135 140 145

cgc cct ggc cct gtt ctg gtg gat att cct aag gat gtc cag aac gct 595
 Arg Pro Gly Pro Val Leu Val Asp Ile Pro Lys Asp Val Gln Asn Ala
 150 155 160 165

gaa ttg gat ttc gtc tgg cca cca aag atc gac ctg cca ggc tac cgc 643
 Glu Leu Asp Phe Val Trp Pro Pro Lys Ile Asp Leu Pro Gly Tyr Arg
 170 175 180

cca gtt tca aca cca cat gct cgc cag atc gag cag gca gtc aag ctg 691
 Pro Val Ser Thr Pro His Ala Arg Gln Ile Glu Gln Ala Val Lys Leu
 185 190 195

atc ggt gag gcc aag aag ccc gtc ctt tac gtt ggt ggt ggc gta atc 739
 Ile Gly Glu Ala Lys Lys Pro Val Leu Tyr Val Gly Gly Gly Val Ile
 200 205 210

aag gct gac gca cac gaa gag ctt cgt gcg ttc gct gag tac acc ggc 787
 Lys Ala Asp Ala His Glu Glu Leu Arg Ala Phe Ala Glu Tyr Thr Gly
 215 220 225

atc cca 793
 Ile Pro
 230

<210> 234

<211> 231

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 234

Met Thr Gly Ala Lys Ala Ile Val Arg Ser Leu Glu Glu Leu Asn Ala
 1 5 10 15

Asp Ile Val Phe Gly Ile Pro Gly Gly Ala Val Leu Pro Val Tyr Asp
 20 25 30

Pro Leu Tyr Ser Ser Thr Lys Val Arg His Val Leu Val Arg His Glu
 35 40 45

Gln Gly Ala Gly His Ala Ala Thr Gly Tyr Ala Gln Val Thr Gly Arg
 50 55 60

Val Gly Val Cys Ile Ala Thr Ser Gly Pro Gly Ala Thr Asn Leu Val
 65 70 75 80

Thr Pro Ile Ala Asp Ala Asn Leu Asp Ser Val Pro Met Val Ala Ile
 85 90 95

Thr Gly Gln Val Gly Ser Gly Leu Leu Gly Thr Asp Ala Phe Gln Glu
 100 105 110

Ala Asp Ile Arg Gly Ile Thr Met Pro Val Thr Lys His Asn Phe Met
 115 120 125

Val Thr Asn Pro Asn Asp Ile Pro Gln Ala Leu Ala Glu Ala Phe His
 130 135 140

Leu Ala Ile Thr Gly Arg Pro Gly Pro Val Leu Val Asp Ile Pro Lys
 145 150 155 160

gtc gtc gac gtg gct cca gac tct gtg gtt att gaa tcc aca ggc acc 499
 Val Val Asp Val Ala Pro Asp Ser Val Val Ile Glu Ser Thr Gly Thr
 120 125 130

cca ggc aag ctc cgc gca ctg ctt gac gtg atg gaa cca ttc gga atc 547
 Pro Gly Lys Leu Arg Ala Leu Leu Asp Val Met Glu Pro Phe Gly Ile
 135 140 145

cgc gaa ctg atc caa tcc gga cag att gca ctc aac cgc ggt ccg aag 595
 Arg Glu Leu Ile Gln Ser Gly Gln Ile Ala Leu Asn Arg Gly Pro Lys
 150 155 160 165

acc atg gct ccg gcc aag atc taaacagcaa ttaatctgat tgc 639
 Thr Met Ala Pro Ala Lys Ile
 170

<210> 236

<211> 172

<212> PRT

<213> Corynebacterium glutamicum .

<400> 236

Met Ala Asn Ser Asp Val Thr Arg His Ile Leu Ser Val Leu Val Gln
 1 5 10 15

Asp Val Asp Gly Ile Ile Ser Arg Val Ser Gly Met Phe Thr Arg Arg
 20 25 30

Ala Phe Asn Leu Val Phe Leu Val Ser Ala Lys Thr Glu Thr His Gly
 35 40 45

Ile Asn Arg Ile Thr Val Val Val Asp Ala Asp Glu Leu Asn Ile Glu
 50 55 60

Gln Ile Thr Lys Gln Leu Asn Lys Leu Ile Pro Val Leu Lys Val Val
 65 70 75 80

Arg Leu Asp Glu Glu Thr Thr Ile Ala Arg Ala Ile Met Leu Val Lys
 85 90 95

Val Ser Ala Asp Ser Thr Asn Arg Pro Gln Ile Val Asp Ala Ala Asn
 100 105 110

Ile Phe Arg Ala Arg Val Val Asp Val Ala Pro Asp Ser Val Val Ile
 115 120 125

Glu Ser Thr Gly Thr Pro Gly Lys Leu Arg Ala Leu Leu Asp Val Met
 130 135 140

Glu Pro Phe Gly Ile Arg Glu Leu Ile Gln Ser Gly Gln Ile Ala Leu
 145 150 155 160

Asn Arg Gly Pro Lys Thr Met Ala Pro Ala Lys Ile
 165 170

<210> 237

<211> 897

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(874)

<223> RXA02474

<400> 237

tgctggtcta ttgtggcgac cgagggcctt tgaaggttcg acaaactgta taaggccttg 60

aatccttgaga atttattttg aggaagcaag aggaagtgtc	atg agc aaa gtt gca	115
	Met Ser Lys Val Ala	
	1 5	

atg gtt acc ggt ggt gca caa ggc atc ggt cgt gga att tca gag aag	163
Met Val Thr Gly Gly Ala Gln Gly Ile Gly Arg Gly Ile Ser Glu Lys	
10 15 20	

ctg gca gca gat ggt ttc gat att gcc gta gcc gac ctg cca caa cag	211
Leu Ala Ala Asp Gly Phe Asp Ile Ala Val Ala Asp Leu Pro Gln Gln	
25 30 35	

gaa gaa caa gct gca gag acc atc aag ttg att gaa gct gca ggt caa	259
Glu Glu Gln Ala Ala Glu Thr Ile Lys Leu Ile Glu Ala Ala Gly Gln	
40 45 50	

aag gct gta ttc gtt gga tta gat gtc acc gat aag gct aat ttc gac	307
Lys Ala Val Phe Val Gly Leu Asp Val Thr Asp Lys Ala Asn Phe Asp	
55 60 65	

agt gca att gat gag gca gca gag aaa ctt ggc ggc ttc gat gtg cta	355
Ser Ala Ile Asp Glu Ala Ala Glu Lys Leu Gly Gly Phe Asp Val Leu	
70 75 80 85	

gta aac aac gcc ggc atc gca caa att aag cca ctt ctg gaa gtc acc	403
Val Asn Asn Ala Gly Ile Ala Gln Ile Lys Pro Leu Leu Glu Val Thr	
90 95 100	

gaa gaa gac cta aag cag atc tac tcc gtg aac gtt ttt agc gta ttt	451
Glu Glu Asp Leu Lys Gln Ile Tyr Ser Val Asn Val Phe Ser Val Phe	
105 110 115	

ttt ggt att caa gca gca tcc cga aag ttc gat gag ctt ggc gta aaa	499
Phe Gly Ile Gln Ala Ala Ser Arg Lys Phe Asp Glu Leu Gly Val Lys	
120 125 130	

ggc aag atc atc aac gct gca tca atc gct gct atc caa ggt ttc cca	547
Gly Lys Ile Ile Asn Ala Ala Ser Ile Ala Ala Ile Gln Gly Phe Pro	
135 140 145	

atc ttg agc gcc tac tcc acc acc aaa ttc gcg gtt cgt ggc ctc acc	595
Ile Leu Ser Ala Tyr Ser Thr Thr Lys Phe Ala Val Arg Gly Leu Thr	
150 155 160 165	

cag gct gct gcg caa gaa ctc gca ccc aag ggt cac acc gtg aat gcc	643
Gln Ala Ala Ala Gln Glu Leu Ala Pro Lys Gly His Thr Val Asn Ala	
170 175 180	

tac gca cct ggc atc gtg ggc acc gga atg tgg gag caa atc gat gcc	691
Tyr Ala Pro Gly Ile Val Gly Thr Gly Met Trp Glu Gln Ile Asp Ala	
185 190 195	

gag ctt tcc aag atc aac ggc aag cca atc ggt gag aac ttc aag gag 739
 Glu Leu Ser Lys Ile Asn Gly Lys Pro Ile Gly Glu Asn Phe Lys Glu
 200 205 210

tac tcc tcc tca atc gca ttg ggc cga cca tca gta cct gag gat gta 787
 Tyr Ser Ser Ser Ile Ala Leu Gly Arg Pro Ser Val Pro Glu Asp Val
 215 220 225

gcc ggt ctg gtt tcg ttc ctg gct tct gaa aac tcc aac tac atc acc 835
 Ala Gly Leu Val Ser Phe Leu Ala Ser Glu Asn Ser Asn Tyr Ile Thr
 230 235 240 245

gga cag gtc atg ctt gtc gac ggc ggc atg ctc tac aac taggggttgc 884
 Gly Gln Val Met Leu Val Asp Gly Gly Met Leu Tyr Asn
 250 255

tttcccgcac tca 897

<210> 238
 <211> 258
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 238
 Met Ser Lys Val Ala Met Val Thr Gly Gly Ala Gln Gly Ile Gly Arg
 1 5 10 15
 Gly Ile Ser Glu Lys Leu Ala Ala Asp Gly Phe Asp Ile Ala Val Ala
 20 25 30
 Asp Leu Pro Gln Gln Glu Glu Gln Ala Ala Glu Thr Ile Lys Leu Ile
 35 40 45
 Glu Ala Ala Gly Gln Lys Ala Val Phe Val Gly Leu Asp Val Thr Asp
 50 55 60
 Lys Ala Asn Phe Asp Ser Ala Ile Asp Glu Ala Ala Glu Lys Leu Gly
 65 70 75 80
 Gly Phe Asp Val Leu Val Asn Asn Ala Gly Ile Ala Gln Ile Lys Pro
 85 90 95
 Leu Leu Glu Val Thr Glu Glu Asp Leu Lys Gln Ile Tyr Ser Val Asn
 100 105 110
 Val Phe Ser Val Phe Phe Gly Ile Gln Ala Ala Ser Arg Lys Phe Asp
 115 120 125
 Glu Leu Gly Val Lys Gly Lys Ile Ile Asn Ala Ala Ser Ile Ala Ala
 130 135 140
 Ile Gln Gly Phe Pro Ile Leu Ser Ala Tyr Ser Thr Thr Lys Phe Ala
 145 150 155 160
 Val Arg Gly Leu Thr Gln Ala Ala Ala Gln Glu Leu Ala Pro Lys Gly
 165 170 175
 His Thr Val Asn Ala Tyr Ala Pro Gly Ile Val Gly Thr Gly Met Trp
 180 185 190

Glu Gln Ile Asp Ala Glu Leu Ser Lys Ile Asn Gly Lys Pro Ile Gly
 195 200 205

Glu Asn Phe Lys Glu Tyr Ser Ser Ser Ile Ala Leu Gly Arg Pro Ser
 210 215 220

Val Pro Glu Asp Val Ala Gly Leu Val Ser Phe Leu Ala Ser Glu Asn
 225 230 235 240

Ser Asn Tyr Ile Thr Gly Gln Val Met Leu Val Asp Gly Gly Met Leu
 245 250 255

Tyr Asn

<210> 239
 <211> 876
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(853)
 <223> RXA02453

<400> 239

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tcgtgccagc tcagggcata tctcacctaa agtaaacacc atg aaa tca atc ttc 115
 Met Lys Ser Ile Phe
 1 5

att tcc ggt gcg gcg aac gga att ggc aaa gct gtg gcg ttg aaa ttt 163
 Ile Ser Gly Ala Ala Asn Gly Ile Gly Lys Ala Val Ala Leu Lys Phe
 10 15 20

ctt cac gaa ggt tgg ctc gtt gga gcc tac gac ctc gcg gaa atc acc 211
 Leu His Glu Gly Trp Leu Val Gly Ala Tyr Asp Leu Ala Glu Ile Thr
 25 30 35

tac tca cac ccc aat ctt cgc tgg ggc tac ctc aat gtt cga cag tcc 259
 Tyr Ser His Pro Asn Leu Arg Trp Gly Tyr Leu Asn Val Arg Gln Ser
 40 45 50

gag tcg tgg gac aaa gcc cta gaa gac ttt gcg acg cac acc gga ggc 307
 Glu Ser Trp Asp Lys Ala Leu Glu Asp Phe Ala Thr His Thr Gly Gly
 55 60 65

acc atc gat gtg gtg gac aat aat gcc ggc gta att att gag gga ccg 355
 Thr Ile Asp Val Val Asp Asn Asn Ala Gly Val Ile Ile Glu Gly Pro
 70 75 80 85

ctg cag gac gca gag gag ggg agc gtc gac aag ctt ctt gca atc aac 403
 Leu Gln Asp Ala Glu Gly Ser Val Asp Lys Leu Leu Ala Ile Asn
 90 95 100

gtc aat ggc gtg act ctt ggt gcc cgc gcc gct cat cct tat ttg gcg 451
 Val Asn Gly Val Thr Leu Gly Ala Arg Ala Ala His Pro Tyr Leu Ala
 105 110 115

cgc acg ccg ggc gcc cag ttg tta aac atg tcc tcg gcg tcg gcg gtg 499
 Arg Thr Pro Gly Ala Gln Leu Leu Asn Met Ser Ser Ala Ser Ala Val
 120 125 130
 tac ggg cag ccc cag atc gcg gtg tat tcg gct tcg aag ttt tac gtc 547
 Tyr Gly Gln Pro Gln Ile Ala Val Tyr Ser Ala Ser Lys Phe Tyr Val
 135 140 145
 gca ggt ctt act gag gcg ctg aat ttg gag tgg cgg aaa gac gat att 595
 Ala Gly Leu Thr Glu Ala Leu Asn Leu Glu Trp Arg Lys Asp Asp Ile
 150 155 160 165
 cgc gtg gtc gat gtt tgg cct ttg tgg gcg aaa acc gat ttg gtg aac 643
 Arg Val Val Asp Val Trp Pro Leu Trp Ala Lys Thr Asp Leu Val Asn
 170 175 180
 ggc gtg aag gct aag tca ctg aag cgt ttg ggt gtc cgg atc act ccg 691
 Gly Val Lys Ala Lys Ser Leu Lys Arg Leu Gly Val Arg Ile Thr Pro
 185 190 195
 gaa cag gtg gca cag gcg gta tgg gat gcg gtg cat ccg aaa tct cgg 739
 Glu Gln Val Ala Gln Ala Val Trp Asp Ala Val His Pro Lys Ser Arg
 200 205 210
 tgg gcg aag gga aag gtg cat cac ggg gtg tca aag ttg gat aag gcg 787
 Trp Ala Lys Gly Lys Val His His Gly Val Ser Lys Leu Asp Lys Ala
 215 220 225
 ctg tat ctc atg aaa tct ctg tcg cct gat cgg gta gcg atg tgt ttt 835
 Leu Tyr Leu Met Lys Ser Leu Ser Pro Asp Arg Val Ala Met Cys Phe
 230 235 240 245
 gcg cga cta atc gcc gga taaatgaatt gattatttta ggc 876
 Ala Arg Leu Ile Ala Gly
 250

<210> 240

<211> 251

<212> PRT

<213> Corynebacterium glutamicum

<400> 240

Met Lys Ser Ile Phe Ile Ser Gly Ala Ala Asn Gly Ile Gly Lys Ala
 1 5 10 15
 Val Ala Leu Lys Phe Leu His Glu Gly Trp Leu Val Gly Ala Tyr Asp
 20 25 30
 Leu Ala Glu Ile Thr Tyr Ser His Pro Asn Leu Arg Trp Gly Tyr Leu
 35 40 45
 Asn Val Arg Gln Ser Glu Ser Trp Asp Lys Ala Leu Glu Asp Phe Ala
 50 55 60
 Thr His Thr Gly Gly Thr Ile Asp Val Val Asp Asn Asn Ala Gly Val
 65 70 75 80
 Ile Ile Glu Gly Pro Leu Gln Asp Ala Glu Glu Gly Ser Val Asp Lys
 85 90 95

Leu Leu Ala Ile Asn Val Asn Gly Val Thr Leu Gly Ala Arg Ala Ala
 100 105 110
 His Pro Tyr Leu Ala Arg Thr Pro Gly Ala Gln Leu Leu Asn Met Ser
 115 120 125
 Ser Ala Ser Ala Val Tyr Gly Gln Pro Gln Ile Ala Val Tyr Ser Ala
 130 135 140
 Ser Lys Phe Tyr Val Ala Gly Leu Thr Glu Ala Leu Asn Leu Glu Trp
 145 150 155 160
 Arg Lys Asp Asp Ile Arg Val Val Asp Val Trp Pro Leu Trp Ala Lys
 165 170 175
 Thr Asp Leu Val Asn Gly Val Lys Ala Lys Ser Leu Lys Arg Leu Gly
 180 185 190
 Val Arg Ile Thr Pro Glu Gln Val Ala Gln Ala Val Trp Asp Ala Val
 195 200 205
 His Pro Lys Ser Arg Trp Ala Lys Gly Lys Val His His Gly Val Ser
 210 215 220
 Lys Leu Asp Lys Ala Leu Tyr Leu Met Lys Ser Leu Ser Pro Asp Arg
 225 230 235 240
 Val Ala Met Cys Phe Ala Arg Leu Ile Ala Gly
 245 250

<210> 241
 <211> 1140
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1117)
 <223> RXS01758

<400> 241
 ccccttatt cagagtgatg gtctaccgga gaagtaccca gaccaatagc atcgaccaac 60
 gatagcgcgc tcagaagttc tttagtga aa gcagaaccaa atg ccc aaa tac att 115
 Met Pro Lys Tyr Ile
 1 5
 gcc atg cag gta tcc gaa tcc ggt gca ccg tta gcc gcg aat ctc gtg 163
 Ala Met Gln Val Ser Glu Ser Gly Ala Pro Leu Ala Ala Asn Leu Val
 10 15 20
 caa cct gct ccg ttg aaa tcg agg gaa gtc cgc gtg gaa atc gct gct 211
 Gln Pro Ala Pro Leu Lys Ser Arg Glu Val Arg Val Glu Ile Ala Ala
 25 30 35
 agt ggt gtg tgc cat gca gat att ggc acg gca gca gca tcg ggg aag 259
 Ser Gly Val Cys His Ala Asp Ile Gly Thr Ala Ala Ala Ser Gly Lys
 40 45 50

cac act gtt ttt cct gtt acc cct ggt cat gag att gca gga acc atc	307
His Thr Val Phe Pro Val Thr Pro Gly His Glu Ile Ala Gly Thr Ile	
55 60 65	
gcg gaa att ggt gaa aac gta tct cgg tgg acg gtt ggt gat cgc gtt	355
Ala Glu Ile Gly Glu Asn Val Ser Arg Trp Thr Val Gly Asp Arg Val	
70 75 80 85	
gca atc ggt tgg ttt ggt ggc aat tgc ggt gac tgc gct ttt tgt cgt	403
Ala Ile Gly Trp Phe Gly Gly Asn Cys Gly Asp Cys Ala Phe Cys Arg	
90 95 100	
gca ggt gat cct gtg cat tgc aga gag cgg aag att cct ggc gtt tct	451
Ala Gly Asp Pro Val His Cys Arg Glu Arg Lys Ile Pro Gly Val Ser	
105 110 115	
tat gcg ggt ggt tgg gca cag aat att gtt gtt cca gcg gag gct ctt	499
Tyr Ala Gly Gly Trp Ala Gln Asn Ile Val Val Pro Ala Glu Ala Leu	
120 125 130	
gct gcg att cca gat ggc atg gac ttt tac gag ccc gcc ccg atg ggc	547
Ala Ala Ile Pro Asp Gly Met Asp Phe Tyr Glu Pro Ala Pro Met Gly	
135 140 145	
tgc gca ggt gtg aca aca ttc aat gcg ttg cga aac ctg aag ctg gat	595
Cys Ala Gly Val Thr Thr Phe Asn Ala Leu Arg Asn Leu Lys Leu Asp	
150 155 160 165	
ccc ggt gcg gct gtc gcg gtc ttt gga atc ggc ggt tta gtg cgc cta	643
Pro Gly Ala Ala Val Ala Val Phe Gly Ile Gly Gly Leu Val Arg Leu	
170 175 180	
gct att cag ttt gct gcg aaa atg ggt tat cga acc atc acc atc gcc	691
Ala Ile Gln Phe Ala Ala Lys Met Gly Tyr Arg Thr Ile Thr Ile Ala	
185 190 195	
cgc ggt tta gag cgt gag gag cta gct agg caa ctt ggc gcc aac cac	739
Arg Gly Leu Glu Arg Glu Glu Leu Ala Arg Gln Leu Gly Ala Asn His	
200 205 210	
tac atc gat agc aat gat ctg cac cct ggc cag gcg tta ttt gaa ctt	787
Tyr Ile Asp Ser Asn Asp Leu His Pro Gly Gln Ala Leu Phe Glu Leu	
215 220 225	
ggc ggg gct gac ttg atc ttg tct act gcg tcc acc acg gag cct ctt	835
Gly Gly Ala Asp Leu Ile Leu Ser Thr Ala Ser Thr Thr Glu Pro Leu	
230 235 240 245	
tcg gag ttg tct acc ggt ctt tct att ggc ggg cag cta acc att atc	883
Ser Glu Leu Ser Thr Gly Leu Ser Ile Gly Gly Gln Leu Thr Ile Ile	
250 255 260	
gga gtt gat ggg gga gat atc acc gtt tcg gca gcc caa ttg atg atg	931
Gly Val Asp Gly Gly Asp Ile Thr Val Ser Ala Ala Gln Leu Met Met	
265 270 275	
aac cgt cag atc atc aca ggt cac ctc act gga agt gcg aat gac acg	979
Asn Arg Gln Ile Ile Thr Gly His Leu Thr Gly Ser Ala Asn Asp Thr	
280 285 290	
gaa cag act atg aaa ttt gct cat ctc cat ggc gtg aaa ccg ctt att	1027

Glu Gln Thr Met Lys Phe Ala His Leu His Gly Val Lys Pro Leu Ile
 295 300 305
 gaa cgg atg cct ctc gat caa gcc aac gag gct att gca cgt att tca 1075
 Glu Arg Met Pro Leu Asp Gln Ala Asn Glu Ala Ile Ala Arg Ile Ser
 310 315 320 325
 gct ggt aaa cca cgt ttc cgt att gtc ttg gag ccg aat tca 1117
 Ala Gly Lys Pro Arg Phe Arg Ile Val Leu Glu Pro Asn Ser
 330 335
 taatgccaac agcaagccca att 1140

 <210> 242
 <211> 339
 <212> PRT
 <213> Corynebacterium glutamicum

 <400> 242
 Met Pro Lys Tyr Ile Ala Met Gln Val Ser Glu Ser Gly Ala Pro Leu
 1 5 10 15
 Ala Ala Asn Leu Val Gln Pro Ala Pro Leu Lys Ser Arg Glu Val Arg
 20 25 30
 Val Glu Ile Ala Ala Ser Gly Val Cys His Ala Asp Ile Gly Thr Ala
 35 40 45
 Ala Ala Ser Gly Lys His Thr Val Phe Pro Val Thr Pro Gly His Glu
 50 55 60
 Ile Ala Gly Thr Ile Ala Glu Ile Gly Glu Asn Val Ser Arg Trp Thr
 65 70 75 80
 Val Gly Asp Arg Val Ala Ile Gly Trp Phe Gly Gly Asn Cys Gly Asp
 85 90 95
 Cys Ala Phe Cys Arg Ala Gly Asp Pro Val His Cys Arg Glu Arg Lys
 100 105 110
 Ile Pro Gly Val Ser Tyr Ala Gly Gly Trp Ala Gln Asn Ile Val Val
 115 120 125
 Pro Ala Glu Ala Leu Ala Ala Ile Pro Asp Gly Met Asp Phe Tyr Glu
 130 135 140
 Pro Ala Pro Met Gly Cys Ala Gly Val Thr Thr Phe Asn Ala Leu Arg
 145 150 155 160
 Asn Leu Lys Leu Asp Pro Gly Ala Ala Val Ala Val Phe Gly Ile Gly
 165 170 175
 Gly Leu Val Arg Leu Ala Ile Gln Phe Ala Ala Lys Met Gly Tyr Arg
 180 185 190
 Thr Ile Thr Ile Ala Arg Gly Leu Glu Arg Glu Glu Leu Ala Arg Gln
 195 200 205
 Leu Gly Ala Asn His Tyr Ile Asp Ser Asn Asp Leu His Pro Gly Gln
 210 215 220

Ala Leu Phe Glu Leu Gly Gly Ala Asp Leu Ile Leu Ser Thr Ala Ser
225 230 235 240

Thr Thr Glu Pro Leu Ser Glu Leu Ser Thr Gly Leu Ser Ile Gly Gly
245 250 255

Gln Leu Thr Ile Ile Gly Val Asp Gly Gly Asp Ile Thr Val Ser Ala
260 265 270

Ala Gln Leu Met Met Asn Arg Gln Ile Ile Thr Gly His Leu Thr Gly
275 280 285

Ser Ala Asn Asp Thr Glu Gln Thr Met Lys Phe Ala His Leu His Gly
290 295 300

Val Lys Pro Leu Ile Glu Arg Met Pro Leu Asp Gln Ala Asn Glu Ala
305 310 315 320

Ile Ala Arg Ile Ser Ala Gly Lys Pro Arg Phe Arg Ile Val Leu Glu
325 330 335

Pro Asn Ser

<210> 243

<211> 1665

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1642)

<223> RXA02737

<400> 243

agcagcgtgc atcagtaacg gcgacatgaa atcgaattag ttcgatctta tgtggccggt 60

acacatcttt cattaagaa aggatcgtga cactaccatc gtg agc aca aac acg 115
Val Ser Thr Asn Thr
1 5

acc ccc tcc agc tgg aca aac cca ctg cgc gac ccg cag gat aaa cga 163
Thr Pro Ser Ser Trp Thr Asn Pro Leu Arg Asp Pro Gln Asp Lys Arg
10 15 20

ctc ccc cgc atc gct ggc cct tcc ggc atg gtg atc ttc ggt gtc act 211
Leu Pro Arg Ile Ala Gly Pro Ser Gly Met Val Ile Phe Gly Val Thr
25 30 35

ggc gac ttg gct cga aag aag ctg ctc ccc gcc att tat gat cta gca 259
Gly Asp Leu Ala Arg Lys Lys Leu Leu Pro Ala Ile Tyr Asp Leu Ala
40 45 50

aac cgc gga ttg ctg ccc cca gga ttc tcg ttg gta ggt tac ggc cgc 307
Asn Arg Gly Leu Leu Pro Pro Gly Phe Ser Leu Val Gly Tyr Gly Arg
55 60 65

cgc gaa tgg tcc aaa gaa gac ttt gaa aaa tac gta cgc gat gcc gca 355
Arg Glu Trp Ser Lys Glu Asp Phe Glu Lys Tyr Val Arg Asp Ala Ala

70	75	80	85
agt gct ggt gct cgt acg gaa ttc cgt gaa aat gtt tgg gag cgc ctc Ser Ala Gly Ala Arg Thr Glu Phe Arg Glu Asn Val Trp Glu Arg Leu 90 95 100	403		
gcc gag ggt atg gaa ttt gtt cgc ggc aac ttt gat gat gat gca gct Ala Glu Gly Met Glu Phe Val Arg Gly Asn Phe Asp Asp Asp Ala Ala 105 110 115	451		
ttc gac aac ctc gct gca aca ctc aag cgc atc gac aaa acc cgc ggc Phe Asp Asn Leu Ala Ala Thr Leu Lys Arg Ile Asp Lys Thr Arg Gly 120 125 130	499		
acc gcc ggc aac tgg gct tac tac ctg tcc att cca cca gat tcc ttc Thr Ala Gly Asn Trp Ala Tyr Tyr Leu Ser Ile Pro Pro Asp Ser Phe 135 140 145	547		
aca gcg gtc tgc cac cag ctg gag cgt tcc ggc atg gct gaa tcc acc Thr Ala Val Cys His Gln Leu Glu Arg Ser Gly Met Ala Glu Ser Thr 150 155 160 165	595		
gaa gaa gca tgg cgc cgc gtg atc atc gag aag cct ttc ggc cac aac Glu Glu Ala Trp Arg Arg Val Ile Ile Glu Lys Pro Phe Gly His Asn 170 175 180	643		
ctc gaa tcc gca cac gag ctc aac cag ctg gtc aac gca gtc ttc cca Leu Glu Ser Ala His Glu Leu Asn Gln Leu Val Asn Ala Val Phe Pro 185 190 195	691		
gaa tct tct gtg ttc cgc atc gac cac tat ttg ggc aag gaa aca gtt Glu Ser Ser Val Phe Arg Ile Asp His Tyr Leu Gly Lys Glu Thr Val 200 205 210	739		
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cgc gac gtc atc cag aac cac ctg atc cag ctc ttg gct ctg gtt gcc Arg Asp Val Ile Gln Asn His Leu Ile Gln Leu Leu Ala Leu Val Ala 265 270 275	931		
atg gaa gaa cca att tct ttc gtg cca gcg cag ctg cag gca gaa aag Met Glu Glu Pro Ile Ser Phe Val Pro Ala Gln Leu Gln Ala Glu Lys 280 285 290	979		
atc aag gtg ctc tct gcg aca aag ccg tgc tac cca ttg gat aaa acc Ile Lys Val Leu Ser Ala Thr Lys Pro Cys Tyr Pro Leu Asp Lys Thr 295 300 305	1027		
tcc gct cgt ggt cag tac gct gcc ggt tgg cag ggc tct gag tta gtc Ser Ala Arg Gly Gln Tyr Ala Ala Gly Trp Gln Gly Ser Glu Leu Val 310 315 320 325	1075		

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330 335 340

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Thr Phe Ala Ala Cys Thr Leu Glu Ile Thr Ser Arg Arg Trp Ala Gly
345 350 355

gtg ccg ttc tac ctg cgc acc ggt aag cgt ctt ggt cgc cgt gtt act 1219
Val Pro Phe Tyr Leu Arg Thr Gly Lys Arg Leu Gly Arg Arg Val Thr
360 365 370

gag att gcc gtg gtg ttt aaa gac gca cca cac cag cct ttc gac ggc 1267
Glu Ile Ala Val Val Phe Lys Asp Ala Pro His Gln Pro Phe Asp Gly
375 380 385

gac atg act gta tcc ctt ggc caa aac gcc atc gtg att cgc gtg cag 1315
Asp Met Thr Val Ser Leu Gly Gln Asn Ala Ile Val Ile Arg Val Gln
390 395 400 405

cct gat gaa ggt gtg ctc atc cgc ttc ggt tcc aag gtt cca ggt tct 1363
Pro Asp Glu Gly Val Leu Ile Arg Phe Gly Ser Lys Val Pro Gly Ser
410 415 420

gcc atg gaa gtc cgt gac gtc aac atg gac ttc tcc tac tca gaa tcc 1411
Ala Met Glu Val Arg Asp Val Asn Met Asp Phe Ser Tyr Ser Glu Ser
425 430 435

ttc act gaa gaa tca cct gaa gca tac gag cgc ctc att ttg gat gcg 1459
Phe Thr Glu Glu Ser Pro Glu Ala Tyr Glu Arg Leu Ile Leu Asp Ala
440 445 450

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Leu Leu Asp Glu Ser Ser Leu Phe Pro Thr Asn Glu Glu Val Glu Leu
455 460 465

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Ser Trp Lys Ile Leu Asp Pro Ile Leu Glu Ala Trp Asp Ala Asp Gly
470 475 480 485

gaa cca gag gat tac cca gcg ggt acg tgg ggt cca aag agc gct gat 1603
Glu Pro Glu Asp Tyr Pro Ala Gly Thr Trp Gly Pro Lys Ser Ala Asp
490 495 500

gaa atg ctt tcc cgc aac ggt cac acc tgg cgc agg cca taatttaggg 1652
Glu Met Leu Ser Arg Asn Gly His Thr Trp Arg Arg Pro
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 35 40 45
 Ile Tyr Asp Leu Ala Asn Arg Gly Leu Leu Pro Pro Gly Phe Ser Leu
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 Val Gly Tyr Gly Arg Arg Glu Trp Ser Lys Glu Asp Phe Glu Lys Tyr
 65 70 75 80
 Val Arg Asp Ala Ala Ser Ala Gly Ala Arg Thr Glu Phe Arg Glu Asn
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 Val Trp Glu Arg Leu Ala Glu Gly Met Glu Phe Val Arg Gly Asn Phe
 100 105 110
 Asp Asp Asp Ala Ala Phe Asp Asn Leu Ala Ala Thr Leu Lys Arg Ile
 115 120 125
 Asp Lys Thr Arg Gly Thr Ala Gly Asn Trp Ala Tyr Tyr Leu Ser Ile
 130 135 140
 Pro Pro Asp Ser Phe Thr Ala Val Cys His Gln Leu Glu Arg Ser Gly
 145 150 155 160
 Met Ala Glu Ser Thr Glu Glu Ala Trp Arg Arg Val Ile Ile Glu Lys
 165 170 175
 Pro Phe Gly His Asn Leu Glu Ser Ala His Glu Leu Asn Gln Leu Val
 180 185 190
 Asn Ala Val Phe Pro Glu Ser Ser Val Phe Arg Ile Asp His Tyr Leu
 195 200 205
 Gly Lys Glu Thr Val Gln Asn Ile Leu Ala Leu Arg Phe Ala Asn Gln
 210 215 220
 Leu Phe Glu Pro Leu Trp Asn Ser Asn Tyr Val Asp His Val Gln Ile
 225 230 235 240
 Thr Met Ala Glu Asp Ile Gly Leu Gly Gly Arg Ala Gly Tyr Tyr Asp
 245 250 255
 Gly Ile Gly Ala Ala Arg Asp Val Ile Gln Asn His Leu Ile Gln Leu
 260 265 270
 Leu Ala Leu Val Ala Met Glu Glu Pro Ile Ser Phe Val Pro Ala Gln
 275 280 285
 Leu Gln Ala Glu Lys Ile Lys Val Leu Ser Ala Thr Lys Pro Cys Tyr
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 Pro Leu Asp Lys Thr Ser Ala Arg Gly Gln Tyr Ala Ala Gly Trp Gln
 305 310 315 320
 Gly Ser Glu Leu Val Lys Gly Leu Arg Glu Glu Asp Gly Phe Asn Pro
 325 330 335
 Glu Ser Thr Thr Glu Thr Phe Ala Ala Cys Thr Leu Glu Ile Thr Ser

340 345 350
 Arg Arg Trp Ala Gly Val Pro Phe Tyr Leu Arg Thr Gly Lys Arg Leu
 355 360 365
 Gly Arg Arg Val Thr Glu Ile Ala Val Val Phe Lys Asp Ala Pro His
 370 375 380
 Gln Pro Phe Asp Gly Asp Met Thr Val Ser Leu Gly Gln Asn Ala Ile
 385 390 395 400
 Val Ile Arg Val Gln Pro Asp Glu Gly Val Leu Ile Arg Phe Gly Ser
 405 410 415
 Lys Val Pro Gly Ser Ala Met Glu Val Arg Asp Val Asn Met Asp Phe
 420 425 430
 Ser Tyr Ser Glu Ser Phe Thr Glu Glu Ser Pro Glu Ala Tyr Glu Arg
 435 440 445
 Leu Ile Leu Asp Ala Leu Leu Asp Glu Ser Ser Leu Phe Pro Thr Asn
 450 455 460
 Glu Glu Val Glu Leu Ser Trp Lys Ile Leu Asp Pro Ile Leu Glu Ala
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 485 490 495
 Pro Lys Ser Ala Asp Glu Met Leu Ser Arg Asn Gly His Thr Trp Arg
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Arg Pro

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 Met Ser His Ile Asp
 1 5
 gat ctt gca cag ctc ggc act tcc act tgg ctc gac gac ctc tcc cgc 163
 Asp Leu Ala Gln Leu Gly Thr Ser Thr Trp Leu Asp Asp Leu Ser Arg
 10 15 20
 gag cgc att act tcc ggc aat ctc agc cag gtt att gag gaa aag tct 211
 Glu Arg Ile Thr Ser Gly Asn Leu Ser Gln Val Ile Glu Glu Lys Ser
 25 30 35

gta gtc ggt gtc acc acc aac cca gct att ttc gca gca gca atg tcc	259
Val Val Gly Val Thr Thr Asn Pro Ala Ile Phe Ala Ala Ala Met Ser	
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Lys Gly Asp Ser Tyr Asp Ala Gln Ile Ala Glu Leu Lys Ala Ala Gly	
55 60 65	
gca tct gtt gac cag gct gtt tac gcc atg agc atc gac gac gtt cgc	355
Ala Ser Val Asp Gln Ala Val Tyr Ala Met Ser Ile Asp Asp Val Arg	
70 75 80 85	
aat gct tgt gat ctg ttc acc ggc atc ttc gag tcc tcc aac ggc tac	403
Asn Ala Cys Asp Leu Phe Thr Gly Ile Phe Glu Ser Ser Asn Gly Tyr	
90 95 100	
gac ggc cgc gtg tcc atc gag gtt gac cca cgt atc tct gct gac cgc	451
Asp Gly Arg Val Ser Ile Glu Val Asp Pro Arg Ile Ser Ala Asp Arg	
105 110 115	
gac gca acc ctg gct cag gcc aag gag ctg tgg gca aag gtt gat cgt	499
Asp Ala Thr Leu Ala Gln Ala Lys Glu Leu Trp Ala Lys Val Asp Arg	
120 125 130	
cca aac gtc atg atc aag atc cct gca acc cca ggt tct ttg cca gca	547
Pro Asn Val Met Ile Lys Ile Pro Ala Thr Pro Gly Ser Leu Pro Ala	
135 140 145	
atc acc gac gct ttg gct gag ggc atc agc gtt aac gtc acc ttg atc	595
Ile Thr Asp Ala Leu Ala Glu Gly Ile Ser Val Asn Val Thr Leu Ile	
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ttc tcc gtt gct cgc tac cgc gag gtc atc gct gcg ttc atc gag ggc	643
Phe Ser Val Ala Arg Tyr Arg Glu Val Ile Ala Ala Phe Ile Glu Gly	
170 175 180	
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Ile Lys Gln Ala Ala Ala Asn Gly His Asp Val Ser Lys Ile His Ser	
185 190 195	
gtg gct tcc ttc ttc gtc tcc cgc gtc gac gtt gag atc gac aag cgc	739
Val Ala Ser Phe Phe Val Ser Arg Val Asp Val Glu Ile Asp Lys Arg	
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ctc gag gca atc gga tcc gat gag gct ttg gct ctg cgc ggc aag gca	787
Leu Glu Ala Ile Gly Ser Asp Glu Ala Leu Ala Leu Arg Gly Lys Ala	
215 220 225	
ggc gtt gcc aac gct cag cgc gct tac gct gtg tac aag gag ctt ttc	835
Gly Val Ala Asn Ala Gln Arg Ala Tyr Ala Val Tyr Lys Glu Leu Phe	
230 235 240 245	
gac gcc gcc gag ctg cct gaa ggt gcc aac act cag cgc cca ctg tgg	883
Asp Ala Ala Glu Leu Pro Glu Gly Ala Asn Thr Gln Arg Pro Leu Trp	
250 255 260	
gca tcc acc ggc gtg aag aac cct gcg tac gct gca act ctt tac gtt	931
Ala Ser Thr Gly Val Lys Asn Pro Ala Tyr Ala Ala Thr Leu Tyr Val	
265 270 275	
tcc gag ctg gct ggt cca aac acc gtc aac acc atg cca gaa ggc acc	979

Ser Glu Leu Ala Gly Pro Asn Thr Val Asn Thr Met Pro Glu Gly Thr
 280 285 290
 atc gac gcg gtt ctg gag cag ggc aac ctg cac ggt gac acc ctg tcc 1027
 Ile Asp Ala Val Leu Glu Gln Gly Asn Leu His Gly Asp Thr Leu Ser
 295 300 305
 aac tcc gcg gca gaa gct gac gct gtg ttc tcc cag ctt gag gct ctg 1075
 Asn Ser Ala Ala Glu Ala Asp Ala Val Phe Ser Gln Leu Glu Ala Leu
 310 315 320 325
 ggc gtt gac ttg gca gat gtc ttc cag gtc ctg gag acc gag ggt gtg 1123
 Gly Val Asp Leu Ala Asp Val Phe Gln Val Leu Glu Thr Glu Gly Val
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 gac aag ttc gtt gct tct tgg agc gaa ctg ctt gag tcc atg gaa gct 1171
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 Arg Leu Lys
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 35 40 45
 Ala Ala Ala Met Ser Lys Gly Asp Ser Tyr Asp Ala Gln Ile Ala Glu
 50 55 60
 Leu Lys Ala Ala Gly Ala Ser Val Asp Gln Ala Val Tyr Ala Met Ser
 65 70 75 80
 Ile Asp Asp Val Arg Asn Ala Cys Asp Leu Phe Thr Gly Ile Phe Glu
 85 90 95
 Ser Ser Asn Gly Tyr Asp Gly Arg Val Ser Ile Glu Val Asp Pro Arg
 100 105 110
 Ile Ser Ala Asp Arg Asp Ala Thr Leu Ala Gln Ala Lys Glu Leu Trp
 115 120 125
 Ala Lys Val Asp Arg Pro Asn Val Met Ile Lys Ile Pro Ala Thr Pro
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<223> RXA02739
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Ser Leu Ala Pro Leu Ala Tyr Thr Leu Tyr Gln Arg Val Met Asn Val	
55 60 65	
gat cca cag gac acc aac tgg gca ggc cgt gac cgc ttc gtt ctt tct	355
Asp Pro Gln Asp Thr Asn Trp Ala Gly Arg Asp Arg Phe Val Leu Ser	
70 75 80 85	
tgt ggc cac tcc tct ttg acc cag tac atc cag ctt tac ttg ggt gga	403
Cys Gly His Ser Ser Leu Thr Gln Tyr Ile Gln Leu Tyr Leu Gly Gly	
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ttc ggc ctt gag atg gat gac ctg aag gct ctg cgc acc tgg gat tcc	451
Phe Gly Leu Glu Met Asp Asp Leu Lys Ala Leu Arg Thr Trp Asp Ser	
105 110 115	
ttg acc cca gga cac cct gag tac cgc cac acc aag ggc gtt gag atc	499
Leu Thr Pro Gly His Pro Glu Tyr Arg His Thr Lys Gly Val Glu Ile	
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acc act ggc cct ctt ggc cag ggt ctt gca tct gca gtt ggt atg gcc	547
Thr Thr Gly Pro Leu Gly Gln Gly Leu Ala Ser Ala Val Gly Met Ala	
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Met Ala Ala Arg Arg Glu Arg Gly Leu Phe Asp Pro Thr Ala Ala Glu	
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Gly Glu Ser Pro Phe Asp His His Ile Tyr Val Ile Ala Ser Asp Gly	
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Asp Leu Gln Glu Gly Val Thr Ser Glu Ala Ser Ser Ile Ala Gly Thr	
185 190 195	
cag cag ctg ggc aac ctc atc gtg ttc tgg gat gac aac cgc atc tcc	739
Gln Gln Leu Gly Asn Leu Ile Val Phe Trp Asp Asp Asn Arg Ile Ser	
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Ile Glu Asp Asn Thr Glu Ile Ala Phe Asn Glu Asp Val Val Ala Arg	
215 220 225	
tac aag gct tac ggc tgg cag acc att gag gtt gag gct ggc gag gac	835
Tyr Lys Ala Tyr Gly Trp Gln Thr Ile Glu Val Glu Ala Gly Glu Asp	
230 235 240 245	
gtt gca gca atc gaa gct gca gtg gct gag gct aag aag gac acc aag	883
Val Ala Ala Ile Glu Ala Ala Val Ala Glu Ala Lys Lys Asp Thr Lys	
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cga cct acc ttc atc cgc gtt cgc acc atc atc ggc ttc cca gct cca	931
Arg Pro Thr Phe Ile Arg Val Arg Thr Ile Ile Gly Phe Pro Ala Pro	

354

atc cca ggt ctg tcc gtc ctg cgt cct gca gat gcg aac gag acc gcc 1699
 Ile Pro Gly Leu Ser Val Leu Arg Pro Ala Asp Ala Asn Glu Thr Ala
 520 525 530

cag gct tgg gct gca gca ctt gag tac aag gaa ggc cct aag ggt ctt 1747
 Gln Ala Trp Ala Ala Ala Leu Glu Tyr Lys Glu Gly Pro Lys Gly Leu
 535 540 545

gca ctg acc cgc cag aac gtt cct gtt ctg gaa ggc acc aag gag aag 1795
 Ala Leu Thr Arg Gln Asn Val Pro Val Leu Glu Gly Thr Lys Glu Lys
 550 555 560 565

gct gct gaa ggc gtt cgc cgc ggt ggc tac gtc ctg gtt gag ggt tcc 1843
 Ala Ala Glu Gly Val Arg Arg Gly Gly Tyr Val Leu Val Glu Gly Ser
 570 575 580

aag gaa acc cca gat gtg atc ctc atg ggc tcc ggc tcc gag gtt cag 1891
 Lys Glu Thr Pro Asp Val Ile Leu Met Gly Ser Gly Ser Glu Val Gln
 585 590 595

ctt gca gtt aac gct gcg aag gct ctg gaa gct gag ggc gtt gca gct 1939
 Leu Ala Val Asn Ala Ala Lys Ala Leu Glu Ala Glu Gly Val Ala Ala
 600 605 610

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 Arg Val Val Ser Val Pro Cys Met Asp Trp Phe Gln Glu Gln Asp Ala
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gag tac atc gag tcc gtt ctg cct gca gct gtg acc gct cgt gtg tct 2035
 Glu Tyr Ile Glu Ser Val Leu Pro Ala Ala Val Thr Ala Arg Val Ser
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gtt gaa gct ggc atc gca atg cct tgg tac cgc ttc ttg ggc acc cag 2083
 Val Glu Ala Gly Ile Ala Met Pro Trp Tyr Arg Phe Leu Gly Thr Gln
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ggc cgt gct gtc tcc ctt gag cac ttc ggt gct tct gcg gat tac cag 2131
 Gly Arg Ala Val Ser Leu Glu His Phe Gly Ala Ser Ala Asp Tyr Gln
 665 670 675

acc ctg ttt gag aag ttc ggc atc acc acc gat gca gtc gtg gca gcg 2179
 Thr Leu Phe Glu Lys Phe Gly Ile Thr Thr Asp Ala Val Val Ala Ala
 680 685 690

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<211> 700

<212> PRT

<213> Corynebacterium glutamicum

<400> 248

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 35 40 45
 Pro Gly Thr Ala Met Ser Leu Ala Pro Leu Ala Tyr Thr Leu Tyr Gln
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 Arg Val Met Asn Val Asp Pro Gln Asp Thr Asn Trp Ala Gly Arg Asp
 65 70 75 80
 Arg Phe Val Leu Ser Cys Gly His Ser Ser Leu Thr Gln Tyr Ile Gln
 85 90 95
 Leu Tyr Leu Gly Gly Phe Gly Leu Glu Met Asp Asp Leu Lys Ala Leu
 100 105 110
 Arg Thr Trp Asp Ser Leu Thr Pro Gly His Pro Glu Tyr Arg His Thr
 115 120 125
 Lys Gly Val Glu Ile Thr Thr Gly Pro Leu Gly Gln Gly Leu Ala Ser
 130 135 140
 Ala Val Gly Met Ala Met Ala Ala Arg Arg Glu Arg Gly Leu Phe Asp
 145 150 155 160
 Pro Thr Ala Ala Glu Gly Glu Ser Pro Phe Asp His His Ile Tyr Val
 165 170 175
 Ile Ala Ser Asp Gly Asp Leu Gln Glu Gly Val Thr Ser Glu Ala Ser
 180 185 190
 Ser Ile Ala Gly Thr Gln Gln Leu Gly Asn Leu Ile Val Phe Trp Asp
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 Asp Asn Arg Ile Ser Ile Glu Asp Asn Thr Glu Ile Ala Phe Asn Glu
 210 215 220
 Asp Val Val Ala Arg Tyr Lys Ala Tyr Gly Trp Gln Thr Ile Glu Val
 225 230 235 240
 Glu Ala Gly Glu Asp Val Ala Ala Ile Glu Ala Ala Val Ala Glu Ala
 245 250 255
 Lys Lys Asp Thr Lys Arg Pro Thr Phe Ile Arg Val Arg Thr Ile Ile
 260 265 270
 Gly Phe Pro Ala Pro Thr Met Met Asn Thr Gly Ala Val His Gly Ala
 275 280 285
 Ala Leu Gly Ala Ala Glu Val Ala Ala Thr Lys Thr Glu Leu Gly Phe
 290 295 300
 Asp Pro Glu Ala His Phe Ala Ile Asp Asp Glu Val Ile Ala His Thr
 305 310 315 320
 Arg Ser Leu Ala Glu Arg Ala Ala Gln Lys Lys Ala Ala Trp Gln Val
 325 330 335
 Lys Phe Asp Glu Trp Ala Ala Ala Asn Pro Glu Asn Lys Ala Leu Phe
 340 345 350

Asp Arg Leu Asn Ser Arg Glu Leu Pro Ala Gly Tyr Ala Asp Glu Leu
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 370 375 380
 Glu Ala Ala Leu Gln Ala Leu Gly Lys Thr Leu Pro Glu Leu Trp Gly
 385 390 395 400
 Gly Ser Ala Asp Leu Ala Gly Ser Asn Asn Thr Val Ile Lys Gly Ser
 405 410 415
 Pro Ser Phe Gly Pro Glu Ser Ile Ser Thr Glu Thr Trp Ser Ala Glu
 420 425 430
 Pro Tyr Gly Arg Asn Leu His Phe Gly Ile Arg Glu His Ala Met Gly
 435 440 445
 Ser Ile Leu Asn Gly Ile Ser Leu His Gly Gly Thr Arg Pro Tyr Gly
 450 455 460
 Gly Thr Phe Leu Ile Phe Ser Asp Tyr Met Arg Pro Ala Val Arg Leu
 465 470 475 480
 Ala Ala Leu Met Glu Thr Asp Ala Tyr Tyr Val Trp Thr His Asp Ser
 485 490 495
 Ile Gly Leu Gly Glu Asp Gly Pro Thr His Gln Pro Val Glu Thr Leu
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 Ala Ala Leu Arg Ala Ile Pro Gly Leu Ser Val Leu Arg Pro Ala Asp
 515 520 525
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 530 535 540
 Gly Pro Lys Gly Leu Ala Leu Thr Arg Gln Asn Val Pro Val Leu Glu
 545 550 555 560
 Gly Thr Lys Glu Lys Ala Ala Glu Gly Val Arg Arg Gly Gly Tyr Val
 565 570 575
 Leu Val Glu Gly Ser Lys Glu Thr Pro Asp Val Ile Leu Met Gly Ser
 580 585 590
 Gly Ser Glu Val Gln Leu Ala Val Asn Ala Ala Lys Ala Leu Glu Ala
 595 600 605
 Glu Gly Val Ala Ala Arg Val Val Ser Val Pro Cys Met Asp Trp Phe
 610 615 620
 Gln Glu Gln Asp Ala Glu Tyr Ile Glu Ser Val Leu Pro Ala Ala Val
 625 630 635 640
 Thr Ala Arg Val Ser Val Glu Ala Gly Ile Ala Met Pro Trp Tyr Arg
 645 650 655
 Phe Leu Gly Thr Gln Gly Arg Ala Val Ser Leu Glu His Phe Gly Ala
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 Ser Ala Asp Tyr Gln Thr Leu Phe Glu Lys Phe Gly Ile Thr Thr Asp

675

680

685

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<223> RXA00965

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 Phe His Asp Leu Pro Leu Glu Glu Arg Leu Thr Leu Ala Arg Leu Gly
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 Thr Ser His Tyr Ser Arg Gln Leu Ser Leu Val Asp Asn Ala Glu Phe
 20 25 30 35

ggc gag cat tcc ctg cta gaa ggg tgg act cgt tcc cac ctc att gcc 200
 Gly Glu His Ser Leu Leu Glu Gly Trp Thr Arg Ser His Leu Ile Ala
 40 45 50

cac gtg gca tac aac gcc atc gca ctg tgc aac ctc atg cac tgg gca 248
 His Val Ala Tyr Asn Ala Ile Ala Leu Cys Asn Leu Met His Trp Ala
 55 60 65

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 Asn Thr Gly Glu Glu Thr Pro Met Tyr Val Ser Pro Glu Ala Arg Asn
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gag gaa att gcc tac ggt tcc acg ctc aat ccc gat gcg ttg cgt aac 344
 Glu Glu Ile Ala Tyr Gly Ser Thr Leu Asn Pro Asp Ala Leu Arg Asn
 85 90 95

ctg cat gaa cac tcc gtc gca cgc ctg gac gtg gct tgg cgt gaa acg 392
 Leu His Glu His Ser Val Ala Arg Leu Asp Val Ala Trp Arg Glu Thr
 100 105 110 115

tct gaa gat gct tgg tca cac gag gtt ctg aca gct cag gga cgc act 440
 Ser Glu Asp Ala Trp Ser His Glu Val Leu Thr Ala Gln Gly Arg Thr
 120 125 130

gtc cca gct agt gaa aca ttg tgg atg cgt tcc cgc gaa gtc tgg atc 488
 Val Pro Ala Ser Glu Thr Leu Trp Met Arg Ser Arg Glu Val Trp Ile
 135 140 145

cac gca gtt gac ctc ggt gca gtg gca acc ttt ggc gac atc cca gag 536
 His Ala Val Asp Leu Gly Ala Val Ala Thr Phe Gly Asp Ile Pro Glu
 150 155 160

gtc atc ctg cgc acc tta gct gca gaa atc aca caa aag tgg aca agc 584
 Val Ile Leu Arg Thr Leu Ala Ala Glu Ile Thr Gln Lys Trp Thr Ser
 165 170 175
 caa gga gcc ggc gag gga ctt gtg ctt ctc gac gag ccc tcc agc act 632
 Gln Gly Ala Gly Glu Gly Leu Val Leu Leu Asp Glu Pro Ser Ser Thr
 180 185 190 195
 cgc tac ccc gcc gcc cca ggg cag gac gag gta gta gtg tcc ggt agc 680
 Arg Tyr Pro Ala Ala Pro Gly Gln Asp Glu Val Val Val Ser Gly Ser
 200 205 210
 ctt gca ggc att gtt cgc tac gcc gct ggc cgc ggt tcc gat gga gtc 728
 Leu Ala Gly Ile Val Arg Tyr Ala Ala Gly Arg Gly Ser Asp Gly Val
 215 220 225
 act tct tcc act gga gag gtt cca gag cca ccg cgc tgg ctg 770
 Thr Ser Ser Thr Gly Glu Val Pro Glu Pro Pro Arg Trp Leu
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 <213> Corynebacterium glutamicum

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 Arg Leu Gly Thr Ser His Tyr Ser Arg Gln Leu Ser Leu Val Asp Asn
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 Ala Glu Phe Gly Glu His Ser Leu Leu Glu Gly Trp Thr Arg Ser His
 35 40 45
 Leu Ile Ala His Val Ala Tyr Asn Ala Ile Ala Leu Cys Asn Leu Met
 50 55 60
 His Trp Ala Asn Thr Gly Glu Glu Thr Pro Met Tyr Val Ser Pro Glu
 65 70 75 80
 Ala Arg Asn Glu Glu Ile Ala Tyr Gly Ser Thr Leu Asn Pro Asp Ala
 85 90 95
 Leu Arg Asn Leu His Glu His Ser Val Ala Arg Leu Asp Val Ala Trp
 100 105 110
 Arg Glu Thr Ser Glu Asp Ala Trp Ser His Glu Val Leu Thr Ala Gln
 115 120 125
 Gly Arg Thr Val Pro Ala Ser Glu Thr Leu Trp Met Arg Ser Arg Glu
 130 135 140
 Val Trp Ile His Ala Val Asp Leu Gly Ala Val Ala Thr Phe Gly Asp
 145 150 155 160
 Ile Pro Glu Val Ile Leu Arg Thr Leu Ala Ala Glu Ile Thr Gln Lys
 165 170 175

Trp Thr Ser Gln Gly Ala Gly Glu Gly Leu Val Leu Leu Asp Glu Pro
 180 185 190

Ser Ser Thr Arg Tyr Pro Ala Ala Pro Gly Gln Asp Glu Val Val Val
 195 200 205

Ser Gly Ser Leu Ala Gly Ile Val Arg Tyr Ala Ala Gly Arg Gly Ser
 210 215 220

Asp Gly Val Thr Ser Ser Thr Gly Glu Val Pro Glu Pro Pro Arg Trp
 225 230 235 240

Leu

<210> 251

<211> 1575

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1552)

<223> RXN00999

<400> 251

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 Met Thr Asn Gly Asp
 1 5

aat ctc gca cag atc ggc gtt gta ggc cta gca gta atg ggc tca aac 163
 Asn Leu Ala Gln Ile Gly Val Val Gly Leu Ala Val Met Gly Ser Asn
 10 15 20

ctc gcc cgc aac ttc gcc cgc aac ggc aac act gtc gct gtc tac aac 211
 Leu Ala Arg Asn Phe Ala Arg Asn Gly Asn Thr Val Ala Val Tyr Asn
 25 30 35

cgc agc act gac aaa acc gac aag ctc atc gcc gat cac ggc tcc gaa 259
 Arg Ser Thr Asp Lys Thr Asp Lys Leu Ile Ala Asp His Gly Ser Glu
 40 45 50

ggc aac ttc atc cct tct gca acc gtc gaa gag ttc gta gca tcc ctg 307
 Gly Asn Phe Ile Pro Ser Ala Thr Val Glu Glu Phe Val Ala Ser Leu
 55 60 65

gaa aag cca cgc cgc gcc atc atc atg gtt cag gct ggt aac gcc acc 355
 Glu Lys Pro Arg Arg Ala Ile Ile Met Val Gln Ala Gly Asn Ala Thr
 70 75 80 85

gac gca gtc atc aac cag ctg gca gat gcc atg gac gaa ggc gac atc 403
 Asp Ala Val Ile Asn Gln Leu Ala Asp Ala Met Asp Glu Gly Asp Ile
 90 95 100

atc atc gac ggc ggc aac gcc ctc tac acc gac acc att cgt cgc gag 451
 Ile Ile Asp Gly Gly Asn Ala Leu Tyr Thr Asp Thr Ile Arg Arg Glu
 105 110 115

aag gaa atc tcc gca cgc ggt ctc cac ttc gtc ggt gct ggt atc tcc Lys Glu Ile Ser Ala Arg Gly Leu His Phe Val Gly Ala Gly Ile Ser 120 125 130	499
ggc ggc gaa gaa ggc gca ctc aac ggc cca tcc atc atg cct ggt ggc Gly Gly Glu Glu Gly Ala Leu Asn Gly Pro Ser Ile Met Pro Gly Gly 135 140 145	547
cca gca aag tcc tac gag tcc ctc gga cca ctg ctt gag tcc atc gct Pro Ala Lys Ser Tyr Glu Ser Leu Gly Pro Leu Leu Glu Ser Ile Ala 150 155 160 165	595
gcc aac gtt gac ggc acc cca tgt gtc acc cac atc ggc cca gac ggc Ala Asn Val Asp Gly Thr Pro Cys Val Thr His Ile Gly Pro Asp Gly 170 175 180	643
gcc ggc cac ttc gtc aag atg gtc cac aac ggc atc gag tac gcc gac Ala Gly His Phe Val Lys Met Val His Asn Gly Ile Glu Tyr Ala Asp 185 190 195	691
atg cag gtc atc ggc gag gca tac cac ctt ctc cgc tac gca gca ggc Met Gln Val Ile Gly Glu Ala Tyr His Leu Leu Arg Tyr Ala Ala Gly 200 205 210	739
atg cag cca gct gaa atc gct gag gtt ttc aag gaa tgg aac gca ggc Met Gln Pro Ala Glu Ile Ala Glu Val Phe Lys Glu Trp Asn Ala Gly 215 220 225	787
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gtg gat gct gaa acc ggc aag cca cta atc gac gtc atc gtt gac gct Val Asp Ala Glu Thr Gly Lys Pro Leu Ile Asp Val Ile Val Asp Ala 250 255 260	883
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ctc tcc ggc gca acc agc cag cgc gct gca gca cag ggc aac cta cct Leu Ser Gly Ala Thr Ser Gln Arg Ala Ala Ala Gln Gly Asn Leu Pro 295 300 305	1027
gca ggt gtc ctc acc gat ctg gaa gca ctt ggc gtg gac aag gca cag Ala Gly Val Leu Thr Asp Leu Glu Ala Leu Gly Val Asp Lys Ala Gln 310 315 320 325	1075
ttc gtc gaa gac gtt cgc cgt gca ctg tac gca tcc aag ctt gtt gct Phe Val Glu Asp Val Arg Arg Ala Leu Tyr Ala Ser Lys Leu Val Ala 330 335 340	1123
tac gca cag ggc ttc gac gag atc aag gct ggc tcc gac gag aac aac Tyr Ala Gln Gly Phe Asp Glu Ile Lys Ala Gly Ser Asp Glu Asn Asn 345 350 355	1171

tgg gac gtt gac cct cgc gac ctc gct acc atc tgg cgc ggc ggc tgc 1219
 Trp Asp Val Asp Pro Arg Asp Leu Ala Thr Ile Trp Arg Gly Gly Cys
 360 365 370

 atc att cgc gct aag ttc ctc aac cgc atc gtc gaa gca tac gat gca 1267
 Ile Ile Arg Ala Lys Phe Leu Asn Arg Ile Val Glu Ala Tyr Asp Ala
 375 380 385

 aac gct gaa ctt gag tcc ctg ctg ctc gat cct tac ttc aag agc gag 1315
 Asn Ala Glu Leu Glu Ser Leu Leu Leu Asp Pro Tyr Phe Lys Ser Glu
 390 395 400 405

 ctc ggc gac ctc atc gat tca tgg cgt cgc gtg att gtc acc gcc acc 1363
 Leu Gly Asp Leu Ile Asp Ser Trp Arg Arg Val Ile Val Thr Ala Thr
 410 415 420

 cag ctt ggc ctg cca atc cca gtg ttc gct tcc tcc ctg tcc tac tac 1411
 Gln Leu Gly Leu Pro Ile Pro Val Phe Ala Ser Ser Leu Ser Tyr Tyr
 425 430 435

 gac agc ctg cgt gca gag cgt ctg cca gca gcc ctg atc caa gga cag 1459
 Asp Ser Leu Arg Ala Glu Arg Leu Pro Ala Ala Leu Ile Gln Gly Gln
 440 445 450

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 Arg Asp Phe Phe Gly Ala His Thr Tyr Lys Arg Ile Asp Lys Asp Gly
 455 460 465

 tcc ttc cac acc gag tgg tcc ggc gac cgc tcc gag gtt gaa gct 1552
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<210> 252

<211> 484

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 252

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 Val Ala Val Tyr Asn Arg Ser Thr Asp Lys Thr Asp Lys Leu Ile Ala
 35 40 45

 Asp His Gly Ser Glu Gly Asn Phe Ile Pro Ser Ala Thr Val Glu Glu
 50 55 60

 Phe Val Ala Ser Leu Glu Lys Pro Arg Arg Ala Ile Ile Met Val Gln
 65 70 75 80

 Ala Gly Asn Ala Thr Asp Ala Val Ile Asn Gln Leu Ala Asp Ala Met
 85 90 95

 Asp Glu Gly Asp Ile Ile Ile Asp Gly Gly Asn Ala Leu Tyr Thr Asp
 100 105 110

Thr Ile Arg Arg Glu Lys Glu Ile Ser Ala Arg Gly Leu His Phe Val
 115 120 125
 Gly Ala Gly Ile Ser Gly Gly Glu Glu Gly Ala Leu Asn Gly Pro Ser
 130 135 140
 Ile Met Pro Gly Gly Pro Ala Lys Ser Tyr Glu Ser Leu Gly Pro Leu
 145 150 155 160
 Leu Glu Ser Ile Ala Ala Asn Val Asp Gly Thr Pro Cys Val Thr His
 165 170 175
 Ile Gly Pro Asp Gly Ala Gly His Phe Val Lys Met Val His Asn Gly
 180 185 190
 Ile Glu Tyr Ala Asp Met Gln Val Ile Gly Glu Ala Tyr His Leu Leu
 195 200 205
 Arg Tyr Ala Ala Gly Met Gln Pro Ala Glu Ile Ala Glu Val Phe Lys
 210 215 220
 Glu Trp Asn Ala Gly Asp Leu Asp Ser Tyr Leu Ile Glu Ile Thr Ala
 225 230 235 240
 Glu Val Leu Ser Gln Val Asp Ala Glu Thr Gly Lys Pro Leu Ile Asp
 245 250 255
 Val Ile Val Asp Ala Ala Gly Gln Lys Gly Thr Gly Arg Trp Thr Val
 260 265 270
 Lys Ala Ala Leu Asp Leu Gly Ile Ala Thr Thr Gly Ile Gly Glu Ala
 275 280 285
 Val Phe Ala Arg Ala Leu Ser Gly Ala Thr Ser Gln Arg Ala Ala Ala
 290 295 300
 Gln Gly Asn Leu Pro Ala Gly Val Leu Thr Asp Leu Glu Ala Leu Gly
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 Val Asp Lys Ala Gln Phe Val Glu Asp Val Arg Arg Ala Leu Tyr Ala
 325 330 335
 Ser Lys Leu Val Ala Tyr Ala Gln Gly Phe Asp Glu Ile Lys Ala Gly
 340 345 350
 Ser Asp Glu Asn Asn Trp Asp Val Asp Pro Arg Asp Leu Ala Thr Ile
 355 360 365
 Trp Arg Gly Gly Cys Ile Ile Arg Ala Lys Phe Leu Asn Arg Ile Val
 370 375 380
 Glu Ala Tyr Asp Ala Asn Ala Glu Leu Glu Ser Leu Leu Leu Asp Pro
 385 390 395 400
 Tyr Phe Lys Ser Glu Leu Gly Asp Leu Ile Asp Ser Trp Arg Arg Val
 405 410 415
 Ile Val Thr Ala Thr Gln Leu Gly Leu Pro Ile Pro Val Phe Ala Ser
 420 425 430

Ser Leu Ser Tyr Tyr Asp Ser Leu Arg Ala Glu Arg Leu Pro Ala Ala
 435 440 445

Leu Ile Gln Gly Gln Arg Asp Phe Phe Gly Ala His Thr Tyr Lys Arg
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Ile Asp Lys Asp Gly Ser Phe His Thr Glu Trp Ser Gly Asp Arg Ser
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Glu Val Glu Ala

<210> 253
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 <212> DNA
 <213> Corynebacterium glutamicum

<220>
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 <222> (101)..(1537)
 <223> FRXA00999

<400> 253
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 Met Thr Asn Gly Asp
 1 5

aat ctg gca cag atc ggc gtt gta ggc cta gca gta atg ggc tca aac 163
 Asn Leu Ala Gln Ile Gly Val Val Gly Leu Ala Val Met Gly Ser Asn
 10 15 20

ctc gcc cgc aac ttc gcc cgc aac ggc aac act gtc gct gtc tac aac 211
 Leu Ala Arg Asn Phe Ala Arg Asn Gly Asn Thr Val Ala Val Tyr Asn
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cgc agc act gac aaa acc gac aag ctc atc gcc gat cac ggc tcc gaa 259
 Arg Ser Thr Asp Lys Thr Asp Lys Leu Ile Ala Asp His Gly Ser Glu
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ggc aac ttc atc cct tct gca acc gtc gaa gag ttc gta gca tcc ctg 307
 Gly Asn Phe Ile Pro Ser Ala Thr Val Glu Glu Phe Val Ala Ser Leu
 55 60 65

gaa aag cca cgc cgc gcc atc atc atg gtt cag gct ggt aac gcc acc 355
 Glu Lys Pro Arg Arg Ala Ile Ile Met Val Gln Ala Gly Asn Ala Thr
 70 75 80 85

gac gca gtc atc aac cag ctg gca gat gcc atg gac gaa ggc gac atc 403
 Asp Ala Val Ile Asn Gln Leu Ala Asp Ala Met Asp Glu Gly Asp Ile
 90 95 100

atc atc gac ggc ggc aac gcc ctc tac acc gac acc att cgt cgc gag 451
 Ile Ile Asp Gly Gly Asn Ala Leu Tyr Thr Asp Thr Ile Arg Arg Glu
 105 110 115

aag gaa atc tcc gca cgc ggt ctc cac ttc gtc ggt gct ggt atc tcc 499
 Lys Glu Ile Ser Ala Arg Gly Leu His Phe Val Gly Ala Gly Ile Ser
 120 125 130

ggc ggc gaa gaa ggc gca ctc aac ggc cca tcc atc atg cct ggt ggc Gly Gly Glu Glu Gly Ala Leu Asn Gly Pro Ser Ile Met Pro Gly Gly 135 140 145	547
cca gca aag tcc tac gag tcc ctc gga cca ctg ctt gag tcc atc gct Pro Ala Lys Ser Tyr Glu Ser Leu Gly Pro Leu Leu Glu Ser Ile Ala 150 155 160 165	595
gcc aac gtt gac ggc acc cca tgt gtc acc cac atc ggc cca gac ggc Ala Asn Val Asp Gly Thr Pro Cys Val Thr His Ile Gly Pro Asp Gly 170 175 180	643
gcc ggc cac ttc gtc aag atg gtc cac aac ggc atc gag tac gcc gac Ala Gly His Phe Val Lys Met Val His Asn Gly Ile Glu Tyr Ala Asp 185 190 195	691
atg cag gtc atc ggc gag gca tac cac ctt ctc cgc tac gca gca ggc Met Gln Val Ile Gly Glu Ala Tyr His Leu Leu Arg Tyr Ala Ala Gly 200 205 210	739
atg cag cca gct gaa atc gct gag gtt ttc aag gaa tgg aac gca ggc Met Gln Pro Ala Glu Ile Ala Glu Val Phe Lys Glu Trp Asn Ala Gly 215 220 225	787
gac ctg gat tcc tac ctc atc gaa atc acc gca gag gtt ctc tcc cag Asp Leu Asp Ser Tyr Leu Ile Glu Ile Thr Ala Glu Val Leu Ser Gln 230 235 240 245	835
gtg gat gct gaa acc ggc aag cca cta atc gac gtc atc gtt gac gct Val Asp Ala Glu Thr Gly Lys Pro Leu Ile Asp Val Ile Val Asp Ala 250 255 260	883
gca ggt cag aag ggc acc gga cgt tgg acc gtc aag gct gct ctt gat Ala Gly Gln Lys Gly Thr Gly Arg Trp Thr Val Lys Ala Ala Leu Asp 265 270 275	931
ctg ggt att gct acc acc ggc atc ggc gaa gct gtt ttc gca cgt gca Leu Gly Ile Ala Thr Thr Gly Ile Gly Glu Ala Val Phe Ala Arg Ala 280 285 290	979
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ttc gtc gaa gac gtt cgc cgt gca ctg tac gca tcc aag ctt gtt gct Phe Val Glu Asp Val Arg Arg Ala Leu Tyr Ala Ser Lys Leu Val Ala 330 335 340	1123
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 Ile Ile Arg Ala Lys Phe Leu Asn Arg Ile Val Glu Ala Tyr Asp Ala
 375 380 385

aac gct gaa ctt gag tcc ctg ctg ctc gat cct tac ttc aag agc gag 1315
 Asn Ala Glu Leu Glu Ser Leu Leu Leu Asp Pro Tyr Phe Lys Ser Glu
 390 395 400 405

ctc ggc gac ctc atc gat tca tgg cgt cgc gtg att gtc acc gcc acc 1363
 Leu Gly Asp Leu Ile Asp Ser Trp Arg Arg Val Ile Val Thr Ala Thr
 410 415 420

cag ctt ggc ctg cca atc cca gtg ttc gct tcc tcc ctg tcc tac tac 1411
 Gln Leu Gly Leu Pro Ile Pro Val Phe Ala Ser Ser Leu Ser Tyr Tyr
 425 430 435

gac agc ctg cgt gca gag cgt ctg cca gca gcc ctg atc caa gga cag 1459
 Asp Ser Leu Arg Ala Glu Arg Leu Pro Ala Ala Leu Ile Gln Gly Gln
 440 445 450

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 Arg Asp Phe Phe Gly Ala His Thr Tyr Lys Arg Ile Asp Lys Asp Gly
 455 460 465

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 Ser Phe His Thr Glu Trp Ser Gly Asp Arg
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<210> 254

<211> 479

<212> PRT

<213> Corynebacterium glutamicum

<400> 254

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 20 25 30

Val Ala Val Tyr Asn Arg Ser Thr Asp Lys Thr Asp Lys Leu Ile Ala
 35 40 45

Asp His Gly Ser Glu Gly Asn Phe Ile Pro Ser Ala Thr Val Glu Glu
 50 55 60

Phe Val Ala Ser Leu Glu Lys Pro Arg Arg Ala Ile Ile Met Val Gln
 65 70 75 80

Ala Gly Asn Ala Thr Asp Ala Val Ile Asn Gln Leu Ala Asp Ala Met
 85 90 95

Asp Glu Gly Asp Ile Ile Ile Asp Gly Gly Asn Ala Leu Tyr Thr Asp
 100 105 110

Thr Ile Arg Arg Glu Lys Glu Ile Ser Ala Arg Gly Leu His Phe Val
 115 120 125

Gly Ala Gly Ile Ser Gly Gly Glu Glu Gly Ala Leu Asn Gly Pro Ser
 130 135 140

Ile Met Pro Gly Gly Pro Ala Lys Ser Tyr Glu Ser Leu Gly Pro Leu
 145 150 155 160
 Leu Glu Ser Ile Ala Ala Asn Val Asp Gly Thr Pro Cys Val Thr His
 165 170 175
 Ile Gly Pro Asp Gly Ala Gly His Phe Val Lys Met Val His Asn Gly
 180 185 190
 Ile Glu Tyr Ala Asp Met Gln Val Ile Gly Glu Ala Tyr His Leu Leu
 195 200 205
 Arg Tyr Ala Ala Gly Met Gln Pro Ala Glu Ile Ala Glu Val Phe Lys
 210 215 220
 Glu Trp Asn Ala Gly Asp Leu Asp Ser Tyr Leu Ile Glu Ile Thr Ala
 225 230 235 240
 Glu Val Leu Ser Gln Val Asp Ala Glu Thr Gly Lys Pro Leu Ile Asp
 245 250 255
 Val Ile Val Asp Ala Ala Gly Gln Lys Gly Thr Gly Arg Trp Thr Val
 260 265 270
 Lys Ala Ala Leu Asp Leu Gly Ile Ala Thr Thr Gly Ile Gly Glu Ala
 275 280 285
 Val Phe Ala Arg Ala Leu Ser Gly Ala Thr Ser Gln Arg Ala Ala Ala
 290 295 300
 Gln Gly Asn Leu Pro Ala Gly Val Leu Thr Asp Leu Glu Ala Leu Gly
 305 310 315 320
 Val Asp Lys Ala Gln Phe Val Glu Asp Val Arg Arg Ala Leu Tyr Ala
 325 330 335
 Ser Lys Leu Val Ala Tyr Ala Gln Gly Phe Asp Glu Ile Lys Ala Gly
 340 345 350
 Ser Asp Glu Asn Asn Trp Asp Val Asp Pro Arg Asp Leu Ala Thr Ile
 355 360 365
 Trp Arg Gly Gly Cys Ile Ile Arg Ala Lys Phe Leu Asn Arg Ile Val
 370 375 380
 Glu Ala Tyr Asp Ala Asn Ala Glu Leu Glu Ser Leu Leu Leu Asp Pro
 385 390 395 400
 Tyr Phe Lys Ser Glu Leu Gly Asp Leu Ile Asp Ser Trp Arg Arg Val
 405 410 415
 Ile Val Thr Ala Thr Gln Leu Gly Leu Pro Ile Pro Val Phe Ala Ser
 420 425 430
 Ser Leu Ser Tyr Tyr Asp Ser Leu Arg Ala Glu Arg Leu Pro Ala Ala
 435 440 445
 Leu Ile Gln Gly Gln Arg Asp Phe Phe Gly Ala His Thr Tyr Lys Arg
 450 455 460

Ile Asp Lys Asp Gly Ser Phe His Thr Glu Trp Ser Gly Asp Arg
 465 470 475

<210> 255

<211> 1326

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1303)

<223> RXN02596

<400> 255

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 Met Thr Glu Ser Lys
 1 5

aat tac gac tta atc gtt gta ggc tcc ggc ctc ttc ggg ctc acc gtg 163
 Asn Tyr Asp Leu Ile Val Val Gly Ser Gly Leu Phe Gly Leu Thr Val
 10 15 20

gct gag cgt gca gct agc cag ctg ggt aag aaa gtc ctc atc gtt gaa 211
 Ala Glu Arg Ala Ala Ser Gln Leu Gly Lys Lys Val Leu Ile Val Glu
 25 30 35

cgc cgc tcg cac ctc ggt ggc aat gct tac tct gaa gca gaa cca gag 259
 Arg Arg Ser His Leu Gly Gly Asn Ala Tyr Ser Glu Ala Glu Pro Glu
 40 45 50

acc ggc att gaa atc cac aaa tac ggc gcg cac ctc ttc cac acc tcc 307
 Thr Gly Ile Glu Ile His Lys Tyr Gly Ala His Leu Phe His Thr Ser
 55 60 65

aac aca cgc gtg tgg gaa tac gtc aac cag ttc acc agt ttc acc ggc 355
 Asn Thr Arg Val Trp Glu Tyr Val Asn Gln Phe Thr Ser Phe Thr Gly
 70 75 80 85

tac cag cac cgc gtc ttc gca atg cac aac ggc acc gcc tac caa ttc 403
 Tyr Gln His Arg Val Phe Ala Met His Asn Gly Thr Ala Tyr Gln Phe
 90 95 100

ccc atg gga ctg ggc ctg att aac cag ttc ttc ggc aag tac tac agc 451
 Pro Met Gly Leu Gly Leu Ile Asn Gln Phe Phe Gly Lys Tyr Tyr Ser
 105 110 115

cca gat gaa gcc cgt gag ctc atc aag gaa cag tct gca gaa atc gat 499
 Pro Asp Glu Ala Arg Glu Leu Ile Lys Glu Gln Ser Ala Glu Ile Asp
 120 125 130

tcc tcc gac gcc acc aac ctc gaa gaa aag gcc att tcc ctc att ggt 547
 Ser Ser Asp Ala Thr Asn Leu Glu Glu Lys Ala Ile Ser Leu Ile Gly
 135 140 145

cgc cca ctt tac gag gca ttc atc cgc gac tac acc gca aag cag tgg 595
 Arg Pro Leu Tyr Glu Ala Phe Ile Arg Asp Tyr Thr Ala Lys Gln Trp
 150 155 160 165

cag act gat cca aag aac ctc cca gcc ggc aac atc acc cgc ctg cca	643
Gln Thr Asp Pro Lys Asn Leu Pro Ala Gly Asn Ile Thr Arg Leu Pro	
170 175 180	
gtt cgc tac aac ttc aac aac cgc tat ttc aac gac acc tac gaa ggc	691
Val Arg Tyr Asn Phe Asn Asn Arg Tyr Phe Asn Asp Thr Tyr Glu Gly	
185 190 195	
ctt ccc aca gac ggc tac gcg gca tgg ttg gaa aag atg gca gag cat	739
Leu Pro Thr Asp Gly Tyr Ala Ala Trp Leu Glu Lys Met Ala Glu His	
200 205 210	
gag ctt atc gac gtc cgc ctc gac acc gac tgg ttc gac gtt cgc gat	787
Glu Leu Ile Asp Val Arg Leu Asp Thr Asp Trp Phe Asp Val Arg Asp	
215 220 225	
gac ctc cgc gca agc aac ccc gac gca cct gtg gtc tac acc ggc cca	835
Asp Leu Arg Ala Ser Asn Pro Asp Ala Pro Val Val Tyr Thr Gly Pro	
230 235 240 245	
ctc gac ctc tac ttc aac tac gca gag ggc aag ctg gga tgg cgc acc	883
Leu Asp Leu Tyr Phe Asn Tyr Ala Glu Gly Lys Leu Gly Trp Arg Thr	
250 255 260	
ctc gac ttt gaa acc gaa gta gta gaa acc ggt gac ttc caa gga acc	931
Leu Asp Phe Glu Thr Glu Val Val Glu Thr Gly Asp Phe Gln Gly Thr	
265 270 275	
cca gtg atg aac tac aac gat gcg gac gta cct ttc acc cgc atc cac	979
Pro Val Met Asn Tyr Asn Asp Ala Asp Val Pro Phe Thr Arg Ile His	
280 285 290	
gag ttc cgt cac ttc cac cca gag cgt gat gac agt tac ccc aag gat	1027
Glu Phe Arg His Phe His Pro Glu Arg Asp Asp Ser Tyr Pro Lys Asp	
295 300 305	
aag acc gtc atc atg cgc gag ttc tcc cgt ttc gca gat aac gag gat	1075
Lys Thr Val Ile Met Arg Glu Phe Ser Arg Phe Ala Asp Asn Glu Asp	
310 315 320 325	
gag cct tat tac cca atc aac act cca gac gac cga gac atg ctg aag	1123
Glu Pro Tyr Tyr Pro Ile Asn Thr Pro Asp Asp Arg Asp Met Leu Lys	
330 335 340	
cag tac cgc ctt ctg gct gct gaa gag gct gct aat aat aag gtg ctg	1171
Gln Tyr Arg Leu Leu Ala Ala Glu Glu Ala Ala Asn Asn Lys Val Leu	
345 350 355	
ttc ggc ggt cga ctg ggc acg tac cag tac ctc gac atg cac atg gct	1219
Phe Gly Gly Arg Leu Gly Thr Tyr Gln Tyr Leu Asp Met His Met Ala	
360 365 370	
atc ggt tct gcg ctg agc atg ttt gac aac aag ctg gtg ccg ttc ttt	1267
Ile Gly Ser Ala Leu Ser Met Phe Asp Asn Lys Leu Val Pro Phe Phe	
375 380 385	
gaa gaa ggc aca ccg cta gag cag gaa cgc gga cac taaaaggaag	1313
Glu Glu Gly Thr Pro Leu Glu Gln Glu Arg Gly His	
390 395 400	
ggcatctctccc aca	1326

<210> 256

<211> 401

<212> PRT

<213> Corynebacterium glutamicum

<400> 256

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Phe Gly Leu Thr Val Ala Glu Arg Ala Ala Ser Gln Leu Gly Lys Lys
      20           25           30

Val Leu Ile Val Glu Arg Arg Ser His Leu Gly Gly Asn Ala Tyr Ser
      35           40           45

Glu Ala Glu Pro Glu Thr Gly Ile Glu Ile His Lys Tyr Gly Ala His
      50           55           60

Leu Phe His Thr Ser Asn Thr Arg Val Trp Glu Tyr Val Asn Gln Phe
      65           70           75           80

Thr Ser Phe Thr Gly Tyr Gln His Arg Val Phe Ala Met His Asn Gly
      85           90           95

Thr Ala Tyr Gln Phe Pro Met Gly Leu Gly Leu Ile Asn Gln Phe Phe
      100          105          110

Gly Lys Tyr Tyr Ser Pro Asp Glu Ala Arg Glu Leu Ile Lys Glu Gln
      115          120          125

Ser Ala Glu Ile Asp Ser Ser Asp Ala Thr Asn Leu Glu Glu Lys Ala
      130          135          140

Ile Ser Leu Ile Gly Arg Pro Leu Tyr Glu Ala Phe Ile Arg Asp Tyr
      145          150          155          160

Thr Ala Lys Gln Trp Gln Thr Asp Pro Lys Asn Leu Pro Ala Gly Asn
      165          170          175

Ile Thr Arg Leu Pro Val Arg Tyr Asn Phe Asn Asn Arg Tyr Phe Asn
      180          185          190

Asp Thr Tyr Glu Gly Leu Pro Thr Asp Gly Tyr Ala Ala Trp Leu Glu
      195          200          205

Lys Met Ala Glu His Glu Leu Ile Asp Val Arg Leu Asp Thr Asp Trp
      210          215          220

Phe Asp Val Arg Asp Asp Leu Arg Ala Ser Asn Pro Asp Ala Pro Val
      225          230          235          240

Val Tyr Thr Gly Pro Leu Asp Leu Tyr Phe Asn Tyr Ala Glu Gly Lys
      245          250          255

Leu Gly Trp Arg Thr Leu Asp Phe Glu Thr Glu Val Val Glu Thr Gly
      260          265          270

Asp Phe Gln Gly Thr Pro Val Met Asn Tyr Asn Asp Ala Asp Val Pro
      275          280          285

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Phe Thr Arg Ile His Glu Phe Arg His Phe His Pro Glu Arg Asp Asp
 290 295 300

Ser Tyr Pro Lys Asp Lys Thr Val Ile Met Arg Glu Phe Ser Arg Phe
 305 310 315 320

Ala Asp Asn Glu Asp Glu Pro Tyr Tyr Pro Ile Asn Thr Pro Asp Asp
 325 330 335

Arg Asp Met Leu Lys Gln Tyr Arg Leu Leu Ala Ala Glu Glu Ala Ala
 340 345 350

Asn Asn Lys Val Leu Phe Gly Gly Arg Leu Gly Thr Tyr Gln Tyr Leu
 355 360 365

Asp Met His Met Ala Ile Gly Ser Ala Leu Ser Met Phe Asp Asn Lys
 370 375 380

Leu Val Pro Phe Phe Glu Glu Gly Thr Pro Leu Glu Gln Glu Arg Gly
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His

<210> 257

<211> 512

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (1)..(489)

<223> FRXA02596

<400> 257

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 Gly Lys Leu Gly Trp Arg Thr Leu Asp Phe Glu Thr Glu Val Val Glu
 20 25 30

acc ggt gac ttc caa gga acc cca gtg atg aac tac aac gat gcg gac 144
 Thr Gly Asp Phe Gln Gly Thr Pro Val Met Asn Tyr Asn Asp Ala Asp
 35 40 45

gta cct ttc acc cgc atc cac gag ttc cgt cac ttc cac cca gag cgt 192
 Val Pro Phe Thr Arg Ile His Glu Phe Arg His Phe His Pro Glu Arg
 50 55 60

gat gac agt tac ccc aag gat aag acc gtc atc atg cgc gag ttc tcc 240
 Asp Asp Ser Tyr Pro Lys Asp Lys Thr Val Ile Met Arg Glu Phe Ser
 65 70 75 80

cgt ttc gca gat aac gag gat gag cct tat tac cca atc aac act cca 288
 Arg Phe Ala Asp Asn Glu Asp Glu Pro Tyr Tyr Pro Ile Asn Thr Pro
 85 90 95

gac gac cga gac atg ctg aag cag tac cgc ctt ctg gct gct gaa gag 336
 Asp Asp Arg Asp Met Leu Lys Gln Tyr Arg Leu Leu Ala Ala Glu Glu
 100 105 110

 gct gct aat aat aag gtg ctg ttc ggc ggt cga ctg ggc acg tac cag 384
 Ala Ala Asn Asn Lys Val Leu Phe Gly Gly Arg Leu Gly Thr Tyr Gln
 115 120 125

 tac ctc gac atg cac atg gct atc ggt tct gcg ctg agc atg ttt gac 432
 Tyr Leu Asp Met His Met Ala Ile Gly Ser Ala Leu Ser Met Phe Asp
 130 135 140

 aac aag ctg gtg ccg ttc ttt gaa gaa ggc aca ccg cta gag cag gaa 480
 Asn Lys Leu Val Pro Phe Phe Glu Glu Gly Thr Pro Leu Glu Gln Glu
 145 150 155 160

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 Arg Gly His

<210> 258
 <211> 163
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 258
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 Gly Lys Leu Gly Trp Arg Thr Leu Asp Phe Glu Thr Glu Val Val Glu
 20 25 30

 Thr Gly Asp Phe Gln Gly Thr Pro Val Met Asn Tyr Asn Asp Ala Asp
 35 40 45

 Val Pro Phe Thr Arg Ile His Glu Phe Arg His Phe His Pro Glu Arg
 50 55 60

 Asp Asp Ser Tyr Pro Lys Asp Lys Thr Val Ile Met Arg Glu Phe Ser
 65 70 75 80

 Arg Phe Ala Asp Asn Glu Asp Glu Pro Tyr Tyr Pro Ile Asn Thr Pro
 85 90 95

 Asp Asp Arg Asp Met Leu Lys Gln Tyr Arg Leu Leu Ala Ala Glu Glu
 100 105 110

 Ala Ala Asn Asn Lys Val Leu Phe Gly Gly Arg Leu Gly Thr Tyr Gln
 115 120 125

 Tyr Leu Asp Met His Met Ala Ile Gly Ser Ala Leu Ser Met Phe Asp
 130 135 140

 Asn Lys Leu Val Pro Phe Phe Glu Glu Gly Thr Pro Leu Glu Gln Glu
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 Arg Gly His

<210> 259
 <211> 598
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(598)
 <223> FRXA02642

<400> 259

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                                         Met Thr Glu Ser Lys
                                         1 5

aat tac gac tta atc gtt gta ggc tcc ggc ctc ttc ggg ctc acc gtg 163
Asn Tyr Asp Leu Ile Val Val Gly Ser Gly Leu Phe Gly Leu Thr Val
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gct gag cgt gca gct agc cag ctg ggt aag aaa gtc ctc atc gtt gaa 211
Ala Glu Arg Ala Ala Ser Gln Leu Gly Lys Lys Val Leu Ile Val Glu
          25          30          35

cgc cgc tcg cac ctc ggt ggc aat gct tac tct gaa gca gaa cca gag 259
Arg Arg Ser His Leu Gly Gly Asn Ala Tyr Ser Glu Ala Glu Pro Glu
          40          45          50

acc ggc att gaa atc cac aaa tac ggc gcg cac ctc ttc cac acc tcc 307
Thr Gly Ile Glu Ile His Lys Tyr Gly Ala His Leu Phe His Thr Ser
          55          60          65

aac aca cgc gtg tgg gaa tac gtc aac cag ttc acc agt ttc acc ggc 355
Asn Thr Arg Val Trp Glu Tyr Val Asn Gln Phe Thr Ser Phe Thr Gly
          70          75          80          85

tac cag cac cgc gtc ttc gca atg cac aac ggc acc gcc tac caa ttc 403
Tyr Gln His Arg Val Phe Ala Met His Asn Gly Thr Ala Tyr Gln Phe
          90          95          100

ccc atg gga ctg ggc ctg att aac cag ttc ttc ggc aag tac tac agc 451
Pro Met Gly Leu Gly Leu Ile Asn Gln Phe Phe Gly Lys Tyr Tyr Ser
          105          110          115

cca gat gaa gcc cgt gag ctc atc aag gaa cag tct gca gaa atc gat 499
Pro Asp Glu Ala Arg Glu Leu Ile Lys Glu Gln Ser Ala Glu Ile Asp
          120          125          130

tcc tcc gac gcc acc aac ctc gaa gaa aag gcc att tcc ctc att ggt 547
Ser Ser Asp Ala Thr Asn Leu Glu Glu Lys Ala Ile Ser Leu Ile Gly
          135          140          145

cgc cca ctt tac gag gca ttc atc cgc gac tac acc gca aag cag tgg 595
Arg Pro Leu Tyr Glu Ala Phe Ile Arg Asp Tyr Thr Ala Lys Gln Trp
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cag
Gln 598

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 <213> Corynebacterium glutamicum

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 20 25 30
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 35 40 45
 Glu Ala Glu Pro Glu Thr Gly Ile Glu Ile His Lys Tyr Gly Ala His
 50 55 60
 Leu Phe His Thr Ser Asn Thr Arg Val Trp Glu Tyr Val Asn Gln Phe
 65 70 75 80
 Thr Ser Phe Thr Gly Tyr Gln His Arg Val Phe Ala Met His Asn Gly
 85 90 95
 Thr Ala Tyr Gln Phe Pro Met Gly Leu Gly Leu Ile Asn Gln Phe Phe
 100 105 110
 Gly Lys Tyr Tyr Ser Pro Asp Glu Ala Arg Glu Leu Ile Lys Glu Gln
 115 120 125
 Ser Ala Glu Ile Asp Ser Ser Asp Ala Thr Asn Leu Glu Glu Lys Ala
 130 135 140
 Ile Ser Leu Ile Gly Arg Pro Leu Tyr Glu Ala Phe Ile Arg Asp Tyr
 145 150 155 160
 Thr Ala Lys Gln Trp Gln
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 <212> DNA
 <213> Corynebacterium glutamicum

<220>
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 <223> RXA02572

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 Val Asp Ala Ile Gly His Asp Asp Arg Ile Gly Arg Lys Phe Leu Gly
 20 25 30
 gcg ggc ctg gga ttc ggt ggc ggt tgt ttg cct aaa gac atc cgc gct 144

Ala Gly Leu Gly Phe Gly Gly Gly Cys Leu Pro Lys Asp Ile Arg Ala
 35 40 45

ttc atg gca cgc gcg ggc gaa ttg ggt gct gac cag gca tta acg ttc 192
 Phe Met Ala Arg Ala Gly Glu Leu Gly Ala Asp Gln Ala Leu Thr Phe
 50 55 60

ttg cgt gag gtc gat tcc atc aat atg cgt cgt cgc gac cgt gtg gtg 240
 Leu Arg Glu Val Asp Ser Ile Asn Met Arg Arg Arg Asp Arg Val Val
 65 70 75 80

cag ctg gcc aaa gag atg tgt ggc ggt tcg ctg ctg ggc aag cgg gtt 288
 Gln Leu Ala Lys Glu Met Cys Gly Gly Ser Leu Leu Gly Lys Arg Val
 85 90 95

aca gtg ctc ggc gcc gca ttc aaa ccc aac tcg gac gat gtc cgc gat 336
 Thr Val Leu Gly Ala Ala Phe Lys Pro Asn Ser Asp Asp Val Arg Asp
 100 105 110

tct ccg gcg ctg tcg gtc gcg ggt tcg ctg tcg ctc cag ggt gcg gcg 384
 Ser Pro Ala Leu Ser Val Ala Gly Ser Leu Ser Leu Gln Gly Ala Ala
 115 120 125

gtc tcg gtc tac gac ccg gaa gct atg gac aac gct cga cgc gtc ttc 432
 Val Ser Val Tyr Asp Pro Glu Ala Met Asp Asn Ala Arg Arg Val Phe
 130 135 140

ccg acg ctc agc tat gcg tcc agc act aaa gag gcg ctt atc gac gcc 480
 Pro Thr Leu Ser Tyr Ala Ser Ser Thr Lys Glu Ala Leu Ile Asp Ala
 145 150 155 160

cac ctc gtc gtt ctt gcc act gaa tgg caa gaa ttc cgc gac ctt gac 528
 His Leu Val Val Leu Ala Thr Glu Trp Gln Glu Phe Arg Asp Leu Asp
 165 170 175

ccc gaa gtg gcg gga ggg gtc gtc gag aag cgc gct att att gat ggc 576
 Pro Glu Val Ala Gly Gly Val Val Glu Lys Arg Ala Ile Ile Asp Gly
 180 185 190

cga aac gtc ctc gat gtt gcc aaa tgg aag gcc gcc ggt tgg gaa atg 624
 Arg Asn Val Leu Asp Val Ala Lys Trp Lys Ala Ala Gly Trp Glu Met
 195 200 205

gaa gcg ctc ggc cgc aac ctt tagtgcggtg gatcaggcgg ggc 668
 Glu Ala Leu Gly Arg Asn Leu
 210 215

<210> 262
 <211> 215
 <212> PRT
 <213> *Corynebacterium glutamicum*

<400> 262
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 20 25 30
 Ala Gly Leu Gly Phe Gly Gly Gly Cys Leu Pro Lys Asp Ile Arg Ala

376

gcc gta cgt tgc cag acc acg gag gcg ctg gtc agc gcc ata aaa ttg	259
Ala Val Arg Cys Gln Thr Thr Glu Ala Leu Val Ser Ala Ile Lys Leu	
40 45 50	
ctt gac gac gcc tcc ctc ccc ctc ctc att gtc ggc ggc ggg tcc aat	307
Leu Asp Asp Ala Ser Leu Pro Leu Leu Ile Val Gly Gly Gly Ser Asn	
55 60 65	
ctc gtc gtg gcc gac ggc gat ctg gat gtt att gcc gtc atc atc gaa	355
Leu Val Val Ala Asp Gly Asp Leu Asp Val Ile Ala Val Ile Ile Glu	
70 75 80 85	
acc gac gac gtc tcc atc aac ctc acc gac ggt ctc ctc acc gcc gat	403
Thr Asp Asp Val Ser Ile Asn Leu Thr Asp Gly Leu Leu Thr Ala Asp	
90 95 100	
gca ggc gct gtt tgg gac gat gtt gtc cac ctt tcg gtg gat gcc ggc	451
Ala Gly Ala Val Trp Asp Asp Val Val His Leu Ser Val Asp Ala Gly	
105 110 115	
ctc ggt gga att gaa tgc ctc tcc gga atc ccc ggc tcc gcc ggc gcc	499
Leu Gly Gly Ile Glu Cys Leu Ser Gly Ile Pro Gly Ser Ala Gly Ala	
120 125 130	
acc cca gtc caa aac gtg ggc gcc tac ggc acg gaa gtt tcc gat gta	547
Thr Pro Val Gln Asn Val Gly Ala Tyr Gly Thr Glu Val Ser Asp Val	
135 140 145	
ctc acc cgc gtc cag ctt ctc gac cgc acc acc cac caa gtc tcc tgg	595
Leu Thr Arg Val Gln Leu Asp Arg Thr Thr His Gln Val Ser Trp	
150 155 160 165	
gtc gac gcc tcc gaa ctc gac ctc tct tac cga tac tcc aat ctc aaa	643
Val Asp Ala Ser Glu Leu Asp Leu Ser Tyr Arg Tyr Ser Asn Leu Lys	
170 175 180	
ttc acc aac cgc gca gtc gtc ttg gcg atc gaa ctc cag ctc ctc acc	691
Phe Thr Asn Arg Ala Val Val Leu Ala Ile Glu Leu Gln Leu Leu Thr	
185 190 195	
gac gga ttg tcc gcg ccg cta cgt ttt ggt gaa ttg gga cgt cga tta	739
Asp Gly Leu Ser Ala Pro Leu Arg Phe Gly Glu Leu Gly Arg Arg Leu	
200 205 210	
gcg atc tcc gag gcc gaa ccc cac cca cgt cgc ccc gtc cgc atg gtc	787
Ala Ile Ser Glu Ala Glu Pro His Pro Arg Arg Pro Val Arg Met Val	
215 220 225	
cgc gac gcc gtc cta gaa ctc cgc cgc gcc aaa ggc atg gtc gtg gaa	835
Arg Asp Ala Val Leu Glu Leu Arg Arg Ala Lys Gly Met Val Val Glu	
230 235 240 245	
cac acc gac cac gac acc tgg tcc gcc gga tcc ttc ttc acc aac cca	883
His Thr Asp His Asp Thr Trp Ser Ala Gly Ser Phe Phe Thr Asn Pro	
250 255 260	
atc gtc gac cca gcc ctt gcc gac gca gtc ttt gaa aaa gtc ggc gaa	931
Ile Val Asp Pro Ala Leu Ala Asp Ala Val Phe Glu Lys Val Gly Glu	
265 270 275	
ccc acc atg ccc cgc ttc cca gcc ggc gat ggc aaa gaa aaa ctc tcc	979

Pro Thr Met Pro Arg Phe Pro Ala Gly Asp Gly Lys Glu Lys Leu Ser
 280 285 290

gca gcc tgg ctc atc gaa cgc gcc ggc ttc aaa aag gga cac ccc ggc 1027
 Ala Ala Trp Leu Ile Glu Arg Ala Gly Phe Lys Lys Gly His Pro Gly
 295 300 305

gca ggc gca aaa gcc tcc ctg agc acc aaa cac acc ctc gca ctc acc 1075
 Ala Gly Ala Lys Ala Ser Leu Ser Thr Lys His Thr Leu Ala Leu Thr
 310 315 320 325

aac cgt ggc gac gcc cgc gcc tcc gac ctc gtc gca tta gcc aaa gaa 1123
 Asn Arg Gly Asp Ala Arg Ala Ser Asp Leu Val Ala Leu Ala Lys Glu
 330 335 340

atc cgc gac gga gtc ctc gaa acc ttc ggc gtc acc ctc gtc cca gaa 1171
 Ile Arg Asp Gly Val Leu Glu Thr Phe Gly Val Thr Leu Val Pro Glu
 345 350 355

ccc gtc tgg att gga atc agc atc gat gac tgaattttcc gacgtccctg 1221
 Pro Val Trp Ile Gly Ile Ser Ile Asp Asp
 360 365

gca 1224

<210> 264
 <211> 367
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 264
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 35 40 45

Ser Ala Ile Lys Leu Leu Asp Asp Ala Ser Leu Pro Leu Leu Ile Val
 50 55 60

Gly Gly Gly Ser Asn Leu Val Val Ala Asp Gly Asp Leu Asp Val Ile
 65 70 75 80

Ala Val Ile Ile Glu Thr Asp Asp Val Ser Ile Asn Leu Thr Asp Gly
 85 90 95

Leu Leu Thr Ala Asp Ala Gly Ala Val Trp Asp Asp Val Val His Leu
 100 105 110

Ser Val Asp Ala Gly Leu Gly Gly Ile Glu Cys Leu Ser Gly Ile Pro
 115 120 125

Gly Ser Ala Gly Ala Thr Pro Val Gln Asn Val Gly Ala Tyr Gly Thr
 130 135 140

Glu Val Ser Asp Val Leu Thr Arg Val Gln Leu Leu Asp Arg Thr Thr
 145 150 155 160

His Gln Val Ser Trp Val Asp Ala Ser Glu Leu Asp Leu Ser Tyr Arg
 165 170 175
 Tyr Ser Asn Leu Lys Phe Thr Asn Arg Ala Val Val Leu Ala Ile Glu
 180 185 190
 Leu Gln Leu Leu Thr Asp Gly Leu Ser Ala Pro Leu Arg Phe Gly Glu
 195 200 205
 Leu Gly Arg Arg Leu Ala Ile Ser Glu Ala Glu Pro His Pro Arg Arg
 210 215 220
 Pro Val Arg Met Val Arg Asp Ala Val Leu Glu Leu Arg Arg Ala Lys
 225 230 235 240
 Gly Met Val Val Glu His Thr Asp His Asp Thr Trp Ser Ala Gly Ser
 245 250 255
 Phe Phe Thr Asn Pro Ile Val Asp Pro Ala Leu Ala Asp Ala Val Phe
 260 265 270
 Glu Lys Val Gly Glu Pro Thr Met Pro Arg Phe Pro Ala Gly Asp Gly
 275 280 285
 Lys Glu Lys Leu Ser Ala Ala Trp Leu Ile Glu Arg Ala Gly Phe Lys
 290 295 300
 Lys Gly His Pro Gly Ala Gly Ala Lys Ala Ser Leu Ser Thr Lys His
 305 310 315 320
 Thr Leu Ala Leu Thr Asn Arg Gly Asp Ala Arg Ala Ser Asp Leu Val
 325 330 335
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 340 345 350
 Thr Leu Val Pro Glu Pro Val Trp Ile Gly Ile Ser Ile Asp Asp
 355 360 365

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 <212> DNA
 <213> Corynebacterium glutamicum

<220>
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 <222> (1)..(1101)
 <223> RXA01216

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 Thr Asp His Thr Leu Ser Ala Leu Leu Asp Ala His Val Glu Val Pro
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 acc gct gtc acc gtg ttg acc atg cgt ctg gat gac ccc acc ggc tac 96
 Thr Ala Val Thr Val Leu Thr Met Arg Leu Asp Asp Pro Thr Gly Tyr
 20 25 30
 ggc cgc atc gtg cgc aac gaa gaa ggc gaa gtc acc gcc atc gtt gag 144

Gly	Arg	Ile	Val	Arg	Asn	Glu	Glu	Gly	Glu	Val	Thr	Ala	Ile	Val	Glu	
		35					40					45				
caa	aaa	gat	gct	tca	gca	gaa	gtc	caa	gcc	atc	gat	gag	gtc	aac	tcc	192
Gln	Lys	Asp	Ala	Ser	Ala	Glu	Val	Gln	Ala	Ile	Asp	Glu	Val	Asn	Ser	
	50					55				60						
ggt	gtc	ttt	gct	ttc	gac	gcc	gcc	atc	ttg	cgt	tcc	gca	ctg	gct	gaa	240
Gly	Val	Phe	Ala	Phe	Asp	Ala	Ala	Ile	Leu	Arg	Ser	Ala	Leu	Ala	Glu	
65				70				75						80		
ctg	aag	tcc	gac	aac	gct	cag	ggc	gag	ctg	tac	ctg	acc	gac	gtt	ttg	288
Leu	Lys	Ser	Asp	Asn	Ala	Gln	Gly	Glu	Leu	Tyr	Leu	Thr	Asp	Val	Leu	
				85				90						95		
ggc	att	gct	cgt	ggc	gag	ggc	cac	cca	gtg	cgc	gcc	cac	acc	gcc	gcc	336
Gly	Ile	Ala	Arg	Gly	Glu	Gly	His	Pro	Val	Arg	Ala	His	Thr	Ala	Ala	
		100						105					110			
gat	gct	cgt	gaa	ctc	gcc	ggc	gtc	aac	gat	cgt	gtg	cag	ctc	gca	gaa	384
Asp	Ala	Arg	Glu	Leu	Ala	Gly	Val	Asn	Asp	Arg	Val	Gln	Leu	Ala	Glu	
		115					120					125				
gcc	ggc	gcc	gaa	cta	aac	cgt	cgc	acc	gtc	atc	gcc	gct	atg	cgt	ggt	432
Ala	Gly	Ala	Glu	Leu	Asn	Arg	Arg	Thr	Val	Ile	Ala	Ala	Met	Arg	Gly	
	130					135					140					
ggc	gca	acc	atc	gtt	gat	cca	gca	acc	acc	tgg	atc	gat	gtg	gag	gtt	480
Gly	Ala	Thr	Ile	Val	Asp	Pro	Ala	Thr	Thr	Trp	Ile	Asp	Val	Glu	Val	
145					150					155				160		
tct	atc	gga	cgc	gac	gtg	atc	atc	cac	cct	ggc	acc	cag	ctc	aag	ggc	528
Ser	Ile	Gly	Arg	Asp	Val	Ile	Ile	His	Pro	Gly	Thr	Gln	Leu	Lys	Gly	
				165					170					175		
gaa	act	gtc	atc	gga	gac	cgc	gtt	gaa	gtt	ggt	cca	gac	acc	acc	ttg	576
Glu	Thr	Val	Ile	Gly	Asp	Arg	Val	Glu	Val	Gly	Pro	Asp	Thr	Thr	Leu	
		180						185					190			
acc	aac	atg	acc	atc	ggc	gac	ggc	gca	tcc	gta	atc	cgc	acc	cac	ggt	624
Thr	Asn	Met	Thr	Ile	Gly	Asp	Gly	Ala	Ser	Val	Ile	Arg	Thr	His	Gly	
		195					200					205				
ttc	gac	tcc	acc	atc	ggt	gaa	aac	gcc	acc	gtt	ggc	ccc	ttc	acc	tac	672
Phe	Asp	Ser	Thr	Ile	Gly	Glu	Asn	Ala	Thr	Val	Gly	Pro	Phe	Thr	Tyr	
	210					215					220					
atc	cgc	cca	gga	acc	aca	ctg	gga	cca	gaa	ggc	aag	ctc	ggt	ggc	ttc	720
Ile	Arg	Pro	Gly	Thr	Thr	Leu	Gly	Pro	Glu	Gly	Lys	Leu	Gly	Gly	Phe	
225					230					235					240	
gta	gaa	acc	aag	aag	gcc	aca	atc	ggc	cgt	ggc	tcc	aag	gtt	cca	cac	768
Val	Glu	Thr	Lys	Lys	Ala	Thr	Ile	Gly	Arg	Gly	Ser	Lys	Val	Pro	His	
				245				250						255		
ctc	acc	tat	gtc	ggc	gac	gcc	acc	atc	ggc	gag	gaa	tcc	aac	atc	gga	816
Leu	Thr	Tyr	Val	Gly	Asp	Ala	Thr	Ile	Gly	Glu	Glu	Ser	Asn	Ile	Gly	
			260					265					270			
gcc	tcc	tct	gtc	ttc	gtg	aac	tac	gac	ggt	gaa	aac	aag	cac	cac	acc	864
Ala	Ser	Ser	Val	Phe	Val	Asn	Tyr	Asp	Gly	Glu	Asn	Lys	His	His	Thr	

275	280	285	
acc atc ggc agc cac gtt cgc act ggt tct gac acc atg ttt atc gct			912
Thr Ile Gly Ser His Val Arg Thr Gly Ser Asp Thr Met Phe Ile Ala			
290	295	300	
cca gtg acc gtg ggt gac gga gcg tat tcc gga gcc ggt aca gta att			960
Pro Val Thr Val Gly Asp Gly Ala Tyr Ser Gly Ala Gly Thr Val Ile			
305	310	315	320
aaa gac gat gtt ccg cca gga gcc ctt gcc gtg tcc ggc gga cgc caa			1008
Lys Asp Asp Val Pro Pro Gly Ala Leu Ala Val Ser Gly Gly Arg Gln			
	325	330	335
cga aac atc gaa ggc tgg gtg caa aag aag cgc cct gga acc gct gca			1056
Arg Asn Ile Glu Gly Trp Val Gln Lys Lys Arg Pro Gly Thr Ala Ala			
	340	345	350
gca caa gcc gca gaa gcc gcc caa aac gtc cac aac cag gaa ggc			1101
Ala Gln Ala Ala Glu Ala Ala Gln Asn Val His Asn Gln Glu Gly			
	355	360	365
taagcaggat cctcatgact gct			1124
<210> 266			
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<400> 266			
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1	5	10	15
Thr Ala Val Thr Val Leu Thr Met Arg Leu Asp Asp Pro Thr Gly Tyr			
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Gly Arg Ile Val Arg Asn Glu Glu Gly Glu Val Thr Ala Ile Val Glu			
	35	40	45
Gln Lys Asp Ala Ser Ala Glu Val Gln Ala Ile Asp Glu Val Asn Ser			
	50	55	60
Gly Val Phe Ala Phe Asp Ala Ala Ile Leu Arg Ser Ala Leu Ala Glu			
	65	70	75
Leu Lys Ser Asp Asn Ala Gln Gly Glu Leu Tyr Leu Thr Asp Val Leu			
	85	90	95
Gly Ile Ala Arg Gly Glu Gly His Pro Val Arg Ala His Thr Ala Ala			
	100	105	110
Asp Ala Arg Glu Leu Ala Gly Val Asn Asp Arg Val Gln Leu Ala Glu			
	115	120	125
Ala Gly Ala Glu Leu Asn Arg Arg Thr Val Ile Ala Ala Met Arg Gly			
	130	135	140
Gly Ala Thr Ile Val Asp Pro Ala Thr Thr Trp Ile Asp Val Glu Val			
	145	150	155
			160

Ser Ile Gly Arg Asp Val Ile Ile His Pro Gly Thr Gln Leu Lys Gly
 165 170 175
 Glu Thr Val Ile Gly Asp Arg Val Glu Val Gly Pro Asp Thr Thr Leu
 180 185 190
 Thr Asn Met Thr Ile Gly Asp Gly Ala Ser Val Ile Arg Thr His Gly
 195 200 205
 Phe Asp Ser Thr Ile Gly Glu Asn Ala Thr Val Gly Pro Phe Thr Tyr
 210 215 220
 Ile Arg Pro Gly Thr Thr Leu Gly Pro Glu Gly Lys Leu Gly Gly Phe
 225 230 235 240
 Val Glu Thr Lys Lys Ala Thr Ile Gly Arg Gly Ser Lys Val Pro His
 245 250 255
 Leu Thr Tyr Val Gly Asp Ala Thr Ile Gly Glu Glu Ser Asn Ile Gly
 260 265 270
 Ala Ser Ser Val Phe Val Asn Tyr Asp Gly Glu Asn Lys His His Thr
 275 280 285
 Thr Ile Gly Ser His Val Arg Thr Gly Ser Asp Thr Met Phe Ile Ala
 290 295 300
 Pro Val Thr Val Gly Asp Gly Ala Tyr Ser Gly Ala Gly Thr Val Ile
 305 310 315 320
 Lys Asp Asp Val Pro Pro Gly Ala Leu Ala Val Ser Gly Gly Arg Gln
 325 330 335
 Arg Asn Ile Glu Gly Trp Val Gln Lys Lys Arg Pro Gly Thr Ala Ala
 340 345 350
 Ala Gln Ala Ala Glu Ala Ala Gln Asn Val His Asn Gln Glu Gly
 355 360 365

 <210> 267
 <211> 981
 <212> DNA
 <213> Corynebacterium glutamicum

 <220>
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 <222> (101)..(958)
 <223> RXA01259

 <400> 267
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 Met Gly Thr Arg Phe
 1 5

 ctt cct gca acg aag aca att cca aag gag ctt ctt cct gta gtt gat 163
 Leu Pro Ala Thr Lys Thr Ile Pro Lys Glu Leu Leu Pro Val Val Asp
 10 15 20

acc ccg ggt att gaa ctt gtt gcc aaa gag gct gct gat ctt ggt gca	211
Thr Pro Gly Ile Glu Leu Val Ala Lys Glu Ala Ala Asp Leu Gly Ala	
25 30 35	
act cgg tta gca att atc act gct ccg aac aaa gac gga att ctt aaa	259
Thr Arg Leu Ala Ile Ile Thr Ala Pro Asn Lys Asp Gly Ile Leu Lys	
40 45 50	
cac ttc gag gag ttc cct gag ctt gag gca act ctt gag gct cgc ggt	307
His Phe Glu Glu Phe Pro Glu Leu Glu Ala Thr Leu Glu Ala Arg Gly	
55 60 65	
aag act gat caa ctg aat aaa gtt cga gca gct cga gaa ttg att gca	355
Lys Thr Asp Gln Leu Asn Lys Val Arg Ala Ala Arg Glu Leu Ile Ala	
70 75 80 85	
aca gtt cca gtg gtt caa gaa aag cca ttg ggg ctt ggt cac gct gtt	403
Thr Val Pro Val Val Gln Glu Lys Pro Leu Gly Leu Gly His Ala Val	
90 95 100	
ggc ctt gct gag tct gtg ctc gat gat gat gaa gat gtt gtg gct gtc	451
Gly Leu Ala Glu Ser Val Leu Asp Asp Asp Glu Asp Val Val Ala Val	
105 110 115	
atg ctg cca gac gat ttg gtg ctg cca ttt ggt gtg acc gag aga atg	499
Met Leu Pro Asp Asp Leu Val Leu Pro Phe Gly Val Thr Glu Arg Met	
120 125 130	
gca gaa gtt cgc gct aag ttt ggc gga tct gtt ctt gca gca att gag	547
Ala Glu Val Arg Ala Lys Phe Gly Gly Ser Val Leu Ala Ala Ile Glu	
135 140 145	
gtg gct gaa gat gaa gtc tca aat tac gga gta ttt aag ctc ggt gaa	595
Val Ala Glu Asp Glu Val Ser Asn Tyr Gly Val Phe Lys Leu Gly Glu	
150 155 160 165	
ctc gat gca gag tcc gaa agt gaa ggc att agg cgt gtt gta gga atg	643
Leu Asp Ala Glu Ser Glu Ser Glu Gly Ile Arg Arg Val Val Gly Met	
170 175 180	
gtt gaa aag cct gcg cct gaa gat gca cca tca agg ttt gcc gca acg	691
Val Glu Lys Pro Ala Pro Glu Asp Ala Pro Ser Arg Phe Ala Ala Thr	
185 190 195	
ggc cgt tat cta ctt gat cga gct att ttt gat gca ctg cgt cga att	739
Gly Arg Tyr Leu Leu Asp Arg Ala Ile Phe Asp Ala Leu Arg Arg Ile	
200 205 210	
gag cct ggt gct ggt gga gaa ctg caa tta aca gat gcc atc gca tta	787
Glu Pro Gly Ala Gly Gly Glu Leu Gln Leu Thr Asp Ala Ile Ala Leu	
215 220 225	
ttg atc gaa gaa ggc cat ccg gta cac att gtg gtt cat gaa gga aag	835
Leu Ile Glu Glu Gly His Pro Val His Ile Val Val His Glu Gly Lys	
230 235 240 245	
cgc cat gac ctt ggt aat cca gct ggg tac att cct gct gtt gtg tac	883
Arg His Asp Leu Gly Asn Pro Ala Gly Tyr Ile Pro Ala Val Val Tyr	
250 255 260	
ttc gga ctt cgt cat gca gag tac ggt tcc aag att cac cgt gcg gtg	931

Phe Gly Leu Arg His Ala Glu Tyr Gly Ser Lys Ile His Arg Ala Val
 265 270 275

aag gaa ata ctc gct gag ttt gaa tct taaaaaggaa accgccttcc 978
 Lys Glu Ile Leu Ala Glu Phe Glu Ser
 280 285

aca 981

<210> 268

<211> 286

<212> PRT

<213> Corynebacterium glutamicum

<400> 268

Met Gly Thr Arg Phe Leu Pro Ala Thr Lys Thr Ile Pro Lys Glu Leu
 1 5 10 15

Leu Pro Val Val Asp Thr Pro Gly Ile Glu Leu Val Ala Lys Glu Ala
 20 25 30

Ala Asp Leu Gly Ala Thr Arg Leu Ala Ile Ile Thr Ala Pro Asn Lys
 35 40 45

Asp Gly Ile Leu Lys His Phe Glu Glu Phe Pro Glu Leu Glu Ala Thr
 50 55 60

Leu Glu Ala Arg Gly Lys Thr Asp Gln Leu Asn Lys Val Arg Ala Ala
 65 70 75 80

Arg Glu Leu Ile Ala Thr Val Pro Val Val Gln Glu Lys Pro Leu Gly
 85 90 95

Leu Gly His Ala Val Gly Leu Ala Glu Ser Val Leu Asp Asp Asp Glu
 100 105 110

Asp Val Val Ala Val Met Leu Pro Asp Asp Leu Val Leu Pro Phe Gly
 115 120 125

Val Thr Glu Arg Met Ala Glu Val Arg Ala Lys Phe Gly Gly Ser Val
 130 135 140

Leu Ala Ala Ile Glu Val Ala Glu Asp Glu Val Ser Asn Tyr Gly Val
 145 150 155 160

Phe Lys Leu Gly Glu Leu Asp Ala Glu Ser Glu Ser Glu Gly Ile Arg
 165 170 175

Arg Val Val Gly Met Val Glu Lys Pro Ala Pro Glu Asp Ala Pro Ser
 180 185 190

Arg Phe Ala Ala Thr Gly Arg Tyr Leu Leu Asp Arg Ala Ile Phe Asp
 195 200 205

Ala Leu Arg Arg Ile Glu Pro Gly Ala Gly Gly Glu Leu Gln Leu Thr
 210 215 220

Asp Ala Ile Ala Leu Leu Ile Glu Glu Gly His Pro Val His Ile Val
 225 230 235 240

Val His Glu Gly Lys Arg His Asp Leu Gly Asn Pro Ala Gly Tyr Ile
 245 250 255

Pro Ala Val Val Tyr Phe Gly Leu Arg His Ala Glu Tyr Gly Ser Lys
 260 265 270

Ile His Arg Ala Val Lys Glu Ile Leu Ala Glu Phe Glu Ser
 275 280 285

<210> 269

<211> 526

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(526)

<223> RXA02028

<400> 269

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 tacgacgatt ggggttgcg gggcaggtac tcttggttcc atg agt ttg cct atc 115
 Met Ser Leu Pro Ile
 1 5
 gat gag cac gtg aac gcg gtt aaa acc gtc gta gtg cct gct gca gga 163
 Asp Glu His Val Asn Ala Val Lys Thr Val Val Val Pro Ala Ala Gly
 10 15 20
 ctg gga acc cga ttc ctt ccg gcc acc aaa acc gta ccc aag gag ttg 211
 Leu Gly Thr Arg Phe Leu Pro Ala Thr Lys Thr Val Pro Lys Glu Leu
 25 30 35
 ctg ccg gtt gtc gat acc cca ggt att gag ctg att gct gct gag gct 259
 Leu Pro Val Val Asp Thr Pro Gly Ile Glu Leu Ile Ala Ala Glu Ala
 40 45 50
 gcc gaa ctt ggt gcg acc agg ctg gcg atc atc act gcg cca aac aaa 307
 Ala Glu Leu Gly Ala Thr Arg Leu Ala Ile Ile Thr Ala Pro Asn Lys
 55 60 65
 gct ggg gta ctt gca cac ttt gag cgt tct tct gaa ttg gaa gaa acg 355
 Ala Gly Val Leu Ala His Phe Glu Arg Ser Ser Glu Leu Glu Glu Thr
 70 75 80 85
 ctg atg gag cgt ggc aag act gac cag gtg gag ata atc cgc cgc gcc 403
 Leu Met Glu Arg Gly Lys Thr Asp Gln Val Glu Ile Ile Arg Arg Ala
 90 95 100
 gcc gat tta atc aag gca gtt cca gta acc cag gac aag ccg ctg ggg 451
 Ala Asp Leu Ile Lys Ala Val Pro Val Thr Gln Asp Lys Pro Leu Gly
 105 110 115
 cta ggt cat gct gtt ggt ttg gct gag tct gtg ttg gat gat gat gaa 499
 Leu Gly His Ala Val Gly Leu Ala Glu Ser Val Leu Asp Asp Asp Glu
 120 125 130
 gat gtc gta gcg gtg atg ttg ccg cac 526
 Asp Val Val Ala Val Met Leu Pro His

135

140

<210> 270

<211> 142

<212> PRT

<213> Corynebacterium glutamicum

<400> 270

Met Ser Leu Pro Ile Asp Glu His Val Asn Ala Val Lys Thr Val Val
 1 5 10 15

Val Pro Ala Ala Gly Leu Gly Thr Arg Phe Leu Pro Ala Thr Lys Thr
 20 25 30

Val Pro Lys Glu Leu Leu Pro Val Val Asp Thr Pro Gly Ile Glu Leu
 35 40 45

Ile Ala Ala Glu Ala Ala Glu Leu Gly Ala Thr Arg Leu Ala Ile Ile
 50 55 60

Thr Ala Pro Asn Lys Ala Gly Val Leu Ala His Phe Glu Arg Ser Ser
 65 70 75 80

Glu Leu Glu Glu Thr Leu Met Glu Arg Gly Lys Thr Asp Gln Val Glu
 85 90 95

Ile Ile Arg Arg Ala Ala Asp Leu Ile Lys Ala Val Pro Val Thr Gln
 100 105 110

Asp Lys Pro Leu Gly Leu Gly His Ala Val Gly Leu Ala Glu Ser Val
 115 120 125

Leu Asp Asp Asp Glu Asp Val Val Ala Val Met Leu Pro His
 130 135 140

<210> 271

<211> 1284

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1261)

<223> RXA01262

<400> 271

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aaacttgctg tatcaataaa acacgaaaag gaatactttt atg aaa att gcc gtc 115
 Met Lys Ile Ala Val
 1 5

gca ggg ctc gga tat gtt ggg ctt tca aat gca gct ctc ctc tct aaa 163
 Ala Gly Leu Gly Tyr Val Gly Leu Ser Asn Ala Ala Leu Leu Ser Lys
 10 15 20

aat cat aaa gtt gtt gca gtt gac att gat gaa gaa cga gtg aaa cta 211
 Asn His Lys Val Val Ala Val Asp Ile Asp Glu Glu Arg Val Lys Leu
 25 30 35

gtt caa gaa ttt cgt tcg cca att gtc gat agc gat ctc gaa gaa tat	259
Val Gln Glu Phe Arg Ser Pro Ile Val Asp Ser Asp Leu Glu Glu Tyr	
40 45 50	
ctg tcc act aag cct caa aac tta act gcc aca acg gac gcc gaa gcc	307
Leu Ser Thr Lys Pro Gln Asn Leu Thr Ala Thr Thr Asp Ala Glu Ala	
55 60 65	
gct tac aaa ggc gca gat ttt att gtt att gca acg cca act aat tac	355
Ala Tyr Lys Gly Ala Asp Phe Ile Val Ile Ala Thr Pro Thr Asn Tyr	
70 75 80 85	
gac cca gag tca aac ttt ttt gat act tcc agc gtt gag tcc gta att	403
Asp Pro Glu Ser Asn Phe Phe Asp Thr Ser Ser Val Glu Ser Val Ile	
90 95 100	
gag ata gtc ctt aag gtt tct cct gga tcc aca atc gta att aaa tcg	451
Glu Ile Val Leu Lys Val Ser Pro Gly Ser Thr Ile Val Ile Lys Ser	
105 110 115	
act atc cct gtt ggt ttt aca tcg gaa cta cgc att aag cat cca gaa	499
Thr Ile Pro Val Gly Phe Thr Ser Glu Leu Arg Ile Lys His Pro Glu	
120 125 130	
gct tcg att att ttt tca cct gag ttc ctg cgt gaa ggc cga gca ttc	547
Ala Ser Ile Ile Phe Ser Pro Glu Phe Leu Arg Glu Gly Arg Ala Phe	
135 140 145	
tac gac aat ctc tac cca tcc aga gtt gtc gtt ggt gat cgc agt cct	595
Tyr Asp Asn Leu Tyr Pro Ser Arg Val Val Val Gly Asp Arg Ser Pro	
150 155 160 165	
ctg ggg gaa gaa ttt gcg act ctg tta gct gag ggg gca aaa gaa aag	643
Leu Gly Glu Glu Phe Ala Thr Leu Leu Ala Glu Gly Ala Lys Glu Lys	
170 175 180	
cct ccg att cta ctt acg gac tca act gag gca gag gcg att aaa tta	691
Pro Pro Ile Leu Thr Asp Ser Thr Glu Ala Glu Ala Ile Lys Leu	
185 190 195	
ttt tct aat aca tat ctt gca ctg cga gtt gct ttt ttc aac gaa ctg	739
Phe Ser Asn Thr Tyr Leu Ala Leu Arg Val Ala Phe Phe Asn Glu Leu	
200 205 210	
gat act tat gcg tct gtt cga agc ttg gat act aag cag att att gaa	787
Asp Thr Tyr Ala Ser Val Arg Ser Leu Asp Thr Lys Gln Ile Ile Glu	
215 220 225	
ggg gta ggg ctc gat cca cgt att gga tct cat tac aat aat cct tca	835
Gly Val Gly Leu Asp Pro Arg Ile Gly Ser His Tyr Asn Asn Pro Ser	
230 235 240 245	
ttt gga tat ggc gga tat tgt ctt ccg aaa gat acg aaa cag ctt ctc	883
Phe Gly Tyr Gly Gly Tyr Cys Leu Pro Lys Asp Thr Lys Gln Leu Leu	
250 255 260	
gcc aac tat aag gat gtc ccg cag aat cta atc tct gca gta gtc caa	931
Ala Asn Tyr Lys Asp Val Pro Gln Asn Leu Ile Ser Ala Val Val Gln	
265 270 275	

gca aat aag act cgt aag gac ttt att gca gag gat atc ctc agt aaa 979
Ala Asn Lys Thr Arg Lys Asp Phe Ile Ala Glu Asp Ile Leu Ser Lys
280 285 290

tca cct act gta gtt gga att tac cgc ctt gta atg aag tct gga tca 1027
Ser Pro Thr Val Val Gly Ile Tyr Arg Leu Val Met Lys Ser Gly Ser
295 300 305

gat aac ttt cgt tct tct tct att caa gga gtc atg aaa cga att aag 1075
Asp Asn Phe Arg Ser Ser Ser Ile Gln Gly Val Met Lys Arg Ile Lys
310 315 320 325

gcc aag gga atc gaa att gta gta ttt gaa ccg aat ctc gga gaa gaa 1123
Ala Lys Gly Ile Glu Ile Val Val Phe Glu Pro Asn Leu Gly Glu Glu
330 335 340

act ttc tac aat tcg aag atc ctt aat gac atc gaa gag ttt aag gat 1171
Thr Phe Tyr Asn Ser Lys Ile Leu Asn Asp Ile Glu Glu Phe Lys Asp
345 350 355

tac tgc gac atc att att gca aat cgt cca acc gat gag ctt tct gat 1219
Tyr Cys Asp Ile Ile Ile Ala Asn Arg Pro Thr Asp Glu Leu Ser Asp
360 365 370

gta cca gaa aaa gtt tat aca cgt gat att ttc cag cgt gac 1261
Val Pro Glu Lys Val Tyr Thr Arg Asp Ile Phe Gln Arg Asp
375 380 385

taagtggaaa gaatcttttg ttg 1284

<210> 272

<211> 387

<212> PRT

<213> Corynebacterium glutamicum

<400> 272

Met Lys Ile Ala Val Ala Gly Leu Gly Tyr Val Gly Leu Ser Asn Ala
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Ala Leu Leu Ser Lys Asn His Lys Val Val Ala Val Asp Ile Asp Glu
20 25 30

Glu Arg Val Lys Leu Val Gln Glu Phe Arg Ser Pro Ile Val Asp Ser
35 40 45

Asp Leu Glu Glu Tyr Leu Ser Thr Lys Pro Gln Asn Leu Thr Ala Thr
50 55 60

Thr Asp Ala Glu Ala Ala Tyr Lys Gly Ala Asp Phe Ile Val Ile Ala
65 70 75 80

Thr Pro Thr Asn Tyr Asp Pro Glu Ser Asn Phe Phe Asp Thr Ser Ser
85 90 95

Val Glu Ser Val Ile Glu Ile Val Leu Lys Val Ser Pro Gly Ser Thr
100 105 110

Ile Val Ile Lys Ser Thr Ile Pro Val Gly Phe Thr Ser Glu Leu Arg
115 120 125

Ile Lys His Pro Glu Ala Ser Ile Ile Phe Ser Pro Glu Phe Leu Arg
 130 135 140
 Glu Gly Arg Ala Phe Tyr Asp Asn Leu Tyr Pro Ser Arg Val Val Val
 145 150 155 160
 Gly Asp Arg Ser Pro Leu Gly Glu Glu Phe Ala Thr Leu Leu Ala Glu
 165 170 175
 Gly Ala Lys Glu Lys Pro Pro Ile Leu Leu Thr Asp Ser Thr Glu Ala
 180 185 190
 Glu Ala Ile Lys Leu Phe Ser Asn Thr Tyr Leu Ala Leu Arg Val Ala
 195 200 205
 Phe Phe Asn Glu Leu Asp Thr Tyr Ala Ser Val Arg Ser Leu Asp Thr
 210 215 220
 Lys Gln Ile Ile Glu Gly Val Gly Leu Asp Pro Arg Ile Gly Ser His
 225 230 235 240
 Tyr Asn Asn Pro Ser Phe Gly Tyr Gly Gly Tyr Cys Leu Pro Lys Asp
 245 250 255
 Thr Lys Gln Leu Leu Ala Asn Tyr Lys Asp Val Pro Gln Asn Leu Ile
 260 265 270
 Ser Ala Val Val Gln Ala Asn Lys Thr Arg Lys Asp Phe Ile Ala Glu
 275 280 285
 Asp Ile Leu Ser Lys Ser Pro Thr Val Val Gly Ile Tyr Arg Leu Val
 290 295 300
 Met Lys Ser Gly Ser Asp Asn Phe Arg Ser Ser Ser Ile Gln Gly Val
 305 310 315 320
 Met Lys Arg Ile Lys Ala Lys Gly Ile Glu Ile Val Val Phe Glu Pro
 325 330 335
 Asn Leu Gly Glu Glu Thr Phe Tyr Asn Ser Lys Ile Leu Asn Asp Ile
 340 345 350
 Glu Glu Phe Lys Asp Tyr Cys Asp Ile Ile Ile Ala Asn Arg Pro Thr
 355 360 365
 Asp Glu Leu Ser Asp Val Pro Glu Lys Val Tyr Thr Arg Asp Ile Phe
 370 375 380
 Gln Arg Asp
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<210> 273

<211> 1209

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1186)

<223> RXA01377

<400> 273

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                                         Met Thr Leu Thr Asp
                                         1 5

aac agc aaa aac gtt gat gct gtc atc ttg gtc ggt ggc aaa ggt acc 163
Asn Ser Lys Asn Val Asp Ala Val Ile Leu Val Gly Gly Lys Gly Thr
                        10 15 20

cga ctg cgc ccc ctg acc gtc aat act cca aag cca atg ctg cca act 211
Arg Leu Arg Pro Leu Thr Val Asn Thr Pro Lys Pro Met Leu Pro Thr
                        25 30 35

gct ggc cac cca ttc ttg acc cac ctt ttg gcc cgc atc aag gcc gca 259
Ala Gly His Pro Phe Leu Thr His Leu Leu Ala Arg Ile Lys Ala Ala
                        40 45 50

ggc atc aca cac gtc gtg ctg gga acg tca ttc aaa gct gaa gtc ttc 307
Gly Ile Thr His Val Val Leu Gly Thr Ser Phe Lys Ala Glu Val Phe
                        55 60 65

gag gaa tac ttc gga gat ggc tcc gaa atg ggc ttg gaa att gaa tat 355
Glu Glu Tyr Phe Gly Asp Gly Ser Glu Met Gly Leu Glu Ile Glu Tyr
                        70 75 80 85

gtc gtc gag gat cag cct ttg ggc act ggt ggt ggc atc cga aac gtc 403
Val Val Glu Asp Gln Pro Leu Gly Thr Gly Gly Gly Ile Arg Asn Val
                        90 95 100

tac gac aag ctg cgt cac gat act gcg att gtg ttc aac ggc gat gtg 451
Tyr Asp Lys Leu Arg His Asp Thr Ala Ile Val Phe Asn Gly Asp Val
                        105 110 115

ctc tcc ggt gcg gat ctc aac agc att ctg gac acc cac cgc gaa aag 499
Leu Ser Gly Ala Asp Leu Asn Ser Ile Leu Asp Thr His Arg Glu Lys
                        120 125 130

gac gca gat ctg acc atg cat ctc gtg cgc gta gct aac cct cgt gcg 547
Asp Ala Asp Leu Thr Met His Leu Val Arg Val Ala Asn Pro Arg Ala
                        135 140 145

ttt ggt tgc gtc ccc acc gat gag gat ggt cgc gtc agc gaa ttc ctt 595
Phe Gly Cys Val Pro Thr Asp Glu Asp Gly Arg Val Ser Glu Phe Leu
                        150 155 160 165

gaa aag acc gaa gat cca cca acc gat cag atc aac gcc ggc tgc tac 643
Glu Lys Thr Glu Asp Pro Pro Thr Asp Gln Ile Asn Ala Gly Cys Tyr
                        170 175 180

gtg ttc aag aag gaa ctc atc gag cag atc ccg gca ggc cga gca gtt 691
Val Phe Lys Lys Glu Leu Ile Glu Gln Ile Pro Ala Gly Arg Ala Val
                        185 190 195

tcc gtc gag cgc gaa acc ttc cct cag ctg ttg gaa gaa ggc aag cga 739
Ser Val Glu Arg Glu Thr Phe Pro Gln Leu Leu Glu Glu Gly Lys Arg
                        200 205 210

gtc ttc ggc cac gtc gac gct tcc tac tgg cgc gac atg ggc acc cca 787

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Val Phe Gly His Val Asp Ala Ser Tyr Trp Arg Asp Met Gly Thr Pro
 215 220 225
 agc gac ttc gtc cgc ggc tcg gct gac ctg gtc cgc ggc att gcg tac 835
 Ser Asp Phe Val Arg Gly Ser Ala Asp Leu Val Arg Gly Ile Ala Tyr
 230 235 240 245
 tcc cca ttg ctc gaa ggc aaa aca gga gag tcg ctt gtc gac gcc tcc 883
 Ser Pro Leu Leu Glu Gly Lys Thr Gly Glu Ser Leu Val Asp Ala Ser
 250 255 260
 gcc ggc gtt cgc gac ggc gtc ctg ctg ctc ggc gga acc gta gtc ggc 931
 Ala Gly Val Arg Asp Gly Val Leu Leu Leu Gly Gly Thr Val Val Gly
 265 270 275
 cgc ggc act gag atc ggt gcc ggc tgc cgc gtt gac aac act gtt att 979
 Arg Gly Thr Glu Ile Gly Ala Gly Cys Arg Val Asp Asn Thr Val Ile
 280 285 290
 ttc gac ggc gtc acc att gaa cca ggt gcg gtc att gaa aat tcc atc 1027
 Phe Asp Gly Val Thr Ile Glu Pro Gly Ala Val Ile Glu Asn Ser Ile
 295 300 305
 att tcc tcg gga gca cgc atc ggt gct aat gcg cac atc tcc ggt tgc 1075
 Ile Ser Ser Gly Ala Arg Ile Gly Ala Asn Ala His Ile Ser Gly Cys
 310 315 320 325
 atc att ggc gag ggc gca cag gtt ggt gct cgg tgt gaa ctc aac gca 1123
 Ile Ile Gly Glu Gly Ala Gln Val Gly Ala Arg Cys Glu Leu Asn Ala
 330 335 340
 ggg atg cgc gtc ttc cca ggc gtt gtg atc cca gac agc gga att cgt 1171
 Gly Met Arg Val Phe Pro Gly Val Val Ile Pro Asp Ser Gly Ile Arg
 345 350 355
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 Phe Ser Ser Asp Gln
 360
 <210> 274
 <211> 362
 <212> PRT
 <213> *Corynebacterium glutamicum*
 <400> 274
 Met Thr Leu Thr Asp Asn Ser Lys Asn Val Asp Ala Val Ile Leu Val
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 20 25 30
 Pro Met Leu Pro Thr Ala Gly His Pro Phe Leu Thr His Leu Leu Ala
 35 40 45
 Arg Ile Lys Ala Ala Gly Ile Thr His Val Val Leu Gly Thr Ser Phe
 50 55 60
 Lys Ala Glu Val Phe Glu Glu Tyr Phe Gly Asp Gly Ser Glu Met Gly
 65 70 75 80

Leu Glu Ile Glu Tyr Val Val Glu Asp Gln Pro Leu Gly Thr Gly Gly
 85 90 95
 Gly Ile Arg Asn Val Tyr Asp Lys Leu Arg His Asp Thr Ala Ile Val
 100 105 110
 Phe Asn Gly Asp Val Leu Ser Gly Ala Asp Leu Asn Ser Ile Leu Asp
 115 120 125
 Thr His Arg Glu Lys Asp Ala Asp Leu Thr Met His Leu Val Arg Val
 130 135 140
 Ala Asn Pro Arg Ala Phe Gly Cys Val Pro Thr Asp Glu Asp Gly Arg
 145 150 155 160
 Val Ser Glu Phe Leu Glu Lys Thr Glu Asp Pro Pro Thr Asp Gln Ile
 165 170 175
 Asn Ala Gly Cys Tyr Val Phe Lys Lys Glu Leu Ile Glu Gln Ile Pro
 180 185 190
 Ala Gly Arg Ala Val Ser Val Glu Arg Glu Thr Phe Pro Gln Leu Leu
 195 200 205
 Glu Glu Gly Lys Arg Val Phe Gly His Val Asp Ala Ser Tyr Trp Arg
 210 215 220
 Asp Met Gly Thr Pro Ser Asp Phe Val Arg Gly Ser Ala Asp Leu Val
 225 230 235 240
 Arg Gly Ile Ala Tyr Ser Pro Leu Leu Glu Gly Lys Thr Gly Glu Ser
 245 250 255
 Leu Val Asp Ala Ser Ala Gly Val Arg Asp Gly Val Leu Leu Leu Gly
 260 265 270
 Gly Thr Val Val Gly Arg Gly Thr Glu Ile Gly Ala Gly Cys Arg Val
 275 280 285
 Asp Asn Thr Val Ile Phe Asp Gly Val Thr Ile Glu Pro Gly Ala Val
 290 295 300
 Ile Glu Asn Ser Ile Ile Ser Ser Gly Ala Arg Ile Gly Ala Asn Ala
 305 310 315 320
 His Ile Ser Gly Cys Ile Ile Gly Glu Gly Ala Gln Val Gly Ala Arg
 325 330 335
 Cys Glu Leu Asn Ala Gly Met Arg Val Phe Pro Gly Val Val Ile Pro
 340 345 350
 Asp Ser Gly Ile Arg Phe Ser Ser Asp Gln
 355 360

<210> 275

<211> 1350

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(1327)

<223> RXA02063

<400> 275

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                                         Met Val Lys Gly Val
                                         1 5

aag ggt aga cca aat gtt cta gca atc gtt ctc gca ggt ggc gag ggc 163
Lys Gly Arg Pro Asn Val Leu Ala Ile Val Leu Ala Gly Gly Glu Gly
                        10 15 20

aaa cga ctt ttt ccg ttg acg gag gac cga gct aag cct gcg gtc cca 211
Lys Arg Leu Phe Pro Leu Thr Glu Asp Arg Ala Lys Pro Ala Val Pro
                        25 30 35

ttc ggc gga act tac aga ttg atc gac ttt gtt ttg tcg aac ctg gtg 259
Phe Gly Gly Thr Tyr Arg Leu Ile Asp Phe Val Leu Ser Asn Leu Val
                        40 45 50

aac tcc gga ttc ctc aag atc gcg gta ctg act cag tac aag tcg cat 307
Asn Ser Gly Phe Leu Lys Ile Ala Val Leu Thr Gln Tyr Lys Ser His
                        55 60 65

tca ttg gat agg cat att tca ttg tcg tgg aac gtg tct ggt cca acg 355
Ser Leu Asp Arg His Ile Ser Leu Ser Trp Asn Val Ser Gly Pro Thr
                        70 75 80 85

ggg cag tac att gct tct gtt cct gcg cag cag cgc ctg ggc aag cga 403
Gly Gln Tyr Ile Ala Ser Val Pro Ala Gln Gln Arg Leu Gly Lys Arg
                        90 95 100

tgg ttc act ggt tcc gcg gat gca att ttg cag tct ctg aac ttg atc 451
Trp Phe Thr Gly Ser Ala Asp Ala Ile Leu Gln Ser Leu Asn Leu Ile
                        105 110 115

tct gat gag aaa ccg gat tat gtc atc gtt ttc ggc gcg gac cac gtg 499
Ser Asp Glu Lys Pro Asp Tyr Val Ile Val Phe Gly Ala Asp His Val
                        120 125 130

tat cgc atg gac cca agc cag atg cta gat gag cac att gca tct ggt 547
Tyr Arg Met Asp Pro Ser Gln Met Leu Asp Glu His Ile Ala Ser Gly
                        135 140 145

cgc gcg gtg tct gtg gca ggt att cgc gtt cca cgt gag gaa gca act 595
Arg Ala Val Ser Val Ala Gly Ile Arg Val Pro Arg Glu Glu Ala Thr
                        150 155 160 165

gcg ttt ggt tgc atc cag tcc gat gtc gac ggc aac ata acc gag ttc 643
Ala Phe Gly Cys Ile Gln Ser Asp Val Asp Gly Asn Ile Thr Glu Phe
                        170 175 180

ttg gaa aag cca gct gac cct ccg gga acc cct gat gat cct gac atg 691
Leu Glu Lys Pro Ala Asp Pro Pro Gly Thr Pro Asp Asp Pro Asp Met
                        185 190 195

act tac gcg tcg atg ggt aac tac att ttc acc act gaa gcc ctg atc 739
Thr Tyr Ala Ser Met Gly Asn Tyr Ile Phe Thr Thr Glu Ala Leu Ile

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200	205	210	
cag gcg ctg aaa gat gat gaa aat aac gag aac agt gat cat gac atg Gln Ala Leu Lys Asp Asp Glu Asn Asn Glu Asn Ser Asp His Asp Met 215 220 225			787
ggc gga gac atc att ccg tac ttc gtc tct cgc aat gat gcg cat gtt Gly Gly Asp Ile Ile Pro Tyr Phe Val Ser Arg Asn Asp Ala His Val 230 235 240 245			835
tat gat ttc tcc gga aac att gtt cct ggc gca act gag cgt gac aag Tyr Asp Phe Ser Gly Asn Ile Val Pro Gly Ala Thr Glu Arg Asp Lys 250 255 260			883
ggc tac tgg cgc gac gtc ggt acc att gat gcg ttc tac gag tgc cac Gly Tyr Trp Arg Asp Val Gly Thr Ile Asp Ala Phe Tyr Glu Cys His 265 270 275			931
atg gac ctg att tcc gtg cac cca atc ttc aat ctg tat aac tct gag Met Asp Leu Ile Ser Val His Pro Ile Phe Asn Leu Tyr Asn Ser Glu 280 285 290			979
tgg cca atc cac acg acc tct gaa ggt aac ttg cct ccg gct aag ttc Trp Pro Ile His Thr Thr Ser Glu Gly Asn Leu Pro Pro Ala Lys Phe 295 300 305			1027
gtt cgg ggc ggt atc gcg cag tcg tcg atg gtg tct tca ggt tcc atc Val Arg Gly Gly Ile Ala Gln Ser Ser Met Val Ser Ser Gly Ser Ile 310 315 320 325			1075
att tct gct ggg act gtt cgc aac tcc gtg ctg tcc aac aac gtt gtc Ile Ser Ala Gly Thr Val Arg Asn Ser Val Leu Ser Asn Asn Val Val 330 335 340			1123
gtc gaa gag ggc gca acg gtg gaa ggt gca gtg ctg atg cca ggc gtg Val Glu Glu Gly Ala Thr Val Glu Gly Ala Val Leu Met Pro Gly Val 345 350 355			1171
cgc atc ggt aag ggt gct gtt gtc cgc cat gcg att ctg gac aag aac Arg Ile Gly Lys Gly Ala Val Val Arg His Ala Ile Leu Asp Lys Asn 360 365 370			1219
gtg gtt gtc cgc gac gga gag ctc atc ggt gtc gac caa gtg cgc gat Val Val Val Arg Asp Gly Glu Leu Ile Gly Val Asp Gln Val Arg Asp 375 380 385			1267
gcg cag cgc ttc aag gtg agc gcc ggc ggc gtc gtg gtt gtc ggt aag Ala Gln Arg Phe Lys Val Ser Ala Gly Gly Val Val Val Val Gly Lys 390 395 400 405			1315
aac cag gta gtc taaacgggaa agggacctta aaa Asn Gln Val Val			1350

<210> 276

<211> 409

<212> PRT

<213> Corynebacterium glutamicum

<400> 276

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 20 25 30
 Lys Pro Ala Val Pro Phe Gly Gly Thr Tyr Arg Leu Ile Asp Phe Val
 35 40 45
 Leu Ser Asn Leu Val Asn Ser Gly Phe Leu Lys Ile Ala Val Leu Thr
 50 55 60
 Gln Tyr Lys Ser His Ser Leu Asp Arg His Ile Ser Leu Ser Trp Asn
 65 70 75 80
 Val Ser Gly Pro Thr Gly Gln Tyr Ile Ala Ser Val Pro Ala Gln Gln
 85 90 95
 Arg Leu Gly Lys Arg Trp Phe Thr Gly Ser Ala Asp Ala Ile Leu Gln
 100 105 110
 Ser Leu Asn Leu Ile Ser Asp Glu Lys Pro Asp Tyr Val Ile Val Phe
 115 120 125
 Gly Ala Asp His Val Tyr Arg Met Asp Pro Ser Gln Met Leu Asp Glu
 130 135 140
 His Ile Ala Ser Gly Arg Ala Val Ser Val Ala Gly Ile Arg Val Pro
 145 150 155 160
 Arg Glu Glu Ala Thr Ala Phe Gly Cys Ile Gln Ser Asp Val Asp Gly
 165 170 175
 Asn Ile Thr Glu Phe Leu Glu Lys Pro Ala Asp Pro Pro Gly Thr Pro
 180 185 190
 Asp Asp Pro Asp Met Thr Tyr Ala Ser Met Gly Asn Tyr Ile Phe Thr
 195 200 205
 Thr Glu Ala Leu Ile Gln Ala Leu Lys Asp Asp Glu Asn Asn Glu Asn
 210 215 220
 Ser Asp His Asp Met Gly Gly Asp Ile Ile Pro Tyr Phe Val Ser Arg
 225 230 235 240
 Asn Asp Ala His Val Tyr Asp Phe Ser Gly Asn Ile Val Pro Gly Ala
 245 250 255
 Thr Glu Arg Asp Lys Gly Tyr Trp Arg Asp Val Gly Thr Ile Asp Ala
 260 265 270
 Phe Tyr Glu Cys His Met Asp Leu Ile Ser Val His Pro Ile Phe Asn
 275 280 285
 Leu Tyr Asn Ser Glu Trp Pro Ile His Thr Thr Ser Glu Gly Asn Leu
 290 295 300
 Pro Pro Ala Lys Phe Val Arg Gly Gly Ile Ala Gln Ser Ser Met Val
 305 310 315 320
 Ser Ser Gly Ser Ile Ile Ser Ala Gly Thr Val Arg Asn Ser Val Leu

	325		330		335
Ser Asn Asn Val Val Val Glu Glu Gly Ala Thr Val Glu Gly Ala Val					
	340		345		350
Leu Met Pro Gly Val Arg Ile Gly Lys Gly Ala Val Val Arg His Ala					
	355		360		365
Ile Leu Asp Lys Asn Val Val Val Arg Asp Gly Glu Leu Ile Gly Val					
	370		375		380
Asp Gln Val Arg Asp Ala Gln Arg Phe Lys Val Ser Ala Gly Gly Val					
	385		390		395
					400
Val Val Val Gly Lys Asn Gln Val Val					
	405				

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 <211> 903
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(880)
 <223> RXN00014

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 Met Ser Lys Tyr Ala
 1 5
 gac gat tta gcc tta gcc ctc gaa ctt gcc gaa ctt gcc gat tcc atc 163
 Asp Asp Leu Ala Leu Ala Leu Glu Leu Ala Glu Leu Ala Asp Ser Ile
 10 15 20
 acc ctc gac cgc ttc gaa gcc tct gac ctg gaa gta tcc tcc aag cca 211
 Thr Leu Asp Arg Phe Glu Ala Ser Asp Leu Glu Val Ser Ser Lys Pro
 25 30 35
 gac atg act ccc gtc agc gat gcc gac ctg gcg acc gaa gaa gca ctc 259
 Asp Met Thr Pro Val Ser Asp Ala Asp Leu Ala Thr Glu Glu Ala Leu
 40 45 50
 cgt gag aaa atc gcc acc gcc cgc ccc gcc gac tcc atc ctc ggt gaa 307
 Arg Glu Lys Ile Ala Thr Ala Arg Pro Ala Asp Ser Ile Leu Gly Glu
 55 60 65
 gaa ttc ggt ggc gac gta gaa ttc agc ggc cgc cag tgg atc atc gac 355
 Glu Phe Gly Gly Asp Val Glu Phe Ser Gly Arg Gln Trp Ile Ile Asp
 70 75 80 85
 ccc atc gac ggc acc aaa aac tac gtc cgc ggc gtc ccc gta tgg gca 403
 Pro Ile Asp Gly Thr Lys Asn Tyr Val Arg Gly Val Pro Val Trp Ala
 90 95 100
 acc ctg atc gcg ctg ctc gac aac ggc aaa ccc gtc gca ggt gtc atc 451
 Thr Leu Ile Ala Leu Leu Asp Asn Gly Lys Pro Val Ala Gly Val Ile

105	110	115	
tcc gca ccc gca ctg gct agg cgt tgg tgg gca tcc gaa ggg gcc ggc			499
Ser Ala Pro Ala Leu Ala Arg Arg Trp Trp Ala Ser Glu Gly Ala Gly			
120	125	130	
gca tgg cgc acc ttc aac ggc agc tcc cca cgc aaa ctg tcc gtg tcc			547
Ala Trp Arg Thr Phe Asn Gly Ser Ser Pro Arg Lys Leu Ser Val Ser			
135	140	145	
cag gtg tcc aag ctt gac gac gcc tcc ctc tcc ttc tcc tcc ctc tcc			595
Gln Val Ser Lys Leu Asp Asp Ala Ser Leu Ser Phe Ser Ser Leu Ser			
150	155	160	165
ggc tgg gcc gaa cga gat ttg cgc gat cag ttc gtc tcc cta act gat			643
Gly Trp Ala Glu Arg Asp Leu Arg Asp Gln Phe Val Ser Leu Thr Asp			
170	175		180
acc acc tgg cga ctc cgc ggc tac ggc gac ttc ttc tcc tac tgc ctc			691
Thr Thr Trp Arg Leu Arg Gly Tyr Gly Asp Phe Phe Ser Tyr Cys Leu			
185	190		195
gtc gcc gaa ggt gcc gtc gat atc gcc gct gaa cca gaa gtc agc ctc			739
Val Ala Glu Gly Ala Val Asp Ile Ala Ala Glu Pro Glu Val Ser Leu			
200	205	210	
tgg gat ctt gct ccc ctg tcc atc ctg gtc acc gaa gcc gga gga aag			787
Trp Asp Leu Ala Pro Leu Ser Ile Leu Val Thr Glu Ala Gly Gly Lys			
215	220	225	
ttc acc tca ctg gct ggc gtc gat gga cca cac ggt ggc gat gca gta			835
Phe Thr Ser Leu Ala Gly Val Asp Gly Pro His Gly Gly Asp Ala Val			
230	235	240	245
gcc acc aac ggc atc ctg cac gat gag acg ctg gat cgt tta aaa			880
Ala Thr Asn Gly Ile Leu His Asp Glu Thr Leu Asp Arg Leu Lys			
250	255	260	
tagactcccg ggttttgctt ggt			903
<210> 278			
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<400> 278			
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Leu Ala Asp Ser Ile Thr Leu Asp Arg Phe Glu Ala Ser Asp Leu Glu			
20	25	30	
Val Ser Ser Lys Pro Asp Met Thr Pro Val Ser Asp Ala Asp Leu Ala			
35	40	45	
Thr Glu Glu Ala Leu Arg Glu Lys Ile Ala Thr Ala Arg Pro Ala Asp			
50	55	60	
Ser Ile Leu Gly Glu Glu Phe Gly Gly Asp Val Glu Phe Ser Gly Arg			
65	70	75	80

398

25	30	35	
gac atg act ccc gtc agc gat gcc gac ctg gcg acc gaa gaa gca ctc Asp Met Thr Pro Val Ser Asp Ala Asp Leu Ala Thr Glu Glu Ala Leu 40 45 50			259
cgc gag aaa atc gcc acc gcc cgc ccc gcc gac tcc atc ctc ggt gaa Arg Glu Lys Ile Ala Thr Ala Arg Pro Ala Asp Ser Ile Leu Gly Glu 55 60 65			307
gaa ttc ggt ggc gac gta gaa ttc agc ggc cgc cag tgg atc atc gac Glu Phe Gly Gly Asp Val Glu Phe Ser Gly Arg Gln Trp Ile Ile Asp 70 75 80 85			355
ccc atc gac ggc acc aaa aac tac gtc cgc ggc gtc ccc gta tgg gca Pro Ile Asp Gly Thr Lys Asn Tyr Val Arg Gly Val Pro Val Trp Ala 90 95 100			403
acc ctg atc gcg ctg ctc gac aac ggc aaa ccc gtc gca ggt gtc atc Thr Leu Ile Ala Leu Leu Asp Asn Gly Lys Pro Val Ala Gly Val Ile 105 110 115			451
tcc gca ccc gca ctg gct agg cgt tgg tgg gca tcc gaa ggg gcc ggc Ser Ala Pro Ala Leu Ala Arg Arg Trp Trp Ala Ser Glu Gly Ala Gly 120 125 130			499
gca tgg cgc acc ttc aac ggc agc tcc cca cgc aaa ctg tcc gtg tcc Ala Trp Arg Thr Phe Asn Gly Ser Ser Pro Arg Lys Leu Ser Val Ser 135 140 145			547
cag gtg tcc aag ctt gac gac gcc tcc ctc tcc ttc tcc tcc ctc tcc Gln Val Ser Lys Leu Asp Asp Ala Ser Leu Ser Phe Ser Ser Leu Ser 150 155 160 165			595
ggc tgg gcc gaa cga gat ttg cgc gat cag ttc gtc tcc cta act gat Gly Trp Ala Glu Arg Asp Leu Arg Asp Gln Phe Val Ser Leu Thr Asp 170 175 180			643
acc acc tgg cga ctc cgc ggc tac ggc gac ttc ttc tcc tac tgc ctc Thr Thr Trp Arg Leu Arg Gly Tyr Gly Asp Phe Phe Ser Tyr Cys Leu 185 190 195			691
gtc gcc gaa ggt gcc gtc gat atc gcc gct gaa cca gaa gtc agc ctc Val Ala Glu Gly Ala Val Asp Ile Ala Ala Glu Pro Glu Val Ser Leu 200 205 210			739
tgg gat ctt gct ccc ctg tcc atc ctg gtc acc gaa gcc gga gga aag Trp Asp Leu Ala Pro Leu Ser Ile Leu Val Thr Glu Ala Gly Gly Lys 215 220 225			787
ttc acc tca ctg gct ggc gtc gat gga cca cac ggt ggc gat gca gta Phe Thr Ser Leu Ala Gly Val Asp Gly Pro His Gly Gly Asp Ala Val 230 235 240 245			835
gcc acc aac ggc atc ctg cac gat gag acg ctg gat cgt tta aaa Ala Thr Asn Gly Ile Leu His Asp Glu Thr Leu Asp Arg Leu Lys 250 255 260			880
tagactcccg ggttttgctt ggt			903

<210> 280
 <211> 260
 <212> PRT
 <213> *Corynebacterium glutamicum*

<400> 280

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Leu Ala Asp Ser Ile Thr Leu Asp Arg Phe Glu Ala Ser Asp Leu Glu
          20           25           30

Val Ser Ser Lys Pro Asp Met Thr Pro Val Ser Asp Ala Asp Leu Ala
      35           40           45

Thr Glu Glu Ala Leu Arg Glu Lys Ile Ala Thr Ala Arg Pro Ala Asp
 50           55           60

Ser Ile Leu Gly Glu Glu Phe Gly Gly Asp Val Glu Phe Ser Gly Arg
 65           70           75           80

Gln Trp Ile Ile Asp Pro Ile Asp Gly Thr Lys Asn Tyr Val Arg Gly
          85           90           95

Val Pro Val Trp Ala Thr Leu Ile Ala Leu Leu Asp Asn Gly Lys Pro
          100          105          110

Val Ala Gly Val Ile Ser Ala Pro Ala Leu Ala Arg Arg Trp Trp Ala
 115           120           125

Ser Glu Gly Ala Gly Ala Trp Arg Thr Phe Asn Gly Ser Ser Pro Arg
 130           135           140

Lys Leu Ser Val Ser Gln Val Ser Lys Leu Asp Asp Ala Ser Leu Ser
 145           150           155           160

Phe Ser Ser Leu Ser Gly Trp Ala Glu Arg Asp Leu Arg Asp Gln Phe
          165          170          175

Val Ser Leu Thr Asp Thr Thr Trp Arg Leu Arg Gly Tyr Gly Asp Phe
          180          185          190

Phe Ser Tyr Cys Leu Val Ala Glu Gly Ala Val Asp Ile Ala Ala Glu
 195           200           205

Pro Glu Val Ser Leu Trp Asp Leu Ala Pro Leu Ser Ile Leu Val Thr
 210           215           220

Glu Ala Gly Gly Lys Phe Thr Ser Leu Ala Gly Val Asp Gly Pro His
 225           230           235           240

Gly Gly Asp Ala Val Ala Thr Asn Gly Ile Leu His Asp Glu Thr Leu
          245          250          255

Asp Arg Leu Lys
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<210> 281
 <211> 978
 <212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(955)

<223> RXA01570

<400> 281

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ggcagacccg cctcaacgac tacctcaagg aactctcaaa gtg aaa ggc atc atc 115
                               Val Lys Gly Ile Ile
                               1 5
ctc gca ggt ggc tcc ggc acc cgg ctc tac ccc atc acc aag ggc atc 163
Leu Ala Gly Gly Ser Gly Thr Arg Leu Tyr Pro Ile Thr Lys Gly Ile
                               10 15 20
tcc aag caa ctg atg ccg att tac gac aaa ccc atg gtc tac tac cca 211
Ser Lys Gln Leu Met Pro Ile Tyr Asp Lys Pro Met Val Tyr Tyr Pro
                               25 30 35
ctg acc acg ctc att cag gcc ggc atc aaa gac atc ctg att atc acc 259
Leu Thr Thr Leu Ile Gln Ala Gly Ile Lys Asp Ile Leu Ile Ile Thr
                               40 45 50
acc cct gaa gac agc gcc tcc ttt gaa cgc ttg ctt ggc gac ggc tcc 307
Thr Pro Glu Asp Ser Ala Ser Phe Glu Arg Leu Leu Gly Asp Gly Ser
                               55 60 65
tcc tgg ggc atc aac ctc acc tac gcc gtc caa ccc tcc ccc gac gga 355
Ser Trp Gly Ile Asn Leu Thr Tyr Ala Val Gln Pro Ser Pro Asp Gly
70 75 80 85
cta gcc caa gca ttc atc atc ggc gag gaa ttc atc ggt gac gac gac 403
Leu Ala Gln Ala Phe Ile Ile Gly Glu Glu Phe Ile Gly Asp Asp Asp
90 95 100
gtc gcg ttg gtg ctt ggc gat aac atc ttc gac ggc gca caa ctt ggc 451
Val Ala Leu Val Leu Gly Asp Asn Ile Phe Asp Gly Ala Gln Leu Gly
105 110 115
cac gca cta aag cag tgc tcc aac ccc gac ggt ggc att gtc ttt gct 499
His Ala Leu Lys Gln Cys Ser Asn Pro Asp Gly Gly Ile Val Phe Ala
120 125 130
tat gag gtc tcc gat cct gag cgt tat ggc gtg gtg gaa ttt gat gct 547
Tyr Glu Val Ser Asp Pro Glu Arg Tyr Gly Val Val Glu Phe Asp Ala
135 140 145
gct aat aag gcg gtg tct att gaa gaa aag ccc acc gcg cca aaa tcc 595
Ala Asn Lys Ala Val Ser Ile Glu Glu Lys Pro Thr Ala Pro Lys Ser
150 155 160 165
aac ttt gcc gtg gta gga cta tat ttc tac gac aat cgc gtg gtg gac 643
Asn Phe Ala Val Val Gly Leu Tyr Phe Tyr Asp Asn Arg Val Val Asp
170 175 180
atc gcc aag tca atc aag cct tcc tcg cgt ggc gaa ctg gaa atc acc 691
Ile Ala Lys Ser Ile Lys Pro Ser Ser Arg Gly Glu Leu Glu Ile Thr
185 190 195

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tcc gtt aac gat gcc tac ctc cag caa ggt gct tta act gtg cag cgc 739
 Ser Val Asn Asp Ala Tyr Leu Gln Gln Gly Ala Leu Thr Val Gln Arg
 200 205 210

ctg gac cgt ggc gat gtc tgg tta gat acc ggc aca atc gat tcc atg 787
 Leu Asp Arg Gly Asp Val Trp Leu Asp Thr Gly Thr Ile Asp Ser Met
 215 220 225

tcc gag gcg tct tcc tat gtt gag gtc ctg caa aaa cgt acc ggc aac 835
 Ser Glu Ala Ser Ser Tyr Val Glu Val Leu Gln Lys Arg Thr Gly Asn
 230 235 240 245

atc atc gga tcc ccc gaa gtc gct gcg tac cgc gaa ggt ttc atc aca 883
 Ile Ile Gly Ser Pro Glu Val Ala Ala Tyr Arg Glu Gly Phe Ile Thr
 250 255 260

gct gaa gaa ctc aca gtg ctt ggt gag gaa ctg aag aaa tca ggc tac 931
 Ala Glu Glu Leu Thr Val Leu Gly Glu Glu Leu Lys Lys Ser Gly Tyr
 265 270 275

gga aac tac ctg ctg aga gct ttg taatttacgg tgtggttggtg gag 978
 Gly Asn Tyr Leu Leu Arg Ala Leu
 280 285

<210> 282

<211> 285

<212> PRT

<213> Corynebacterium glutamicum

<400> 282

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 20 25 30

Met Val Tyr Tyr Pro Leu Thr Thr Leu Ile Gln Ala Gly Ile Lys Asp
 35 40 45

Ile Leu Ile Ile Thr Thr Pro Glu Asp Ser Ala Ser Phe Glu Arg Leu
 50 55 60

Leu Gly Asp Gly Ser Ser Trp Gly Ile Asn Leu Thr Tyr Ala Val Gln
 65 70 75 80

Pro Ser Pro Asp Gly Leu Ala Gln Ala Phe Ile Ile Gly Glu Glu Phe
 85 90 95

Ile Gly Asp Asp Asp Val Ala Leu Val Leu Gly Asp Asn Ile Phe Asp
 100 105 110

Gly Ala Gln Leu Gly His Ala Leu Lys Gln Cys Ser Asn Pro Asp Gly
 115 120 125

Gly Ile Val Phe Ala Tyr Glu Val Ser Asp Pro Glu Arg Tyr Gly Val
 130 135 140

Val Glu Phe Asp Ala Ala Asn Lys Ala Val Ser Ile Glu Glu Lys Pro
 145 150 155 160

Thr	Ala	Pro	Lys	Ser	Asn	Phe	Ala	Val	Val	Gly	Leu	Tyr	Phe	Tyr	Asp
				165						170					175
Asn	Arg	Val	Val	Asp	Ile	Ala	Lys	Ser	Ile	Lys	Pro	Ser	Ser	Arg	Gly
			180					185					190		
Glu	Leu	Glu	Ile	Thr	Ser	Val	Asn	Asp	Ala	Tyr	Leu	Gln	Gln	Gly	Ala
		195					200					205			
Leu	Thr	Val	Gln	Arg	Leu	Asp	Arg	Gly	Asp	Val	Trp	Leu	Asp	Thr	Gly
	210					215					220				
Thr	Ile	Asp	Ser	Met	Ser	Glu	Ala	Ser	Ser	Tyr	Val	Glu	Val	Leu	Gln
225					230					235					240
Lys	Arg	Thr	Gly	Asn	Ile	Ile	Gly	Ser	Pro	Glu	Val	Ala	Ala	Tyr	Arg
				245					250					255	
Glu	Gly	Phe	Ile	Thr	Ala	Glu	Glu	Leu	Thr	Val	Leu	Gly	Glu	Glu	Leu
			260					265					270		
Lys	Lys	Ser	Gly	Tyr	Gly	Asn	Tyr	Leu	Leu	Arg	Ala	Leu			
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<210> 283
<211> 891
<212> DNA
<213> Corynebacterium glutamicum
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<220>  
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<222> (101)..(868)  
<223> RXA02666
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				Met	Ser	Ser	Thr	Arg	5							
				1												
atc	ccc	gtc	atc	gca	ctc	ctc	gcg	gcg	gcg	ggg	cgc	gga	acc	cgc	ctc	163
Ile	Pro	Val	Ile	Ala	Leu	Leu	Ala	Ala	Ala	Gly	Arg	Gly	Thr	Arg	Leu	
				10					15					20		
ggc	gga	ccc	atc	ccc	aaa	gca	ttc	gtc	acg	ttg	cgt	gaa	cgc	aca	ctt	211
Gly	Gly	Pro	Ile	Pro	Lys	Ala	Phe	Val	Thr	Leu	Arg	Glu	Arg	Thr	Leu	
			25					30					35			
tta	gag	cgc	tcg	ctc	caa	gcc	atg	ctc	acc	tcc	gaa	agc	gtc	gac	gaa	259
Leu	Glu	Arg	Ser	Leu	Gln	Ala	Met	Leu	Thr	Ser	Glu	Ser	Val	Asp	Glu	
		40					45					50				
atc	atc	atc	ctc	gtc	agc	ccc	gac	atg	gaa	acc	tac	gcc	cgc	gat	ttg	307
Ile	Ile	Ile	Leu	Val	Ser	Pro	Asp	Met	Glu	Thr	Tyr	Ala	Arg	Asp	Leu	
	55					60					65					
ctg	cgc	aaa	cgc	ggt	ctt	ttg	aac	gac	ccc	gaa	ggg	gta	cgc	gta	cgg	355
Leu	Arg	Lys	Arg	Gly	Leu	Leu	Asn	Asp	Pro	Glu	Gly	Val	Arg	Val	Arg	

70	75	80	85	
ctc gtg cac ggc ggc ggg gag cgc gcg gac tcg gtc tgg gca ggc ctt				403
Leu Val His Gly Gly Gly Glu Arg Ala Asp Ser Val Trp Ala Gly Leu	90	95	100	
cag gca att tcg ctt gac gac gcc acc ccc gat gca att gtc tta atc				451
Gln Ala Ile Ser Leu Asp Asp Ala Thr Pro Asp Ala Ile Val Leu Ile	105	110	115	
cac gac agc gcc cga gcg ctc aca cca ccc ggc atg att gcg cgc gtg				499
His Asp Ser Ala Arg Ala Leu Thr Pro Pro Gly Met Ile Ala Arg Val	120	125	130	
gtg cgc aaa gtc cac gaa ggc gcc acc gca gtc atc cca gta ctg cca				547
Val Arg Lys Val His Glu Gly Ala Thr Ala Val Ile Pro Val Leu Pro	135	140	145	
gta tcg gac acc atc aaa cga gtg tcc cct gat ggc gga gta gtt gtc				595
Val Ser Asp Thr Ile Lys Arg Val Ser Pro Asp Gly Gly Val Val Val	150	155	160	165
gac aca ccc aac cgt gca gaa ctt cgc gcc gtc caa acc cca caa ggc				643
Asp Thr Pro Asn Arg Ala Glu Leu Arg Ala Val Gln Thr Pro Gln Gly	170	175	180	
ttc ctg ctg tcc gaa ctt gtt gca gcg aat gag aaa ttc ttc gcc gac				691
Phe Leu Leu Ser Glu Leu Val Ala Ala Asn Glu Lys Phe Phe Ala Asp	185	190	195	
ccc aac cca ggc ttc atc cca acc gat gac gcc agc ttg atg gaa tgg				739
Pro Asn Pro Gly Phe Ile Pro Thr Asp Asp Ala Ser Leu Met Glu Trp	200	205	210	
tac ggc gca gat gta gtc tgc gta caa ggc gac cca atg gcg ttt aaa				787
Tyr Gly Ala Asp Val Val Cys Val Gln Gly Asp Pro Met Ala Phe Lys	215	220	225	
gta aca acc ccc att gat atg atg ctg gca caa cgc atc acc gac gaa				835
Val Thr Thr Pro Ile Asp Met Met Leu Ala Gln Arg Ile Thr Asp Glu	230	235	240	245
gcc gaa ccc aca ata ttt gag gta cca ggt gac taacccaatc atccccgcg				888
Ala Glu Pro Thr Ile Phe Glu Val Pro Gly Asp	250	255		
tag				891
<210> 284				
<211> 256				
<212> PRT				
<213> Corynebacterium glutamicum				
<400> 284				
Met Ser Ser Thr Arg Ile Pro Val Ile Ala Leu Leu Ala Ala Ala Gly	1	5	10	15
Arg Gly Thr Arg Leu Gly Gly Pro Ile Pro Lys Ala Phe Val Thr Leu	20	25	30	

Arg Glu Arg Thr Leu Leu Glu Arg Ser Leu Gln Ala Met Leu Thr Ser
 35 40 45
 Glu Ser Val Asp Glu Ile Ile Ile Leu Val Ser Pro Asp Met Glu Thr
 50 55 60
 Tyr Ala Arg Asp Leu Leu Arg Lys Arg Gly Leu Leu Asn Asp Pro Glu
 65 70 75 80
 Gly Val Arg Val Arg Leu Val His Gly Gly Gly Glu Arg Ala Asp Ser
 85 90 95
 Val Trp Ala Gly Leu Gln Ala Ile Ser Leu Asp Asp Ala Thr Pro Asp
 100 105 110
 Ala Ile Val Leu Ile His Asp Ser Ala Arg Ala Leu Thr Pro Pro Gly
 115 120 125
 Met Ile Ala Arg Val Val Arg Lys Val His Glu Gly Ala Thr Ala Val
 130 135 140
 Ile Pro Val Leu Pro Val Ser Asp Thr Ile Lys Arg Val Ser Pro Asp
 145 150 155 160
 Gly Gly Val Val Val Asp Thr Pro Asn Arg Ala Glu Leu Arg Ala Val
 165 170 175
 Gln Thr Pro Gln Gly Phe Leu Leu Ser Glu Leu Val Ala Ala Asn Glu
 180 185 190
 Lys Phe Phe Ala Asp Pro Asn Pro Gly Phe Ile Pro Thr Asp Asp Ala
 195 200 205
 Ser Leu Met Glu Trp Tyr Gly Ala Asp Val Val Cys Val Gln Gly Asp
 210 215 220
 Pro Met Ala Phe Lys Val Thr Thr Pro Ile Asp Met Met Leu Ala Gln
 225 230 235 240
 Arg Ile Thr Asp Glu Ala Glu Pro Thr Ile Phe Glu Val Pro Gly Asp
 245 250 255

<210> 285

<211> 1056

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(1033)

<223> RXA00825

<400> 285

cccggttcattg ctgggctttg gtgcggtgat ggcaactatt tgtctgatca ttgtgagttt 60
 tagtgcacgc cgattctgag aaacaactaa agtgagccac atg cgc aca gta gtt 115
 Met Arg Thr Val Val

1															5
acc ggc ggt gcc ggc ttc atc gga tcc cat ctc gtt gac ctt ttg atc	163														
Thr Gly Gly Ala Gly Phe Ile Gly Ser His Leu Val Asp Leu Leu Ile															
	10						15					20			
aag gaa ggc cac gag gtc gtt gtg atc gat aac ctc tcc cgc gga cgc	211														
Lys Glu Gly His Glu Val Val Val Ile Asp Asn Leu Ser Arg Gly Arg															
	25						30					35			
ctg gag aat ctc tcc gat gcg gaa gcc acc gga aaa ctc acc ttt gtg	259														
Leu Glu Asn Leu Ser Asp Ala Glu Ala Thr Gly Lys Leu Thr Phe Val															
	40					45					50				
gaa gcc gat ctt ctc gac gtt gat ttc aac gag ttt cta gga acc cac	307														
Glu Ala Asp Leu Leu Asp Val Asp Phe Asn Glu Phe Leu Gly Thr His															
	55					60				65					
aag cct gag gtt att ttc cac ctg gca gcg caa atc gat gtg cgc cac	355														
Lys Pro Glu Val Ile Phe His Leu Ala Ala Gln Ile Asp Val Arg His															
	70				75				80					85	
tct gtt gta gat cct ctt cac gac gcc gaa acc aac att ttg tcc acc	403														
Ser Val Val Asp Pro Leu His Asp Ala Glu Thr Asn Ile Leu Ser Thr															
	90						95						100		
atc cgc atc gct gac gct gcc cgc cag cac ggt gtt cgc aag gtt gtc	451														
Ile Arg Ile Ala Asp Ala Ala Arg Gln His Gly Val Arg Lys Val Val															
	105						110					115			
ttt acc tcc tca ggc ggt tcc att tac ggt gag cct tcg gaa ttc cca	499														
Phe Thr Ser Ser Gly Gly Ser Ile Tyr Gly Glu Pro Ser Glu Phe Pro															
	120					125					130				
gtt gat gaa acc gtg cca gtg gat cca cat tcc cct tat gcg gca tcc	547														
Val Asp Glu Thr Val Pro Val Asp Pro His Ser Pro Tyr Ala Ala Ser															
	135					140				145					
aag gtg tcc ggt gaa att tac ctg aac acc ttc cgc cac ctg tac ggc	595														
Lys Val Ser Gly Glu Ile Tyr Leu Asn Thr Phe Arg His Leu Tyr Gly															
	150				155				160					165	
tta gac tgt tct cac atc gca ccg gca aat gtt tac ggc cca cgc caa	643														
Leu Asp Cys Ser His Ile Ala Pro Ala Asn Val Tyr Gly Pro Arg Gln															
	170						175						180		
gat cca cac ggt gaa gca gga gtt gtg gcc att ttc gcg ctg cga ctt	691														
Asp Pro His Gly Glu Ala Gly Val Val Ala Ile Phe Ala Leu Arg Leu															
	185						190					195			
ctg gga ggc ctg gac acc aag gta ttc ggc gac ggc gga aac acc cgc	739														
Leu Gly Gly Leu Asp Thr Lys Val Phe Gly Asp Gly Gly Asn Thr Arg															
	200					205					210				
gac tac gtc tac gtc ggt gac gta gtt cgt gct ttc tac ctg gct tct	787														
Asp Tyr Val Tyr Val Gly Asp Val Val Arg Ala Phe Tyr Leu Ala Ser															
	215					220				225					
ggg gaa atc ggt ggg gga gag cgc ttc aac att ggc acc tct gtg gaa	835														
Gly Glu Ile Gly Gly Gly Glu Arg Phe Asn Ile Gly Thr Ser Val Glu															
	230				235				240					245	

acc tct gac cgc cag ctg cac acc ctc gtg gcc act gcg gca ggt tcc 883
 Thr Ser Asp Arg Gln Leu His Thr Leu Val Ala Thr Ala Ala Gly Ser
 250 255 260

aaa gat gat cct gaa tat gca cct gca cgt ctc ggc gat gtg cca cgc 931
 Lys Asp Asp Pro Glu Tyr Ala Pro Ala Arg Leu Gly Asp Val Pro Arg
 265 270 275

agt gca ctc agc ttc ggc aag gcc aaa gag gtg ctt ggt tgg gag cct 979
 Ser Ala Leu Ser Phe Gly Lys Ala Lys Glu Val Leu Gly Trp Glu Pro
 280 285 290

gag gtg aac atc gaa caa ggt gtg gcc aag act gtg gag tac ttc cgc 1027
 Glu Val Asn Ile Glu Gln Gly Val Ala Lys Thr Val Glu Tyr Phe Arg
 295 300 305

act cac taggggaaaa tccaccacaa atc 1056
 Thr His
 310

<210> 286

<211> 311

<212> PRT

<213> Corynebacterium glutamicum

<400> 286

Met Arg Thr Val Val Thr Gly Gly Ala Gly Phe Ile Gly Ser His Leu
 1 5 10 15

Val Asp Leu Leu Ile Lys Glu Gly His Glu Val Val Val Ile Asp Asn
 20 25 30

Leu Ser Arg Gly Arg Leu Glu Asn Leu Ser Asp Ala Glu Ala Thr Gly
 35 40 45

Lys Leu Thr Phe Val Glu Ala Asp Leu Leu Asp Val Asp Phe Asn Glu
 50 55 60

Phe Leu Gly Thr His Lys Pro Glu Val Ile Phe His Leu Ala Ala Gln
 65 70 75 80

Ile Asp Val Arg His Ser Val Val Asp Pro Leu His Asp Ala Glu Thr
 85 90 95

Asn Ile Leu Ser Thr Ile Arg Ile Ala Asp Ala Ala Arg Gln His Gly
 100 105 110

Val Arg Lys Val Val Phe Thr Ser Ser Gly Gly Ser Ile Tyr Gly Glu
 115 120 125

Pro Ser Glu Phe Pro Val Asp Glu Thr Val Pro Val Asp Pro His Ser
 130 135 140

Pro Tyr Ala Ala Ser Lys Val Ser Gly Glu Ile Tyr Leu Asn Thr Phe
 145 150 155 160

Arg His Leu Tyr Gly Leu Asp Cys Ser His Ile Ala Pro Ala Asn Val
 165 170 175

Tyr Gly Pro Arg Gln Asp Pro His Gly Glu Ala Gly Val Val Ala Ile
 180 185 190
 Phe Ala Leu Arg Leu Leu Gly Gly Leu Asp Thr Lys Val Phe Gly Asp
 195 200 205
 Gly Gly Asn Thr Arg Asp Tyr Val Tyr Val Gly Asp Val Val Arg Ala
 210 215 220
 Phe Tyr Leu Ala Ser Gly Glu Ile Gly Gly Gly Glu Arg Phe Asn Ile
 225 230 235 240
 Gly Thr Ser Val Glu Thr Ser Asp Arg Gln Leu His Thr Leu Val Ala
 245 250 255
 Thr Ala Ala Gly Ser Lys Asp Asp Pro Glu Tyr Ala Pro Ala Arg Leu
 260 265 270
 Gly Asp Val Pro Arg Ser Ala Leu Ser Phe Gly Lys Ala Lys Glu Val
 275 280 285
 Leu Gly Trp Glu Pro Glu Val Asn Ile Glu Gln Gly Val Ala Lys Thr
 290 295 300
 Val Glu Tyr Phe Arg Thr His
 305 310

<210> 287
 <211> 1134
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1111)
 <223> RXA01887

<400> 287
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 ttatagtaga acgttctagt aaaacttgga aggatgaaaa atg tca gtc aaa ctt 115
 Met Ser Val Lys Leu
 1 5
 gcc ctc atc ggt gct gga cgc atc gga tca aat cac gca cgc ctg atc 163
 Ala Leu Ile Gly Ala Gly Arg Ile Gly Ser Asn His Ala Arg Leu Ile
 10 15 20
 aca aac cac gtg atc ggc tct gaa ctg gtc gcc gtc gtt gac cca act 211
 Thr Asn His Val Ile Gly Ser Glu Leu Val Ala Val Val Asp Pro Thr
 25 30 35
 ccc aac gca gaa acc ctc gct gat gaa ttg ggc gcc gtt gcg ttc tct 259
 Pro Asn Ala Glu Thr Leu Ala Asp Glu Leu Gly Ala Val Ala Phe Ser
 40 45 50
 aac cca gat gac gtc ctg acc cgc gat gac att gac gcg gtt ttg att 307
 Asn Pro Asp Asp Val Leu Thr Arg Asp Asp Ile Asp Ala Val Leu Ile
 55 60 65

gct aca cca gca cga acc cac gcg gat ctc gtg gtc aaa gca gcg gca	355
Ala Thr Pro Ala Arg Thr His Ala Asp Leu Val Val Lys Ala Ala Ala	
70 75 80 85	
gcg ggc aag cac gtg ttt gtg gaa aag ccc atg gcc gtc acc ctc gag	403
Ala Gly Lys His Val Phe Val Glu Lys Pro Met Ala Val Thr Leu Glu	
90 95 100	
gac gca gat cgt gcc atc aac gca gca cgc gaa gca aac act gtc ctg	451
Asp Ala Asp Arg Ala Ile Asn Ala Ala Arg Glu Ala Asn Thr Val Leu	
105 110 115	
cag gtg ggc ttc aat cgt cgt ttc gcg gca ggt ttc gct gca gca cgc	499
Gln Val Gly Phe Asn Arg Arg Phe Ala Ala Gly Phe Ala Ala Ala Arg	
120 125 130	
gca cgc att gac gca ggc gat atc ggc acc cca cag ctg ctt cgt tcc	547
Ala Arg Ile Asp Ala Gly Asp Ile Gly Thr Pro Gln Leu Leu Arg Ser	
135 140 145	
gtg acc cgc gat cca gga cca ttc acc gct gac ccc aac aag atc cct	595
Val Thr Arg Asp Pro Gly Pro Phe Thr Ala Asp Pro Asn Lys Ile Pro	
150 155 160 165	
cag tgg acc atc ttc ctg gaa acc ctc atc cac gat ttc gat gcg ctg	643
Gln Trp Thr Ile Phe Leu Glu Thr Leu Ile His Asp Phe Asp Ala Leu	
170 175 180	
tgc tac ctc aac cca ggc gca acc cca gtg gaa gta acc gct cac gct	691
Cys Tyr Leu Asn Pro Gly Ala Thr Pro Val Glu Val Thr Ala His Ala	
185 190 195	
gat tgc ctc gtc gtt cca gaa gct gct ggc act ggc ttc ctc gac acc	739
Asp Cys Leu Val Val Pro Glu Ala Ala Gly Thr Gly Phe Leu Asp Thr	
200 205 210	
gca gtg gtg act gtc cgt ttt gat aac gga gca att ggt act gca gaa	787
Ala Val Val Thr Val Arg Phe Asp Asn Gly Ala Ile Gly Thr Ala Glu	
215 220 225	
gca agc ttc agc gca gcc tat ggt tat gac gtt cgc ggt gaa gtc ttc	835
Ala Ser Phe Ser Ala Ala Tyr Gly Tyr Asp Val Arg Gly Glu Val Phe	
230 235 240 245	
gga tcc aag ggc atg atg acc gca ggc gac gcg cgc gca acc aac atg	883
Gly Ser Lys Gly Met Met Thr Ala Gly Asp Ala Arg Ala Thr Asn Met	
250 255 260	
act ttc tac ggc gct gag ggc atc gcg gct gcc acc tca cgc gcg gat	931
Thr Phe Tyr Gly Ala Glu Gly Ile Ala Ala Ala Thr Ser Arg Ala Asp	
265 270 275	
acc gat ctg ctc tcc gat gct tac cga gct gaa ttc caa gct ttc gtc	979
Thr Asp Leu Leu Ser Asp Ala Tyr Arg Ala Glu Phe Gln Ala Phe Val	
280 285 290	
gac tcc atc cgt acc aac acc cct tcc aag gtt cca ggc gaa gct gca	1027
Asp Ser Ile Arg Thr Asn Thr Pro Ser Lys Val Pro Gly Glu Ala Ala	
295 300 305	
cgc acc gca cta ctc atc gca ctc ggc gcc atc cga agc gta gaa acc	1075

Arg Thr Ala Leu Leu Ile Ala Leu Gly Ala Ile Arg Ser Val Glu Thr
 310 315 320 325

ggc gca acc atc aac ctt gct gaa agc atc gag gtt taaccatgac 1121
 Gly Ala Thr Ile Asn Leu Ala Glu Ser Ile Glu Val
 330 335

ttttaaaactc gca 1134

<210> 288

<211> 337

<212> PRT

<213> Corynebacterium glutamicum

<400> 288

Met Ser Val Lys Leu Ala Leu Ile Gly Ala Gly Arg Ile Gly Ser Asn
 1 5 10 15

His Ala Arg Leu Ile Thr Asn His Val Ile Gly Ser Glu Leu Val Ala
 20 25 30

Val Val Asp Pro Thr Pro Asn Ala Glu Thr Leu Ala Asp Glu Leu Gly
 35 40 45

Ala Val Ala Phe Ser Asn Pro Asp Asp Val Leu Thr Arg Asp Asp Ile
 50 55 60

Asp Ala Val Leu Ile Ala Thr Pro Ala Arg Thr His Ala Asp Leu Val
 65 70 75 80

Val Lys Ala Ala Ala Gly Lys His Val Phe Val Glu Lys Pro Met
 85 90 95

Ala Val Thr Leu Glu Asp Ala Asp Arg Ala Ile Asn Ala Ala Arg Glu
 100 105 110

Ala Asn Thr Val Leu Gln Val Gly Phe Asn Arg Arg Phe Ala Ala Gly
 115 120 125

Phe Ala Ala Ala Arg Ala Arg Ile Asp Ala Gly Asp Ile Gly Thr Pro
 130 135 140

Gln Leu Leu Arg Ser Val Thr Arg Asp Pro Gly Pro Phe Thr Ala Asp
 145 150 155 160

Pro Asn Lys Ile Pro Gln Trp Thr Ile Phe Leu Glu Thr Leu Ile His
 165 170 175

Asp Phe Asp Ala Leu Cys Tyr Leu Asn Pro Gly Ala Thr Pro Val Glu
 180 185 190

Val Thr Ala His Ala Asp Cys Leu Val Val Pro Glu Ala Ala Gly Thr
 195 200 205

Gly Phe Leu Asp Thr Ala Val Val Thr Val Arg Phe Asp Asn Gly Ala
 210 215 220

Ile Gly Thr Ala Glu Ala Ser Phe Ser Ala Ala Tyr Gly Tyr Asp Val
 225 230 235 240

Arg Gly Glu Val Phe Gly Ser Lys Gly Met Met Thr Ala Gly Asp Ala
245 250 255

Arg Ala Thr Asn Met Thr Phe Tyr Gly Ala Glu Gly Ile Ala Ala Ala
260 265 270

Thr Ser Arg Ala Asp Thr Asp Leu Leu Ser Asp Ala Tyr Arg Ala Glu
275 280 285

Phe Gln Ala Phe Val Asp Ser Ile Arg Thr Asn Thr Pro Ser Lys Val
290 295 300

Pro Gly Glu Ala Ala Arg Thr Ala Leu Leu Ile Ala Leu Gly Ala Ile
305 310 315 320

Arg Ser Val Glu Thr Gly Ala Thr Ile Asn Leu Ala Glu Ser Ile Glu
325 330 335

Val

<210> 289

<211> 996

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(973)

<223> RXN00013

<400> 289

ctgcagaaaaa ttcgggacgc atgattgcac atattaccgc caccgattgt gattcttaga 60

acgccacctt attcagcaca cttggccgac ggcattgcaca atg gaa ggc atg act 115
Met Glu Gly Met Thr
1 5

aat cca gag cag aca cat ccc gct gca agc ctc gaa gac atg atc aaa 163
Asn Pro Glu Gln Thr His Pro Ala Ala Ser Leu Glu Asp Met Ile Lys
10 15 20

acc atc aca aag acc ttc gtg att gct cac gat cag gat tct gat gag 211
Thr Ile Thr Lys Thr Phe Val Ile Ala His Asp Gln Asp Ser Asp Glu
25 30 35

cat ctt gcg cag gca ctg gtg tac aac gct gga cgt ttg gca tgg cgc 259
His Leu Ala Gln Ala Leu Val Tyr Asn Ala Gly Arg Leu Ala Trp Arg
40 45 50

atg cgc gaa aac ggt gtg gat acg gat tac aag act tct gtg tct gat 307
Met Arg Glu Asn Gly Val Asp Thr Asp Tyr Lys Thr Ser Val Ser Asp
55 60 65

gtg gtc acg gat gcc gat cgt gcg gcc gag gcc ttc gtc gca ggc gtt 355
Val Val Thr Asp Ala Asp Arg Ala Ala Glu Ala Phe Val Ala Gly Val
70 75 80 85

ctt gaa gcg ttg cgg cct gag gac ggc gtg ctt ggc gag gaa ggc gcg 403
Leu Glu Ala Leu Arg Pro Glu Asp Gly Val Leu Gly Glu Glu Gly Ala

90	95	100	
gac cgg gcg tcg aaa agc gga aaa acc tgg gtc atc gac ccg gtt gat			451
Asp Arg Ala Ser Lys Ser Gly Lys Thr Trp Val Ile Asp Pro Val Asp			
105	110	115	
ggc acc tac aac ttc acc cag ggc tca gat tat tgg tgc tcg gcg ctc			499
Gly Thr Tyr Asn Phe Thr Gln Gly Ser Asp Tyr Trp Cys Ser Ala Leu			
120	125	130	
gcg ctg gtc gag ggc gat cca tcc gcg cca tcg cgc gtg ctt ttc ggc			547
Ala Leu Val Glu Gly Asp Pro Ser Ala Pro Ser Arg Val Leu Phe Gly			
135	140	145	
gcc gta cac cgc cca gcc atg ggt tat acg tgg ttc ggt ggc ccg gga			595
Ala Val His Arg Pro Ala Met Gly Tyr Thr Trp Phe Gly Gly Pro Gly			
150	155	160	165
atc cgc acc acg ctc gac ggc aag gag cta gat ttg ctt gtc gac gcc			643
Ile Arg Thr Thr Leu Asp Gly Lys Glu Leu Asp Leu Leu Val Asp Ala			
170	175	180	
ccc ctc aat caa atc tcc ctg gcc acc tac atc cac ccg tca cgc atc			691
Pro Leu Asn Gln Ile Ser Leu Ala Thr Tyr Ile His Pro Ser Arg Ile			
185	190	195	
gcg gaa cct gat att caa aag gcg tgg atg agc gtt gcc acc cac cct			739
Ala Glu Pro Asp Ile Gln Lys Ala Trp Met Ser Val Ala Thr His Pro			
200	205	210	
gca acg ctg cgc atg ttc ggc gcc ggc tcc atc gat ttg gcc aac atc			787
Ala Thr Leu Arg Met Phe Gly Ala Gly Ser Ile Asp Leu Ala Asn Ile			
215	220	225	
gcc gac ggc agc atg ggc gca tgg gtg cag cac agc gtc gca gat tgg			835
Ala Asp Gly Ser Met Gly Ala Trp Val Gln His Ser Val Ala Asp Trp			
230	235	240	245
gac tgg cta ccc ggc cgc gca ctc atc gaa ggc gtc ggc gga gca tgc			883
Asp Trp Leu Pro Gly Arg Ala Leu Ile Glu Gly Val Gly Gly Ala Cys			
250	255	260	
atc aaa gtg acc gcc ggc ggc gtc gaa tgg tcc gtt gca gga aac gcg			931
Ile Lys Val Thr Ala Gly Gly Val Glu Trp Ser Val Ala Gly Asn Ala			
265	270	275	
gaa gca gtt agt gag atc tcc gaa act tta agc gca cta gac			973
Glu Ala Val Ser Glu Ile Ser Glu Thr Leu Ser Ala Leu Asp			
280	285	290	
taacaacaca tgagcaaata tgc			996

<210> 290

<211> 291

<212> PRT

<213> Corynebacterium glutamicum

<400> 290

Met	Glu	Gly	Met	Thr	Asn	Pro	Glu	Gln	Thr	His	Pro	Ala	Ala	Ser	Leu
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									10						

Glu Asp Met Ile Lys Thr Ile Thr Lys Thr Phe Val Ile Ala His Asp
 20 25 30
 Gln Asp Ser Asp Glu His Leu Ala Gln Ala Leu Val Tyr Asn Ala Gly
 35 40 45
 Arg Leu Ala Trp Arg Met Arg Glu Asn Gly Val Asp Thr Asp Tyr Lys
 50 55 60
 Thr Ser Val Ser Asp Val Val Thr Asp Ala Asp Arg Ala Ala Glu Ala
 65 70 75 80
 Phe Val Ala Gly Val Leu Glu Ala Leu Arg Pro Glu Asp Gly Val Leu
 85 90 95
 Gly Glu Glu Gly Ala Asp Arg Ala Ser Lys Ser Gly Lys Thr Trp Val
 100 105 110
 Ile Asp Pro Val Asp Gly Thr Tyr Asn Phe Thr Gln Gly Ser Asp Tyr
 115 120 125
 Trp Cys Ser Ala Leu Ala Leu Val Glu Gly Asp Pro Ser Ala Pro Ser
 130 135 140
 Arg Val Leu Phe Gly Ala Val His Arg Pro Ala Met Gly Tyr Thr Trp
 145 150 155 160
 Phe Gly Gly Pro Gly Ile Arg Thr Thr Leu Asp Gly Lys Glu Leu Asp
 165 170 175
 Leu Leu Val Asp Ala Pro Leu Asn Gln Ile Ser Leu Ala Thr Tyr Ile
 180 185 190
 His Pro Ser Arg Ile Ala Glu Pro Asp Ile Gln Lys Ala Trp Met Ser
 195 200 205
 Val Ala Thr His Pro Ala Thr Leu Arg Met Phe Gly Ala Gly Ser Ile
 210 215 220
 Asp Leu Ala Asn Ile Ala Asp Gly Ser Met Gly Ala Trp Val Gln His
 225 230 235 240
 Ser Val Ala Asp Trp Asp Trp Leu Pro Gly Arg Ala Leu Ile Glu Gly
 245 250 255
 Val Gly Gly Ala Cys Ile Lys Val Thr Ala Gly Gly Val Glu Trp Ser
 260 265 270
 Val Ala Gly Asn Ala Glu Ala Val Ser Glu Ile Ser Glu Thr Leu Ser
 275 280 285
 Ala Leu Asp
 290

<210> 291

<211> 996

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(973)

<223> FRXA00013

<400> 291

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acgccacctt attcagcaca cttggccgac ggcattgcaca atg gaa ggc atg act 115
 Met Glu Gly Met Thr
 1 5

aat cca gag cag aca cat ccc gct gca agc ctc gaa gac atg atc aaa 163
 Asn Pro Glu Gln Thr His Pro Ala Ala Ser Leu Glu Asp Met Ile Lys
 10 15 20

acc atc aca aag acc ttc gtg att gct cac gat cag gat tct gat gag 211
 Thr Ile Thr Lys Thr Phe Val Ile Ala His Asp Gln Asp Ser Asp Glu
 25 30 35

cat ctt gcg cag gca ctg gtg tac aac gct gga cgt ttg gca tgg cgc 259
 His Leu Ala Gln Ala Leu Val Tyr Asn Ala Gly Arg Leu Ala Trp Arg
 40 45 50

atg cgc gaa aac ggt gtg gat acg gat tac aag act tct gtg tct gat 307
 Met Arg Glu Asn Gly Val Asp Thr Asp Tyr Lys Thr Ser Val Ser Asp
 55 60 65

gtg gtc acg gat gcc gat cgt gcg gcc gag gcc ttc gtc gca ggc gtt 355
 Val Val Thr Asp Ala Asp Arg Ala Ala Glu Ala Phe Val Ala Gly Val
 70 75 80 85

ctt gaa gcg ttg cgg cct gag gac ggc gtg ctt ggc gag gaa ggc gcg 403
 Leu Glu Ala Leu Arg Pro Glu Asp Gly Val Leu Gly Glu Glu Gly Ala
 90 95 100

gac cgg gcg tcg aaa agc gga aaa acc tgg gtc atc gac ccg gtt gat 451
 Asp Arg Ala Ser Lys Ser Gly Lys Thr Trp Val Ile Asp Pro Val Asp
 105 110 115

ggc acc tac aac ttc acc cag ggc tca gat tat tgg tgc tcg gcg ctc 499
 Gly Thr Tyr Asn Phe Thr Gln Gly Ser Asp Tyr Trp Cys Ser Ala Leu
 120 125 130

gcg ctg gtc gag ggc gat cca tcc gcg cca tcg cgc gtg ctt ttc ggc 547
 Ala Leu Val Glu Gly Asp Pro Ser Ala Pro Ser Arg Val Leu Phe Gly
 135 140 145

gcc gta cac cgc cca gcc atg ggt tat acg tgg ttc ggt ggc ccg gga 595
 Ala Val His Arg Pro Ala Met Gly Tyr Thr Trp Phe Gly Gly Pro Gly
 150 155 160 165

atc cgc acc acg ctc gac ggc aag gag cta gat ttg ctt gtc gac gcc 643
 Ile Arg Thr Thr Leu Asp Gly Lys Glu Leu Asp Leu Leu Val Asp Ala
 170 175 180

ccc ctc aat caa atc tcc ctg gcc acc tac atc cac ccg tca cgc atc 691
 Pro Leu Asn Gln Ile Ser Leu Ala Thr Tyr Ile His Pro Ser Arg Ile
 185 190 195

gcg gaa cct gat att caa aag gcg tgg atg agc gtt gcc acc cac cct 739

Ala Glu Pro Asp Ile Gln Lys Ala Trp Met Ser Val Ala Thr His Pro
 200 205 210

gca acg ctg cgc atg ttc ggc gcc ggc tcc atc gat ttg gcc aac atc 787
 Ala Thr Leu Arg Met Phe Gly Ala Gly Ser Ile Asp Leu Ala Asn Ile
 215 220 225

gcc gac ggc agc atg ggc gca tgg gtg cag cac agc gtc gca gat tgg 835
 Ala Asp Gly Ser Met Gly Ala Trp Val Gln His Ser Val Ala Asp Trp
 230 235 240 245

gac tgg cta ccc ggc cgc gca ctc atc gaa ggc gtc ggc gga gcg tgc 883
 Asp Trp Leu Pro Gly Arg Ala Leu Ile Glu Gly Val Gly Gly Ala Cys
 250 255 260

atc aaa gtg acc gcc ggc ggc gtc gaa tgg tcc gtt gca gga aac gcg 931
 Ile Lys Val Thr Ala Gly Gly Val Glu Trp Ser Val Ala Gly Asn Ala
 265 270 275

gaa gca gtt agt gag atc tcc gaa act tta agc gca cta gac 973
 Glu Ala Val Ser Glu Ile Ser Glu Thr Leu Ser Ala Leu Asp
 280 285 290

tagcaacaca tgagcaaata tgc 996

<210> 292
 <211> 291
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 292
 Met Glu Gly Met Thr Asn Pro Glu Gln Thr His Pro Ala Ala Ser Leu
 1 5 10 15

Glu Asp Met Ile Lys Thr Ile Thr Lys Thr Phe Val Ile Ala His Asp
 20 25 30

Gln Asp Ser Asp Glu His Leu Ala Gln Ala Leu Val Tyr Asn Ala Gly
 35 40 45

Arg Leu Ala Trp Arg Met Arg Glu Asn Gly Val Asp Thr Asp Tyr Lys
 50 55 60

Thr Ser Val Ser Asp Val Val Thr Asp Ala Asp Arg Ala Ala Glu Ala
 65 70 75 80

Phe Val Ala Gly Val Leu Glu Ala Leu Arg Pro Glu Asp Gly Val Leu
 85 90 95

Gly Glu Glu Gly Ala Asp Arg Ala Ser Lys Ser Gly Lys Thr Trp Val
 100 105 110

Ile Asp Pro Val Asp Gly Thr Tyr Asn Phe Thr Gln Gly Ser Asp Tyr
 115 120 125

Trp Cys Ser Ala Leu Ala Leu Val Glu Gly Asp Pro Ser Ala Pro Ser
 130 135 140

Arg Val Leu Phe Gly Ala Val His Arg Pro Ala Met Gly Tyr Thr Trp
 145 150 155 160

Phe Gly Gly Pro Gly Ile Arg Thr Thr Leu Asp Gly Lys Glu Leu Asp
165 170 175

Leu Leu Val Asp Ala Pro Leu Asn Gln Ile Ser Leu Ala Thr Tyr Ile
180 185 190

His Pro Ser Arg Ile Ala Glu Pro Asp Ile Gln Lys Ala Trp Met Ser
195 200 205

Val Ala Thr His Pro Ala Thr Leu Arg Met Phe Gly Ala Gly Ser Ile
210 215 220

Asp Leu Ala Asn Ile Ala Asp Gly Ser Met Gly Ala Trp Val Gln His
225 230 235 240

Ser Val Ala Asp Trp Asp Trp Leu Pro Gly Arg Ala Leu Ile Glu Gly
245 250 255

Val Gly Gly Ala Cys Ile Lys Val Thr Ala Gly Gly Val Glu Trp Ser
260 265 270

Val Ala Gly Asn Ala Glu Ala Val Ser Glu Ile Ser Glu Thr Leu Ser
275 280 285

Ala Leu Asp
290

<210> 293

<211> 948

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(925)

<223> RXA01099

<400> 293

ggatgagggc attgattccg tcatcattgg caaggcactt tatgagcaca agttcaccct 60

cgaagaggct ttggctgcag tagaaaagct cggttaatac atg gat gct cgt ggg 115
Met Asp Ala Arg Gly
1 5

atg ttg gcc att gcg gag gcc gtt gta gat gat gcc gaa gcc ctc ttc 163
Met Leu Ala Ile Ala Glu Ala Val Val Asp Ala Glu Ala Leu Phe
10 15 20

atg cag ggc ttc gga gct gca cct gcc cat atg aaa tcc ccg ggg gat 211
Met Gln Gly Phe Gly Ala Ala Pro Ala His Met Lys Ser Pro Gly Asp
25 30 35

ttt gcc acg gaa gtg gat atg gcc atc gaa tcc cat atg cgt tcg atg 259
Phe Ala Thr Glu Val Asp Met Ala Ile Glu Ser His Met Arg Ser Met
40 45 50

ctg aac atg atg aca ggc att gct gtc atc ggt gaa gaa ggt ggc ggt 307
Leu Asn Met Met Thr Gly Ile Ala Val Ile Gly Glu Glu Gly Gly Gly
55 60 65

gcg acc tcc ggc acg cgc tgg gtg att gat ccc atc gac ggc acc gcc 355
 Ala Thr Ser Gly Thr Arg Trp Val Ile Asp Pro Ile Asp Gly Thr Ala
 70 75 80 85
 aac ttc gcg gcg tcc aac ccg atg agc gcg atc ctg gtg tct ttg ctt 403
 Asn Phe Ala Ala Ser Asn Pro Met Ser Ala Ile Leu Val Ser Leu Leu
 90 95 100
 gtc gac gac cag ccc gtc ctg ggt att acc tcc atg ccc atg ctg ggt 451
 Val Asp Asp Gln Pro Val Leu Gly Ile Thr Ser Met Pro Met Leu Gly
 105 110 115
 aaa cgc ctc acc gct ttt gaa ggt tca ccg ctg atg atc aac ggt gaa 499
 Lys Arg Leu Thr Ala Phe Glu Gly Ser Pro Leu Met Ile Asn Gly Glu
 120 125 130
 cct cag gaa cca ttg caa gaa caa tcc agt ttg gta tcc cac att ggt 547
 Pro Gln Glu Pro Leu Gln Glu Gln Ser Ser Leu Val Ser His Ile Gly
 135 140 145
 ttt agt tcc atg gcc tcc ccg cgc aat aca gcg ttt cct gtg gag ttg 595
 Phe Ser Ser Met Ala Ser Pro Arg Asn Thr Ala Phe Pro Val Glu Leu
 150 155 160 165
 cgt cgg gat ctt ctg acc gag ctc acg gaa tcg tat ctt cgt ccc cgc 643
 Arg Arg Asp Leu Leu Thr Glu Leu Thr Glu Ser Tyr Leu Arg Pro Arg
 170 175 180
 att aca ggt tcg gtg ggt gtt gat ctc gcg ttc act gcg cag ggc att 691
 Ile Thr Gly Ser Val Gly Val Asp Leu Ala Phe Thr Ala Gln Gly Ile
 185 190 195
 ttt gga gca tgc gta tcg ttt agt cct cat gtt tgg gac aat tcc gca 739
 Phe Gly Ala Cys Val Ser Phe Ser Pro His Val Trp Asp Asn Ser Ala
 200 205 210
 ggc gtg atg ttg atg cgc gct gct ggt gca caa gtt act gac acc gaa 787
 Gly Val Met Leu Met Arg Ala Ala Gly Ala Gln Val Thr Asp Thr Glu
 215 220 225
 ggc cat ccg tgg gca cca ggt agg gga gtc gtg gcc gga aca aaa agg 835
 Gly His Pro Trp Ala Pro Gly Arg Gly Val Val Ala Gly Thr Lys Arg
 230 235 240 245
 gct cac gat gtg ctg tta agt aag att gaa aaa gtt cgg ttg atg cat 883
 Ala His Asp Val Leu Leu Ser Lys Ile Glu Lys Val Arg Leu Met His
 250 255 260
 gca gat gca ggt aat gac cag tcg tta aat gag gag tac aag 925
 Ala Asp Ala Gly Asn Asp Gln Ser Leu Asn Glu Glu Tyr Lys
 265 270 275
 taaaatgggc gtggcaattc gag 948

<210> 294

<211> 275

<212> PRT

<213> Corynebacterium glutamicum

<400> 294

Met Asp Ala Arg Gly Met Leu Ala Ile Ala Glu Ala Val Val Asp Asp
 1 5 10 15

Ala Glu Ala Leu Phe Met Gln Gly Phe Gly Ala Ala Pro Ala His Met
 20 25 30

Lys Ser Pro Gly Asp Phe Ala Thr Glu Val Asp Met Ala Ile Glu Ser
 35 40 45

His Met Arg Ser Met Leu Asn Met Met Thr Gly Ile Ala Val Ile Gly
 50 55 60

Glu Glu Gly Gly Gly Ala Thr Ser Gly Thr Arg Trp Val Ile Asp Pro
 65 70 75 80

Ile Asp Gly Thr Ala Asn Phe Ala Ala Ser Asn Pro Met Ser Ala Ile
 85 90 95

Leu Val Ser Leu Leu Val Asp Asp Gln Pro Val Leu Gly Ile Thr Ser
 100 105 110

Met Pro Met Leu Gly Lys Arg Leu Thr Ala Phe Glu Gly Ser Pro Leu
 115 120 125

Met Ile Asn Gly Glu Pro Gln Glu Pro Leu Gln Glu Gln Ser Ser Leu
 130 135 140

Val Ser His Ile Gly Phe Ser Ser Met Ala Ser Pro Arg Asn Thr Ala
 145 150 155 160

Phe Pro Val Glu Leu Arg Arg Asp Leu Leu Thr Glu Leu Thr Glu Ser
 165 170 175

Tyr Leu Arg Pro Arg Ile Thr Gly Ser Val Gly Val Asp Leu Ala Phe
 180 185 190

Thr Ala Gln Gly Ile Phe Gly Ala Cys Val Ser Phe Ser Pro His Val
 195 200 205

Trp Asp Asn Ser Ala Gly Val Met Leu Met Arg Ala Ala Gly Ala Gln
 210 215 220

Val Thr Asp Thr Glu Gly His Pro Trp Ala Pro Gly Arg Gly Val Val
 225 230 235 240

Ala Gly Thr Lys Arg Ala His Asp Val Leu Leu Ser Lys Ile Glu Lys
 245 250 255

Val Arg Leu Met His Ala Asp Ala Gly Asn Asp Gln Ser Leu Asn Glu
 260 265 270

Glu Tyr Lys
 275

<210> 295

<211> 576

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(576)

<223> RXN01332

<400> 295

cac atc tct gcc att att gag ccc gac gca gca cgt gcc gct gca gct	48
His Ile Ser Ala Ile Ile Glu Pro Asp Ala Ala Arg Ala Ala Ala Ala	
1 5 10 15	
gca gaa gac gcg ccg ggt gca cag gcc ttc act cgc att gaa gat gct	96
Ala Glu Asp Ala Pro Gly Ala Gln Ala Phe Thr Arg Ile Glu Asp Ala	
20 25 30	
atc gca gcc gat gct gtc gac gca gtg ctg atc gcc gta cca ggt cag	144
Ile Ala Ala Asp Ala Val Asp Ala Val Leu Ile Ala Val Pro Gly Gln	
35 40 45	
ttc cat gag cca gta ctt gtc cca gca cta gaa gca ggc ctt ccc atc	192
Phe His Glu Pro Val Leu Val Pro Ala Leu Glu Ala Gly Leu Pro Ile	
50 55 60	
ctg tgt gaa aag cca ctg acc cca gat tct gaa tcc tca ctg cgc atc	240
Leu Cys Glu Lys Pro Leu Thr Pro Asp Ser Glu Ser Ser Leu Arg Ile	
65 70 75 80	
gtc gag ctg gag cag aag ctg gac aag cca cac atc cag gtt ggt ttc	288
Val Glu Leu Glu Gln Lys Leu Asp Lys Pro His Ile Gln Val Gly Phe	
85 90 95	
atg cgc cgc ttc gac cct gag tac aac aac ttg cgc aaa ttg gtg gaa	336
Met Arg Arg Phe Asp Pro Glu Tyr Asn Asn Leu Arg Lys Leu Val Glu	
100 105 110	
tcc ggc gaa gct ggc gaa ctg ctc atg ctc cgc ggc ctg cac cgc aac	384
Ser Gly Glu Ala Gly Glu Leu Leu Met Leu Arg Gly Leu His Arg Asn	
115 120 125	
cca agt gtt ggt gag agc tac acc cag tcc atg ctg atc acc gac tcc	432
Pro Ser Val Gly Glu Ser Tyr Thr Gln Ser Met Leu Ile Thr Asp Ser	
130 135 140	
gtc gtc cac gaa ttc gat gtc atc cca tgg ctc gca ggc tcc cga gtt	480
Val Val His Glu Phe Asp Val Ile Pro Trp Leu Ala Gly Ser Arg Val	
145 150 155 160	
gtc tcc gtt gaa gtg aag tac cca aag acc tcc tca ctg gcg cac tcc	528
Val Ser Val Glu Val Lys Tyr Pro Lys Thr Ser Ser Leu Ala His Ser	
165 170 175	
ggc ctc aag gaa cca atc ctg gtg atc atg gag ctc gaa aac ggc gtg	576
Gly Leu Lys Glu Pro Ile Leu Val Ile Met Glu Leu Glu Asn Gly Val	
180 185 190	

<210> 296

<211> 192

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 296

His Ile Ser Ala Ile Ile Glu Pro Asp Ala Ala Arg Ala Ala Ala Ala
 1 5 10 15
 Ala Glu Asp Ala Pro Gly Ala Gln Ala Phe Thr Arg Ile Glu Asp Ala
 20 25 30
 Ile Ala Ala Asp Ala Val Asp Ala Val Leu Ile Ala Val Pro Gly Gln
 35 40 45
 Phe His Glu Pro Val Leu Val Pro Ala Leu Glu Ala Gly Leu Pro Ile
 50 55 60
 Leu Cys Glu Lys Pro Leu Thr Pro Asp Ser Glu Ser Ser Leu Arg Ile
 65 70 75 80
 Val Glu Leu Glu Gln Lys Leu Asp Lys Pro His Ile Gln Val Gly Phe
 85 90 95
 Met Arg Arg Phe Asp Pro Glu Tyr Asn Asn Leu Arg Lys Leu Val Glu
 100 105 110
 Ser Gly Glu Ala Gly Glu Leu Leu Met Leu Arg Gly Leu His Arg Asn
 115 120 125
 Pro Ser Val Gly Glu Ser Tyr Thr Gln Ser Met Leu Ile Thr Asp Ser
 130 135 140
 Val Val His Glu Phe Asp Val Ile Pro Trp Leu Ala Gly Ser Arg Val
 145 150 155 160
 Val Ser Val Glu Val Lys Tyr Pro Lys Thr Ser Ser Leu Ala His Ser
 165 170 175
 Gly Leu Lys Glu Pro Ile Leu Val Ile Met Glu Leu Glu Asn Gly Val
 180 185 190

<210> 297
 <211> 549
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (1)..(549)
 <223> FRXA01332

<400> 297
 gca gca cgt gcc gct gca gct gca gaa gac gcg ccg ggt gca cag gcc 48
 Ala Ala Arg Ala Ala Ala Ala Ala Glu Asp Ala Pro Gly Ala Gln Ala
 1 5 10 15
 ttc act cgc att gaa gat gct atc gca gcc gat gct gtc gac gca gtg 96
 Phe Thr Arg Ile Glu Asp Ala Ile Ala Ala Asp Ala Val Asp Ala Val
 20 25 30
 ctg atc gcc gta cca ggt cag ttc cat gag cca gta ctt gtc cca gca 144
 Leu Ile Ala Val Pro Gly Gln Phe His Glu Pro Val Leu Val Pro Ala

35	40	45	
cta gaa gca ggc ctt ccc atc ctg tgt gaa aag cca ctg acc cca gat			192
Leu Glu Ala Gly Leu Pro Ile Leu Cys Glu Lys Pro Leu Thr Pro Asp			
50	55	60	
tct gaa tcc tca ctg cgc atc gtc gag ctg gag cag aag ctg gac aag			240
Ser Glu Ser Ser Leu Arg Ile Val Glu Leu Glu Gln Lys Leu Asp Lys			
65	70	75	80
cca cac atc cag gtt ggt ttc atg cgc cgc ttc gac cct gag tac aac			288
Pro His Ile Gln Val Gly Phe Met Arg Arg Phe Asp Pro Glu Tyr Asn			
	85	90	95
aac ttg cgc aaa ttg gtg gaa tcc ggc gaa gct ggc gaa ctg ctc atg			336
Asn Leu Arg Lys Leu Val Glu Ser Gly Glu Ala Gly Glu Leu Leu Met			
	100	105	110
ctc cgc ggc ctg cac cgc aac cca agt gtt ggt gag agc tac acc cag			384
Leu Arg Gly Leu His Arg Asn Pro Ser Val Gly Glu Ser Tyr Thr Gln			
	115	120	125
tcc atg ctg atc acc gac tcc gtc gtc cac gaa ttc gat gtc atc cca			432
Ser Met Leu Ile Thr Asp Ser Val Val His Glu Phe Asp Val Ile Pro			
	130	135	140
tgg ctc gca ggc tcc cga gtt gtc tcc gtt gaa gtg aag tac cca aag			480
Trp Leu Ala Gly Ser Arg Val Val Ser Val Glu Val Lys Tyr Pro Lys			
145	150	155	160
acc tcc tca ctg gcg cac tcc ggc ctc aag gaa cca atc ctg gtg atc			528
Thr Ser Ser Leu Ala His Ser Gly Leu Lys Glu Pro Ile Leu Val Ile			
	165	170	175
atg gag ctc gaa aac ggc gtg			549
Met Glu Leu Glu Asn Gly Val			
	180		

<210> 298

<211> 183

<212> PRT

<213> Corynebacterium glutamicum

<400> 298

Ala Ala Arg Ala Ala Ala Ala Glu Asp Ala Pro Gly Ala Gln Ala			
1	5	10	15
Phe Thr Arg Ile Glu Asp Ala Ile Ala Ala Asp Ala Val Asp Ala Val			
	20	25	30
Leu Ile Ala Val Pro Gly Gln Phe His Glu Pro Val Leu Val Pro Ala			
	35	40	45
Leu Glu Ala Gly Leu Pro Ile Leu Cys Glu Lys Pro Leu Thr Pro Asp			
	50	55	60
Ser Glu Ser Ser Leu Arg Ile Val Glu Leu Glu Gln Lys Leu Asp Lys			
	65	70	75
Pro His Ile Gln Val Gly Phe Met Arg Arg Phe Asp Pro Glu Tyr Asn			

	85	90	95
Asn Leu Arg Lys Leu Val Glu Ser Gly Glu Ala Gly Glu Leu Leu Met	100	105	110
Leu Arg Gly Leu His Arg Asn Pro Ser Val Gly Glu Ser Tyr Thr Gln	115	120	125
Ser Met Leu Ile Thr Asp Ser Val Val His Glu Phe Asp Val Ile Pro	130	135	140
Trp Leu Ala Gly Ser Arg Val Val Ser Val Glu Val Lys Tyr Pro Lys	145	150	155
Thr Ser Ser Leu Ala His Ser Gly Leu Lys Glu Pro Ile Leu Val Ile	165	170	175
Met Glu Leu Glu Asn Gly Val	180		
<210> 299			
<211> 1128			
<212> DNA			
<213> Corynebacterium glutamicum			
<220>			
<221> CDS			
<222> (101)..(1105)			
<223> RXA01632			
<400> 299			
aagggctgca acgtgctttc gacaccacca tcgcagcggt tgaacaagct gctcgtctcg	60		
ccccctccac taactgatct ttgaaaggct gaaaaaactc atg act ctt cgt atc	115		
	Met Thr Leu Arg Ile		
	1 5		
gcc ctt ttc ggc gct ggc cgc atc ggt cac gtc cac gct gcc aac att	163		
Ala Leu Phe Gly Ala Gly Arg Ile Gly His Val His Ala Ala Asn Ile			
	10 15 20		
gct gca aac cct gat ctt gaa ctc gtt gtt atc gcc gat cct ttc att	211		
Ala Ala Asn Pro Asp Leu Glu Leu Val Val Ile Ala Asp Pro Phe Ile			
	25 30 35		
gaa ggc gca cag cgt ttg gca gaa gcc aat ggg gca gaa gcg gtt gca	259		
Glu Gly Ala Gln Arg Leu Ala Glu Ala Asn Gly Ala Glu Ala Val Ala			
	40 45 50		
tca cca gat gag gtg ttc gcc cgc gat gat atc gat ggc atc gtg atc	307		
Ser Pro Asp Glu Val Phe Ala Arg Asp Asp Ile Asp Gly Ile Val Ile			
	55 60 65		
ggt tca cca acc agc acc cac gtt gat ctg atc acc cgc gcc gtg gaa	355		
Gly Ser Pro Thr Ser Thr His Val Asp Leu Ile Thr Arg Ala Val Glu			
	70 75 80 85		
cgt ggc att cct gca ctg tgc gaa aaa ccc att gat tta gac att gaa	403		
Arg Gly Ile Pro Ala Leu Cys Glu Lys Pro Ile Asp Leu Asp Ile Glu			
	90 95 100		

atg gtg cgt gcc tgc aaa gag aag atc ggc gac ggc gct tcc aag gtg	451
Met Val Arg Ala Cys Lys Glu Lys Ile Gly Asp Gly Ala Ser Lys Val	
105 110 115	
atg ctg ggg ttt aac cga cgc ttc gat cct tct ttc gct gcc atc aat	499
Met Leu Gly Phe Asn Arg Arg Phe Asp Pro Ser Phe Ala Ala Ile Asn	
120 125 130	
gcg cga gtg gca aac cag gag atc ggc aac ctg gag cag ttg gtg atc	547
Ala Arg Val Ala Asn Gln Glu Ile Gly Asn Leu Glu Gln Leu Val Ile	
135 140 145	
atc agc cgc gat cca gcg ccc gca ccg aag gac tac atc gca ggt tcc	595
Ile Ser Arg Asp Pro Ala Pro Ala Pro Lys Asp Tyr Ile Ala Gly Ser	
150 155 160 165	
ggt gga atc ttc cgc gat atg acc atc cac gat ctg gat atg gcg cgt	643
Gly Gly Ile Phe Arg Asp Met Thr Ile His Asp Leu Asp Met Ala Arg	
170 175 180	
ttc ttt gtg ccc aat atc gtg gaa gtg act gca acc ggc gcc aat gtt	691
Phe Phe Val Pro Asn Ile Val Glu Val Thr Ala Thr Gly Ala Asn Val	
185 190 195	
ttc agc cag gaa atc gcg gag ttc aat gac tac gac cag gtt atc gtc	739
Phe Ser Gln Glu Ile Ala Glu Phe Asn Asp Tyr Asp Gln Val Ile Val	
200 205 210	
acg ctt cgt ggc tca aag ggc gag ttg atc aac atc gtg aac tcc cgc	787
Thr Leu Arg Gly Ser Lys Gly Glu Leu Ile Asn Ile Val Asn Ser Arg	
215 220 225	
cac tgc tcc tac ggc tac gac cag cga ctt gag gct ttc ggc tct aag	835
His Cys Ser Tyr Gly Tyr Asp Gln Arg Leu Glu Ala Phe Gly Ser Lys	
230 235 240 245	
ggc atg ctc gcc gcc gac aac atc agg ccc acc acg gtg cgc aag cac	883
Gly Met Leu Ala Ala Asp Asn Ile Arg Pro Thr Thr Val Arg Lys His	
250 255 260	
aat gcg gaa agc acc gag cag gca gat ccg att ttc aac ttc ttc ctc	931
Asn Ala Glu Ser Thr Glu Gln Ala Asp Pro Ile Phe Asn Phe Phe Leu	
265 270 275	
gag cgc tac gac gcc gct tac aag gca gag ctc gca act ttt gct caa	979
Glu Arg Tyr Asp Ala Ala Tyr Lys Ala Glu Leu Ala Thr Phe Ala Gln	
280 285 290	
gga atc cgc gac ggc caa ggc ttc tca cca aac ttc gag gac ggc gtc	1027
Gly Ile Arg Asp Gly Gln Gly Phe Ser Pro Asn Phe Glu Asp Gly Val	
295 300 305	
atc gcc ctt gaa cta gcg aat gca tgc ctt gaa tca gct caa acc ggc	1075
Ile Ala Leu Glu Leu Ala Asn Ala Cys Leu Glu Ser Ala Gln Thr Gly	
310 315 320 325	
cgc acc gtc acc ctc aac cct gcc aac gtt tagtcaacgt ctagttaatg	1125
Arg Thr Val Thr Leu Asn Pro Ala Asn Val	
330 335	

cct

1128

<210> 300

<211> 335

<212> PRT

<213> Corynebacterium glutamicum

<400> 300

Met Thr Leu Arg Ile Ala Leu Phe Gly Ala Gly Arg Ile Gly His Val
 1 5 10 15

His Ala Ala Asn Ile Ala Ala Asn Pro Asp Leu Glu Leu Val Val Ile
 20 25 30

Ala Asp Pro Phe Ile Glu Gly Ala Gln Arg Leu Ala Glu Ala Asn Gly
 35 40 45

Ala Glu Ala Val Ala Ser Pro Asp Glu Val Phe Ala Arg Asp Asp Ile
 50 55 60

Asp Gly Ile Val Ile Gly Ser Pro Thr Ser Thr His Val Asp Leu Ile
 65 70 75 80

Thr Arg Ala Val Glu Arg Gly Ile Pro Ala Leu Cys Glu Lys Pro Ile
 85 90 95

Asp Leu Asp Ile Glu Met Val Arg Ala Cys Lys Glu Lys Ile Gly Asp
 100 105 110

Gly Ala Ser Lys Val Met Leu Gly Phe Asn Arg Arg Phe Asp Pro Ser
 115 120 125

Phe Ala Ala Ile Asn Ala Arg Val Ala Asn Gln Glu Ile Gly Asn Leu
 130 135 140

Glu Gln Leu Val Ile Ile Ser Arg Asp Pro Ala Pro Ala Pro Lys Asp
 145 150 155 160

Tyr Ile Ala Gly Ser Gly Gly Ile Phe Arg Asp Met Thr Ile His Asp
 165 170 175

Leu Asp Met Ala Arg Phe Phe Val Pro Asn Ile Val Glu Val Thr Ala
 180 185 190

Thr Gly Ala Asn Val Phe Ser Gln Glu Ile Ala Glu Phe Asn Asp Tyr
 195 200 205

Asp Gln Val Ile Val Thr Leu Arg Gly Ser Lys Gly Glu Leu Ile Asn
 210 215 220

Ile Val Asn Ser Arg His Cys Ser Tyr Gly Tyr Asp Gln Arg Leu Glu
 225 230 235 240

Ala Phe Gly Ser Lys Gly Met Leu Ala Ala Asp Asn Ile Arg Pro Thr
 245 250 255

Thr Val Arg Lys His Asn Ala Glu Ser Thr Glu Gln Ala Asp Pro Ile
 260 265 270

Phe Asn Phe Phe Leu Glu Arg Tyr Asp Ala Ala Tyr Lys Ala Glu Leu

275

280

285

Ala Thr Phe Ala Gln Gly Ile Arg Asp Gly Gln Gly Phe Ser Pro Asn
 290 295 300

Phe Glu Asp Gly Val Ile Ala Leu Glu Leu Ala Asn Ala Cys Leu Glu
 305 310 315 320

Ser Ala Gln Thr Gly Arg Thr Val Thr Leu Asn Pro Ala Asn Val
 325 330 335

<210> 301

<211> 1206

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(1183)

<223> RXA01633

<400> 301

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gtttagtcaa cgtctagtta atgcctaagg agaaaacctc atg aaa aac atc acc 115
 Met Lys Asn Ile Thr
 1 5

atc gga atg gtc ggc gtc ggc cgc att ggc cgc atg cac gtc gcc aac 163
 Ile Gly Met Val Gly Val Gly Arg Ile Gly Arg Met His Val Ala Asn
 10 15 20

atg ctt gcc gtt gct gaa act ttg aag gaa cgc gac ctc aac att gag 211
 Met Leu Ala Val Ala Glu Thr Leu Lys Glu Arg Asp Leu Asn Ile Glu
 25 30 35

atc gtg ctc gca gac gca atg ccc ggt ttt gcg gag cag gtg ggc gcg 259
 Ile Val Leu Ala Asp Ala Met Pro Gly Phe Ala Glu Gln Val Gly Ala
 40 45 50

gac atg ggc gtg aag gcg gcg gca agc gtc gat aag ctt att gag gac 307
 Asp Met Gly Val Lys Ala Ala Ala Ser Val Asp Lys Leu Ile Glu Asp
 55 60 65

ggg gtg gat gcc ctt ttc att gcc acc agc acc gct ggc cac gtc gat 355
 Gly Val Asp Ala Leu Phe Ile Ala Thr Ser Thr Ala Gly His Val Asp
 70 75 80 85

gtt ttg cgc aag ggc atc gcg gca aag ctg ccg atg ttc tgc gag aag 403
 Val Leu Arg Lys Gly Ile Ala Ala Lys Leu Pro Met Phe Cys Glu Lys
 90 95 100

ccg atc gcg tcg gat gtg cct gag tcg ctg aac atc atc cgc gaa att 451
 Pro Ile Ala Ser Asp Val Pro Glu Ser Leu Asn Ile Ile Arg Glu Ile
 105 110 115

gat gcg gct ggc gcg acg gtt cag gtc ggc cac cag cgc cgt ttt gac 499
 Asp Ala Ala Gly Ala Thr Val Gln Val Gly His Gln Arg Arg Phe Asp
 120 125 130

ctc ggt tac cag gaa gct aaa cga cgc cta gat gca ggc gac ctc ggc Leu Gly Tyr Gln Glu Ala Lys Arg Arg Leu Asp Ala Gly Asp Leu Gly 135 140 145	547
tgg ctt cat tcg ctc aag gcc gta tcg agc gat gcg ttt ccg cca ccg Trp Leu His Ser Leu Lys Ala Val Ser Ser Asp Ala Phe Pro Pro Pro 150 155 160 165	595
gtg tcc tac tgc gct acc tct ggt gga ctt ttc cgc gat gtg tcg ctg Val Ser Tyr Cys Ala Thr Ser Gly Gly Leu Phe Arg Asp Val Ser Leu 170 175 180	643
cac gat ttc gac atc att cgc tgg ctg acc ggc cag gat att gtc gag His Asp Phe Asp Ile Ile Arg Trp Leu Thr Gly Gln Asp Ile Val Glu 185 190 195	691
gtg tac gcc aag ggc agc aac aac ggc gac cca gaa atc ggc gca gtc Val Tyr Ala Lys Gly Ser Asn Asn Gly Asp Pro Glu Ile Gly Ala Val 200 205 210	739
ggt gac atc gat acc gga gcg gcc cta ctc acg ctt gcc gac ggc acc Gly Asp Ile Asp Thr Gly Ala Ala Leu Leu Thr Leu Ala Asp Gly Thr 215 220 225	787
ctc gcc acc gcc atc gcc act cgt tac aac ggt gca ggc cac gac gtt Leu Ala Thr Ala Ile Ala Thr Arg Tyr Asn Gly Ala Gly His Asp Val 230 235 240 245	835
cgc ctc gat gtt atg ggc tct aaa gat tcc acg atc gtt ggc ctg gat Arg Leu Asp Val Met Gly Ser Lys Asp Ser Thr Ile Val Gly Leu Asp 250 255 260	883
gaa aag tct gcg ttc gct tct gcg gag gag ggc atc gat ttc cca acc Glu Lys Ser Ala Phe Ala Ser Ala Glu Glu Gly Ile Asp Phe Pro Thr 265 270 275	931
ggc gaa tcg cac cca acg ttt gcc gag cgc ttc gcc gac gca tac aag Gly Glu Ser His Pro Thr Phe Ala Glu Arg Phe Ala Asp Ala Tyr Lys 280 285 290	979
aat gag tgc att gcg ttc gtg gag ttg atc ctg gga gag cgg gaa aac Asn Glu Cys Ile Ala Phe Val Glu Leu Ile Leu Gly Glu Arg Glu Asn 295 300 305	1027
cct tgt acc cct gca gac gct gtg gct gcg gcg att gtt gcc gat gca Pro Cys Thr Pro Ala Asp Ala Val Ala Ala Ala Ile Val Ala Asp Ala 310 315 320 325	1075
gct cag ctg tcg ctg gtc act ggc gag cca gtg aag att cct act gta Ala Gln Leu Ser Leu Val Thr Gly Glu Pro Val Lys Ile Pro Thr Val 330 335 340	1123
cgg gaa att ctt gaa ggt tct gcg cag cca gtt gag gtg cgt gcg ctg Arg Glu Ile Leu Glu Gly Ser Ala Gln Pro Val Glu Val Arg Ala Leu 345 350 355	1171
gtt cca tct gct taaaacctta ctgcttatct aaa Val Pro Ser Ala 360	1206

<210> 302
 <211> 361
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 302

Met Lys Asn Ile Thr Ile Gly Met Val Gly Val Gly Arg Ile Gly Arg
 1 5 10 15

Met His Val Ala Asn Met Leu Ala Val Ala Glu Thr Leu Lys Glu Arg
 20 25 30

Asp Leu Asn Ile Glu Ile Val Leu Ala Asp Ala Met Pro Gly Phe Ala
 35 40 45

Glu Gln Val Gly Ala Asp Met Gly Val Lys Ala Ala Ala Ser Val Asp
 50 55 60

Lys Leu Ile Glu Asp Gly Val Asp Ala Leu Phe Ile Ala Thr Ser Thr
 65 70 75 80

Ala Gly His Val Asp Val Leu Arg Lys Gly Ile Ala Ala Lys Leu Pro
 85 90 95

Met Phe Cys Glu Lys Pro Ile Ala Ser Asp Val Pro Glu Ser Leu Asn
 100 105 110

Ile Ile Arg Glu Ile Asp Ala Ala Gly Ala Thr Val Gln Val Gly His
 115 120 125

Gln Arg Arg Phe Asp Leu Gly Tyr Gln Glu Ala Lys Arg Arg Leu Asp
 130 135 140

Ala Gly Asp Leu Gly Trp Leu His Ser Leu Lys Ala Val Ser Ser Asp
 145 150 155 160

Ala Phe Pro Pro Pro Val Ser Tyr Cys Ala Thr Ser Gly Gly Leu Phe
 165 170 175

Arg Asp Val Ser Leu His Asp Phe Asp Ile Ile Arg Trp Leu Thr Gly
 180 185 190

Gln Asp Ile Val Glu Val Tyr Ala Lys Gly Ser Asn Asn Gly Asp Pro
 195 200 205

Glu Ile Gly Ala Val Gly Asp Ile Asp Thr Gly Ala Ala Leu Leu Thr
 210 215 220

Leu Ala Asp Gly Thr Leu Ala Thr Ala Ile Ala Thr Arg Tyr Asn Gly
 225 230 235 240

Ala Gly His Asp Val Arg Leu Asp Val Met Gly Ser Lys Asp Ser Thr
 245 250 255

Ile Val Gly Leu Asp Glu Lys Ser Ala Phe Ala Ser Ala Glu Glu Gly
 260 265 270

Ile Asp Phe Pro Thr Gly Glu Ser His Pro Thr Phe Ala Glu Arg Phe
 275 280 285

Ala Asp Ala Tyr Lys Asn Glu Cys Ile Ala Phe Val Glu Leu Ile Leu

290 295 300

Gly Glu Arg Glu Asn Pro Cys Thr Pro Ala Asp Ala Val Ala Ala Ala
305 310 315 320

Ile Val Ala Asp Ala Ala Gln Leu Ser Leu Val Thr Gly Glu Pro Val
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Lys Ile Pro Thr Val Arg Glu Ile Leu Glu Gly Ser Ala Gln Pro Val
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Glu Val Arg Ala Leu Val Pro Ser Ala
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<222> (101)..(1123)
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Met Thr Ile Arg Ile
1 5

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Gly Leu Val Gly Tyr Gly Val Gly Gly Arg Leu Phe His Thr Pro Tyr
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Ile Gln Ala Ser Thr His Cys Glu Leu Val Gly Val Val Ala Arg Ser
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Glu Gly Thr Lys Ala Ala Val Ala Glu Asp Leu Pro Asp Val Ala Ile
40 45 50

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Val Gly Ser Leu Thr Glu Leu Leu Glu Leu Gly Val Asp Ala Val Val
55 60 65

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Ile Ser Thr Pro Pro Ala Thr Arg Arg Glu Leu Ala Leu Glu Ala Ile
70 75 80 85

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Asn Ala Gly Val Ala Val Val Ala Asp Lys Pro Phe Ala Pro Ser Ala
90 95 100

gca gat gcc atg gaa ctt gtc gaa gcc gcc gaa aag gct gga gtg ctg 451
Ala Asp Ala Met Glu Leu Val Glu Ala Ala Glu Lys Ala Gly Val Leu
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ctc aac gtc ttc cac aac agg cgc aac gac acc cac att gtc acg gca 499

Leu Asn Val Phe His Asn Arg Arg Asn Asp Thr His Ile Val Thr Ala
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 Leu Gly Ile Gln Glu Glu Leu Gly Ala Met Arg Gly Leu Asp Leu Arg
 135 140 145
 cta gac ctg atc gaa cct gat tcc ttg gag gca ggt cct gaa ggt ggt 595
 Leu Asp Leu Ile Glu Pro Asp Ser Leu Glu Ala Gly Pro Glu Gly Gly
 150 155 160 165
 ttg ctg cgc gat ctg ggc tca cac gta gtc gat cag acc ctg gtt ctc 643
 Leu Leu Arg Asp Leu Gly Ser His Val Val Asp Gln Thr Leu Val Leu
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 Met Gly Pro Ala Thr Ser Val Thr Ala Gln Leu Gly Ser Ile Asp Leu
 185 190 195
 cca gaa ggc cca acc aac gca agg ttc cgc atc gtg ttg gaa cat gaa 739
 Pro Glu Gly Pro Thr Asn Ala Arg Phe Arg Ile Val Leu Glu His Glu
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 Ser Gly Ala Val Ser His Ile Ser Ala Ser Lys Ile Asp Arg Leu Glu
 215 220 225
 tcc tgg gaa atc cgc ttg gtg ggc gag cgc gcc tcc tac gta tcc aac 835
 Ser Trp Glu Ile Arg Leu Val Gly Glu Arg Gly Ser Tyr Val Ser Asn
 230 235 240 245
 tac acc gac gtg cag acc gtg gcg atc aaa cag gga ctt cga cca acc 883
 Tyr Thr Asp Val Gln Thr Val Ala Ile Lys Gln Gly Leu Arg Pro Thr
 250 255 260
 aat gac cgc gaa cac tgg ggc tac gaa tcg gag gag cgg tgg ggc acc 931
 Asn Asp Arg Glu His Trp Gly Tyr Glu Ser Glu Glu Arg Trp Gly Thr
 265 270 275
 ttg gtt acc gat gaa ggc tca aag gtg att cct tca gca caa ggc gat 979
 Leu Val Thr Asp Glu Gly Ser Lys Val Ile Pro Ser Ala Gln Gly Asp
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 tac acc cgc ttc tac gat gcc ttt gcc ttg gct gtg gaa aac ggt ggc 1027
 Tyr Thr Arg Phe Tyr Asp Ala Phe Ala Leu Ala Val Glu Asn Gly Gly
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 Ala Gly Pro Val Pro Ala Arg Glu Gly Val Ala Val Leu Lys Val Leu
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 gat gct gta gcc cag agc gct gcg gaa aaa cgc acc att gag ttg agc 1123
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<212> PRT

<213> Corynebacterium glutamicum

<400> 304

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Val Val Ala Arg Ser Glu Gly Thr Lys Ala Ala Val Ala Glu Asp Leu
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Pro Asp Val Ala Ile Val Gly Ser Leu Thr Glu Leu Leu Glu Leu Gly
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Val Asp Ala Val Val Ile Ser Thr Pro Pro Ala Thr Arg Arg Glu Leu
          65           70           75           80
Ala Leu Glu Ala Ile Asn Ala Gly Val Ala Val Val Ala Asp Lys Pro
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Phe Ala Pro Ser Ala Ala Asp Ala Met Glu Leu Val Glu Ala Ala Glu
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Lys Ala Gly Val Leu Leu Asn Val Phe His Asn Arg Arg Asn Asp Thr
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His Ile Val Thr Ala Leu Gly Ile Gln Glu Glu Leu Gly Ala Met Arg
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Gly Leu Asp Leu Arg Leu Asp Leu Ile Glu Pro Asp Ser Leu Glu Ala
          145          150          155          160
Gly Pro Glu Gly Gly Leu Leu Arg Asp Leu Gly Ser His Val Val Asp
          165          170          175
Gln Thr Leu Val Leu Met Gly Pro Ala Thr Ser Val Thr Ala Gln Leu
          180          185          190
Gly Ser Ile Asp Leu Pro Glu Gly Pro Thr Asn Ala Arg Phe Arg Ile
          195          200          205
Val Leu Glu His Glu Ser Gly Ala Val Ser His Ile Ser Ala Ser Lys
          210          215          220
Ile Asp Arg Leu Glu Ser Trp Glu Ile Arg Leu Val Gly Glu Arg Gly
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Ser Tyr Val Ser Asn Tyr Thr Asp Val Gln Thr Val Ala Ile Lys Gln
          245          250          255
Gly Leu Arg Pro Thr Asn Asp Arg Glu His Trp Gly Tyr Glu Ser Glu
          260          265          270
Glu Arg Trp Gly Thr Leu Val Thr Asp Glu Gly Ser Lys Val Ile Pro
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					Met	Ser	Asp	Gln	Lys								
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Ile	Val	Val	Gly	Leu	Leu	Gly	Ile	Thr	His	Pro	His	Ala	Ser	Ala	Arg		
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gtg	cgt	gcc	ctc	cgt	gaa	att	gat	ggg	gta	gag	gtc	gtc	gcc	gcc	gcg	211	
Val	Arg	Ala	Leu	Arg	Glu	Ile	Asp	Gly	Val	Glu	Val	Val	Ala	Ala	Ala		
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Asp	Thr	Asp	Ser	Arg	Leu	Gln	Tyr	Phe	Thr	Asp	Lys	Tyr	Asp	Val	Glu		
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ccc	cgc	gag	atc	gat	gac	gtc	ttg	aac	gac	gat	cgc	atc	aac	gcc	atc	307	
Pro	Arg	Glu	Ile	Asp	Asp	Val	Leu	Asn	Asp	Asp	Arg	Ile	Asn	Ala	Ile		
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Met	Val	His	Ser	Lys	Ser	Lys	Asp	Met	Val	Pro	His	Ala	Lys	Arg	Ala		
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ctc	gcg	gcc	gga	aaa	tcc	gtc	gtc	gtg	gag	aag	ccc	ggc	ggg	gga	aca	403	
Leu	Ala	Ala	Gly	Lys	Ser	Val	Val	Val	Glu	Lys	Pro	Gly	Gly	Gly	Thr		
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gtg	gcg	gat	ctt	gag	gag	ctc	ctg	gcc	ctc	aaa	gaa	gct	gcc	gat	cct	451	
Val	Ala	Asp	Leu	Glu	Glu	Leu	Leu	Ala	Leu	Lys	Glu	Ala	Ala	Asp	Pro		
				105					110					115			
cag	cga	atc	gtg	cag	gtc	ggg	tac	aac	gtc	cgc	ctg	tct	gaa	tcg	gtt	499	
Gln	Arg	Ile	Val	Gln	Val	Gly	Tyr	Asn	Val	Arg	Leu	Ser	Glu	Ser	Val		
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cag	aga	tta	aaa	gag	ctt	ctc	gac	gcc	ggc	ctc	atc	ggc	gaa	gtc	gtc	547	
Gln	Arg	Leu	Lys	Glu	Leu	Leu	Asp	Ala	Gly	Leu	Ile	Gly	Glu	Val	Val		
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 Ser Val Gln Ala Arg Gly Ala Ala Lys Val Gly Glu His Ile Thr Glu
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 His Leu Asn Gln Pro Ala Asp Met Gly Gly Val Leu Trp Ile Leu Gly
 170 175 180

 tgc cac atg ctc gat gca ttg gtg gaa gtc ttc gga gct cca gaa tcc 691
 Cys His Met Leu Asp Ala Leu Val Glu Val Phe Gly Ala Pro Glu Ser
 185 190 195

 gtg aac gcc cga gtg cat aag acc gca aaa ctc tct gac gac acc agc 739
 Val Asn Ala Arg Val His Lys Thr Ala Lys Leu Ser Asp Asp Thr Ser
 200 205 210

 cgc gaa gac tca gcc tcc gca ctg ctg tac tac cca gat ttc tcc gtc 787
 Arg Glu Asp Ser Ala Ser Ala Leu Leu Tyr Tyr Pro Asp Phe Ser Val
 215 220 225

 agc ttc agc ttc gac ggc cac gat gat ctg gaa tgg ttc gaa agc tcc 835
 Ser Phe Ser Phe Asp Gly His Asp Asp Leu Glu Trp Phe Glu Ser Ser
 230 235 240 245

 cga ctc acg gtc tat gga acc aag ggc atg atc gaa gcc gga atc ctc 883
 Arg Leu Thr Val Tyr Gly Thr Lys Gly Met Ile Glu Ala Gly Ile Leu
 250 255 260

 cct cag aca ctg cgc gta tac ctc aat gag tca cgc cag ggc tgg cca 931
 Pro Gln Thr Leu Arg Val Tyr Leu Asn Glu Ser Arg Gln Gly Trp Pro
 265 270 275

 cag ggt tgg acc gag tgg acc cag agc tac ttc acc cca ccg ttt gct 979
 Gln Gly Trp Thr Glu Trp Thr Gln Ser Tyr Phe Thr Pro Pro Phe Ala
 280 285 290

 cgc aca gaa tcc aac aaa ttc tca gag ctt cca gag cta gaa aac atc 1027
 Arg Thr Glu Ser Asn Lys Phe Ser Glu Leu Pro Glu Leu Glu Asn Ile
 295 300 305

 agc aac ttc cgc aca gaa atg cag ggg tgg gtg aat tcc att cgc act 1075
 Ser Asn Phe Arg Thr Glu Met Gln Gly Trp Val Asn Ser Ile Arg Thr
 310 315 320 325

 gga tcc cgc aat gtg gcg cca gtt gag gat gct ctc aca gtc gct cgc 1123
 Gly Ser Arg Asn Val Ala Pro Val Glu Asp Ala Leu Thr Val Ala Arg
 330 335 340

 att gtc agt gca tgc tac gaa tcc gac aac aac cag ggc att tcc gta 1171
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 Asn Ile

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<211> 359

<212> PRT

<213> Corynebacterium glutamicum

<400> 306

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 Val Val Ala Ala Asp Thr Asp Ser Arg Leu Gln Tyr Phe Thr Asp
 35 40 45
 Lys Tyr Asp Val Glu Pro Arg Glu Ile Asp Asp Val Leu Asn Asp Asp
 50 55 60
 Arg Ile Asn Ala Ile Met Val His Ser Lys Ser Lys Asp Met Val Pro
 65 70 75 80
 His Ala Lys Arg Ala Leu Ala Ala Gly Lys Ser Val Val Val Glu Lys
 85 90 95
 Pro Gly Gly Gly Thr Val Ala Asp Leu Glu Glu Leu Leu Ala Leu Lys
 100 105 110
 Glu Ala Ala Asp Pro Gln Arg Ile Val Gln Val Gly Tyr Asn Val Arg
 115 120 125
 Leu Ser Glu Ser Val Gln Arg Leu Lys Glu Leu Leu Asp Ala Gly Leu
 130 135 140
 Ile Gly Glu Val Val Ser Val Gln Ala Arg Gly Ala Ala Lys Val Gly
 145 150 155 160
 Glu His Ile Thr Glu His Leu Asn Gln Pro Ala Asp Met Gly Gly Val
 165 170 175
 Leu Trp Ile Leu Gly Cys His Met Leu Asp Ala Leu Val Glu Val Phe
 180 185 190
 Gly Ala Pro Glu Ser Val Asn Ala Arg Val His Lys Thr Ala Lys Leu
 195 200 205
 Ser Asp Asp Thr Ser Arg Glu Asp Ser Ala Ser Ala Leu Leu Tyr Tyr
 210 215 220
 Pro Asp Phe Ser Val Ser Phe Ser Phe Asp Gly His Asp Asp Leu Glu
 225 230 235 240
 Trp Phe Glu Ser Ser Arg Leu Thr Val Tyr Gly Thr Lys Gly Met Ile
 245 250 255
 Glu Ala Gly Ile Leu Pro Gln Thr Leu Arg Val Tyr Leu Asn Glu Ser
 260 265 270
 Arg Gln Gly Trp Pro Gln Gly Trp Thr Glu Trp Thr Gln Ser Tyr Phe
 275 280 285
 Thr Pro Pro Phe Ala Arg Thr Glu Ser Asn Lys Phe Ser Glu Leu Pro
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1 5																
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Ile Arg Val Ala Ile Ala Gly Val Gly Asn Cys Ala Thr Ser Leu Ile																
10 15 20																
cag ggt gtg gaa tat tac cga aat gcg gat cct tcc gaa act gtc ccg																211
Gln Gly Val Glu Tyr Tyr Arg Asn Ala Asp Pro Ser Glu Thr Val Pro																
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Gly Leu Met His Val Lys Phe Gly Asp Tyr His Val Gly Asp Ile Glu																
40 45 50																
ttc gtg gcc gcg ttc gac gtc gac gcc gaa aaa gta ggc atc gat ctt																307
Phe Val Ala Ala Phe Asp Val Asp Ala Glu Lys Val Gly Ile Asp Leu																
55 60 65																
gcc gac gcc acc gag gct tca caa aac tgc act atc aaa atc gcc gat																355
Ala Asp Ala Thr Glu Ala Ser Gln Asn Cys Thr Ile Lys Ile Ala Asp																
70 75 80 85																
gtc cca cag acc ggc atc aac gtg ctg cgt ggc ccg act ctc gac ggc																403
Val Pro Gln Thr Gly Ile Asn Val Leu Arg Gly Pro Thr Leu Asp Gly																
90 95 100																
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Leu Gly Asp His Tyr Arg Ala Thr Ile Asp Glu Ser Thr Ala Glu Pro																
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Val Asp Val Val Gln Ala Leu Ile Asp Ala Lys Ala Asp Val Leu Val																
120 125 130																

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Ser Tyr Leu Pro Val Gly Ser Glu Glu Ala Asp Lys Phe Tyr Ala Gln	
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Ala Ala Ile Asp Ala Gly Cys Ala Phe Val Asn Ala Leu Pro Val Phe	
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Ile Ala Ser Asp Pro Glu Trp Ala Lys Lys Phe Thr Asp Ala Gly Ile	
170 175 180	
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Pro Ile Val Gly Asp Asp Ile Lys Ser Gln Ile Gly Ala Thr Ile Thr	
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His Arg Val Leu Ala Arg Leu Phe Glu Glu Arg Gly Val Arg Val Asp	
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cgc acc atg cag ctc aac gtc ggc ggc aac atg gac ttc aaa aac atg	787
Arg Thr Met Gln Leu Asn Val Gly Gly Asn Met Asp Phe Lys Asn Met	
215 220 225	
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Leu Asp Arg Asn Arg Leu Glu Ser Lys Lys Val Ser Lys Thr Gln Ala	
230 235 240 245	
gtg acc tcc aac att cca gat ggt cca ctg tct gga aag gtg gaa gac	883
Val Thr Ser Asn Ile Pro Asp Gly Pro Leu Ser Gly Lys Val Glu Asp	
250 255 260	
cgc aac gtc cac atc gga cca tcc gac cac gtc caa tgg ctc gat gac	931
Arg Asn Val His Ile Gly Pro Ser Asp His Val Gln Trp Leu Asp Asp	
265 270 275	
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Arg Lys Trp Ala Tyr Val Arg Leu Glu Gly Thr Ala Phe Gly Gly Val	
280 285 290	
ccc ctc aac ctt gag tac aaa ctc gag gtg tgg gat tca ccc aac tct	1027
Pro Leu Asn Leu Glu Tyr Lys Leu Glu Val Trp Asp Ser Pro Asn Ser	
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Ala Gly Ile Ile Ile Asp Ala Val Arg Ala Ala Lys Ile Ala Leu Asp	
310 315 320 325	
cgc ggt atc ggc gga ccg atc atg cca gca agc tcc tac ctg atg aag	1123
Arg Gly Ile Gly Gly Pro Ile Met Pro Ala Ser Ser Tyr Leu Met Lys	
330 335 340	
tcc cca cct gag cag ctt cca gac gat gtt gct tgt gaa cgc cta gag	1171
Ser Pro Pro Glu Gln Leu Pro Asp Asp Val Ala Cys Glu Arg Leu Glu	
345 350 355	
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Ala Phe Ile Ile Glu Ala	
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<211> 363

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 308

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 35 40 45

Val Gly Asp Ile Glu Phe Val Ala Ala Phe Asp Val Asp Ala Glu Lys
 50 55 60

Val Gly Ile Asp Leu Ala Asp Ala Thr Glu Ala Ser Gln Asn Cys Thr
 65 70 75 80

Ile Lys Ile Ala Asp Val Pro Gln Thr Gly Ile Asn Val Leu Arg Gly
 85 90 95

Pro Thr Leu Asp Gly Leu Gly Asp His Tyr Arg Ala Thr Ile Asp Glu
 100 105 110

Ser Thr Ala Glu Pro Val Asp Val Val Gln Ala Leu Ile Asp Ala Lys
 115 120 125

Ala Asp Val Leu Val Ser Tyr Leu Pro Val Gly Ser Glu Glu Ala Asp
 130 135 140

Lys Phe Tyr Ala Gln Ala Ala Ile Asp Ala Gly Cys Ala Phe Val Asn
 145 150 155 160

Ala Leu Pro Val Phe Ile Ala Ser Asp Pro Glu Trp Ala Lys Lys Phe
 165 170 175

Thr Asp Ala Gly Ile Pro Ile Val Gly Asp Asp Ile Lys Ser Gln Ile
 180 185 190

Gly Ala Thr Ile Thr His Arg Val Leu Ala Arg Leu Phe Glu Glu Arg
 195 200 205

Gly Val Arg Val Asp Arg Thr Met Gln Leu Asn Val Gly Gly Asn Met
 210 215 220

Asp Phe Lys Asn Met Leu Asp Arg Asn Arg Leu Glu Ser Lys Lys Val
 225 230 235 240

Ser Lys Thr Gln Ala Val Thr Ser Asn Ile Pro Asp Gly Pro Leu Ser
 245 250 255

Gly Lys Val Glu Asp Arg Asn Val His Ile Gly Pro Ser Asp His Val
 260 265 270

Gln Trp Leu Asp Asp Arg Lys Trp Ala Tyr Val Arg Leu Glu Gly Thr
 275 280 285

Ala Phe Gly Gly Val Pro Leu Asn Leu Glu Tyr Lys Leu Glu Val Trp

290 295 300

Asp Ser Pro Asn Ser Ala Gly Ile Ile Ile Asp Ala Val Arg Ala Ala
305 310 315 320

Lys Ile Ala Leu Asp Arg Gly Ile Gly Gly Pro Ile Met Pro Ala Ser
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<222> (101)..(772)
<223> RXN03057

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1 5

ggt att aag ttc gtc gca gtg gtg gat aaa gat cta gag act gct gag 163
Gly Ile Lys Phe Val Ala Val Val Asp Lys Asp Leu Glu Thr Ala Glu
10 15 20

aaa ttt gcg acg gga ctt gga gct gct ggc gat tct tca gaa agc agc 211
Lys Phe Ala Thr Gly Leu Gly Ala Ala Gly Asp Ser Ser Glu Ser Ser
25 30 35

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Val Lys Ala His Gly Ser Leu Pro Ala Leu Phe Ser Lys Lys Lys Ile
40 45 50

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Asp Val Leu His Ile Thr Thr Pro His Asp Gln His Ile Gly Leu Ala
55 60 65

ctc gaa gcg cta cac cac ggt gta aat gtc atc ctg gaa aag ccg ttg 355
Leu Glu Ala Leu His His Gly Val Asn Val Ile Leu Glu Lys Pro Leu
70 75 80 85

gct aat gag ttg gac cag gcg cag cgt ctc atc gac tac ttg gat gaa 403
Ala Asn Glu Leu Asp Gln Ala Gln Arg Leu Ile Asp Tyr Leu Asp Glu
90 95 100

aac ccc gat ggt cca aag att gca gtg tgc tat cag aac cgt tac aac 451
Asn Pro Asp Gly Pro Lys Ile Ala Val Cys Tyr Gln Asn Arg Tyr Asn
105 110 115

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Val Ser Ser Gln Glu Leu Arg Arg Leu Leu Asp Ser Gly Asp Leu Gly
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 Ala Ile Asn Gly Ala Tyr Ser Ser Val Val Trp Thr Arg Thr Pro Gly
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 Tyr Tyr Thr Gln Lys Pro Trp Arg Gly Gln Gln Ala His Ser Gly Gly
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 ggc ctg ctg atg aac caa gca att cac acc ctg gat ctg ctg cag tgg 643
 Gly Leu Leu Met Asn Gln Ala Ile His Thr Leu Asp Leu Leu Gln Trp
 170 175 180
 ttc ctt gga aag gca aca gaa gtc aag ggc act gtc tcc acc gat aag 691
 Phe Leu Gly Lys Ala Thr Glu Val Lys Gly Thr Val Ser Thr Asp Lys
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 tat gcc gat gtc atc gat gtt gaa gac acc gca cac gca tac atc ggt 739
 Tyr Ala Asp Val Ile Asp Val Glu Asp Thr Ala His Ala Tyr Ile Gly
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 1 5 10 15
 Leu Glu Thr Ala Glu Lys Phe Ala Thr Gly Leu Gly Ala Ala Gly Asp
 20 25 30
 Ser Ser Glu Ser Ser Val Lys Ala His Gly Ser Leu Pro Ala Leu Phe
 35 40 45
 Ser Lys Lys Lys Ile Asp Val Leu His Ile Thr Thr Pro His Asp Gln
 50 55 60
 His Ile Gly Leu Ala Leu Glu Ala Leu His His Gly Val Asn Val Ile
 65 70 75 80
 Leu Glu Lys Pro Leu Ala Asn Glu Leu Asp Gln Ala Gln Arg Leu Ile
 85 90 95
 Asp Tyr Leu Asp Glu Asn Pro Asp Gly Pro Lys Ile Ala Val Cys Tyr
 100 105 110
 Gln Asn Arg Tyr Asn Val Ser Ser Gln Glu Leu Arg Arg Leu Leu Asp
 115 120 125
 Ser Gly Asp Leu Gly Ala Ile Asn Gly Ala Tyr Ser Ser Val Val Trp

130	135	140
Thr Arg Thr Pro Gly Tyr Tyr Thr Gln Lys Pro Trp Arg Gly Gln Gln		
145	150	155 160
Ala His Ser Gly Gly Gly Leu Leu Met Asn Gln Ala Ile His Thr Leu		
	165	170 175
Asp Leu Leu Gln Trp Phe Leu Gly Lys Ala Thr Glu Val Lys Gly Thr		
	180	185 190
Val Ser Thr Asp Lys Tyr Ala Asp Val Ile Asp Val Glu Asp Thr Ala		
	195	200 205
His Ala Tyr Ile Gly His Glu Ser Gly Val His Thr Ser Glu Val Ser		
	210	215 220

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 <211> 795
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
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 <222> (101)..(772)
 <223> FRXA02902

<400> 311

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 Leu Ala Ser Asp Leu
 1 5

ggt att aag ttc gtc gca gtg gtg gat aaa gat cta gag act gct gag 163
 Gly Ile Lys Phe Val Ala Val Val Asp Lys Asp Leu Glu Thr Ala Glu
 10 15 20

aaa ttt gcg acg gga ctt gga gct gct ggc gat tct tca gaa agc agc 211
 Lys Phe Ala Thr Gly Leu Gly Ala Ala Gly Asp Ser Ser Glu Ser Ser
 25 30 35

gtc aag gcc cac ggc agc ctg ccg gct ttg ttc tcc aaa aag aag atc 259
 Val Lys Ala His Gly Ser Leu Pro Ala Leu Phe Ser Lys Lys Lys Ile
 40 45 50

gat gtt cta cac atc acc acc ccc cac gac caa cac att ggt ttg gct 307
 Asp Val Leu His Ile Thr Thr Pro His Asp Gln His Ile Gly Leu Ala
 55 60 65

ctc gaa gcg cta cac cac ggt gta aat gtc atc ctg gaa aag ccg ttg 355
 Leu Glu Ala Leu His His Gly Val Asn Val Ile Leu Glu Lys Pro Leu
 70 75 80 85

gct aat gag ttg gac cag gcg cag cgt ctc atc gac tac ttg gat gaa 403
 Ala Asn Glu Leu Asp Gln Ala Gln Arg Leu Ile Asp Tyr Leu Asp Glu
 90 95 100

aac ccc gat ggt cca aag att gca gtg tgc tat cag aac cgt tac aac 451
 Asn Pro Asp Gly Pro Lys Ile Ala Val Cys Tyr Gln Asn Arg Tyr Asn
 105 110 115

gtt tcc tcc cag gaa ctg cgt cgt ctg ctc gat tca ggt gac ctc ggt 499
 Val Ser Ser Gln Glu Leu Arg Arg Leu Leu Asp Ser Gly Asp Leu Gly
 120 125 130

gcc atc aat ggt gca tat tcc tct gtg gtg tgg acc cgc acc cca ggc 547
 Ala Ile Asn Gly Ala Tyr Ser Ser Val Val Trp Thr Arg Thr Pro Gly
 135 140 145

tac tac acc cag aaa cct tgg cgt ggc cag caa gca cac tcc ggt ggt 595
 Tyr Tyr Thr Gln Lys Pro Trp Arg Gly Gln Gln Ala His Ser Gly Gly
 150 155 160 165

ggc ctg ctg atg aac caa gca att cac acc ctg gat ctg ctg cag tgg 643
 Gly Leu Leu Met Asn Gln Ala Ile His Thr Leu Asp Leu Leu Gln Trp
 170 175 180

ttc ctt gga aag gca aca gaa gtc aag ggc act gtc tcc acc gat aag 691
 Phe Leu Gly Lys Ala Thr Glu Val Lys Gly Thr Val Ser Thr Asp Lys
 185 190 195

tat gcc gat gtc atc gat gtt gaa gac acc gca cac gca tac atc ggt 739
 Tyr Ala Asp Val Ile Asp Val Glu Asp Thr Ala His Ala Tyr Ile Gly
 200 205 210

cac gag tcc gga gtc cac acc agt gaa gtg agt tgaaccatgc tattggtgat 792
 His Glu Ser Gly Val His Thr Ser Glu Val Ser
 215 220

aca 795

<210> 312
 <211> 224
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 312
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Leu Glu Thr Ala Glu Lys Phe Ala Thr Gly Leu Gly Ala Ala Gly Asp
 20 25 30

Ser Ser Glu Ser Ser Val Lys Ala His Gly Ser Leu Pro Ala Leu Phe
 35 40 45

Ser Lys Lys Lys Ile Asp Val Leu His Ile Thr Thr Pro His Asp Gln
 50 55 60

His Ile Gly Leu Ala Leu Glu Ala Leu His His Gly Val Asn Val Ile
 65 70 75 80

Leu Glu Lys Pro Leu Ala Asn Glu Leu Asp Gln Ala Gln Arg Leu Ile
 85 90 95

Asp Tyr Leu Asp Glu Asn Pro Asp Gly Pro Lys Ile Ala Val Cys Tyr

100					105					110					
Gln	Asn	Arg	Tyr	Asn	Val	Ser	Ser	Gln	Glu	Leu	Arg	Arg	Leu	Leu	Asp
	115						120					125			
Ser	Gly	Asp	Leu	Gly	Ala	Ile	Asn	Gly	Ala	Tyr	Ser	Ser	Val	Val	Trp
	130					135					140				
Thr	Arg	Thr	Pro	Gly	Tyr	Tyr	Thr	Gln	Lys	Pro	Trp	Arg	Gly	Gln	Gln
145					150					155					160
Ala	His	Ser	Gly	Gly	Gly	Leu	Leu	Met	Asn	Gln	Ala	Ile	His	Thr	Leu
			165					170					175		
Asp	Leu	Leu	Gln	Trp	Phe	Leu	Gly	Lys	Ala	Thr	Glu	Val	Lys	Gly	Thr
	180							185					190		
Val	Ser	Thr	Asp	Lys	Tyr	Ala	Asp	Val	Ile	Asp	Val	Glu	Asp	Thr	Ala
	195						200					205			
His	Ala	Tyr	Ile	Gly	His	Glu	Ser	Gly	Val	His	Thr	Ser	Glu	Val	Ser
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 <212> DNA
 <213> Corynebacterium glutamicum

<220>
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 <222> (101)..(808)
 <223> RXA00251

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 acatggggttt tatacagaaa attcatacga aaggttgatc atg aag aag aag att 115
 Met Lys Lys Lys Ile
 1 5
 gcg gtc gtt acc gga gcg acc gga ggc atg gga att gag atc gtc aaa 163
 Ala Val Val Thr Gly Ala Thr Gly Gly Met Gly Ile Glu Ile Val Lys
 10 15 20
 gac ctc tcc cgc gac cac att gtc tac gcc ttg ggc cga aat cca gag 211
 Asp Leu Ser Arg Asp His Ile Val Tyr Ala Leu Gly Arg Asn Pro Glu
 25 30 35
 cat ctg gca gct ctc gca gag atc gag gga gta gag cct atc gag tcc 259
 His Leu Ala Ala Leu Ala Glu Ile Glu Gly Val Glu Pro Ile Glu Ser
 40 45 50
 gat atc gtg aag gaa gtg ttg gaa gag gga ggc gtc gac aag cta aaa 307
 Asp Ile Val Lys Glu Val Leu Glu Glu Gly Gly Val Asp Lys Leu Lys
 55 60 65
 aac ctc gac cac gtg gat acg ctg gtg cac gcc gcg gcg gtg gcg cgt 355

Asn Leu Asp His Val Asp Thr Leu Val His Ala Ala Ala Val Ala Arg
 70 75 80 85
 gac acg acc atc gaa gcc ggc agt gtg gcc gaa tgg cac gca cac ctt 403
 Asp Thr Thr Ile Glu Ala Gly Ser Val Ala Glu Trp His Ala His Leu
 90 95 100
 gat ctc aac gtc att gtc ccg gcc gag ttg agt cgc caa ctc ttg ccc 451
 Asp Leu Asn Val Ile Val Pro Ala Glu Leu Ser Arg Gln Leu Leu Pro
 105 110 115
 gcc ctc cgc gcg gca tcc ggc tgc gtc atc tac atc aac tcc ggc gcc 499
 Ala Leu Arg Ala Ala Ser Gly Cys Val Ile Tyr Ile Asn Ser Gly Ala
 120 125 130
 ggc aac gga cca cac ccc ggc aac acc atc tac gcc gcc agc aaa cac 547
 Gly Asn Gly Pro His Pro Gly Asn Thr Ile Tyr Ala Ala Ser Lys His
 135 140 145
 gcc ctc cgc gga ctc gcc gac gcc ttc cgc aaa gaa gaa gcc aac aac 595
 Ala Leu Arg Gly Leu Ala Asp Ala Phe Arg Lys Glu Glu Ala Asn Asn
 150 155 160 165
 ggc atc cgc gtc agc act gtc agc ccc ggc ccc acc aac acc ccc atg 643
 Gly Ile Arg Val Ser Thr Val Ser Pro Gly Pro Thr Asn Thr Pro Met
 170 175 180
 ctg caa ggc ctc atg gac tca caa ggc acc aac ttc cgc cca gag atc 691
 Leu Gln Gly Leu Met Asp Ser Gln Gly Thr Asn Phe Arg Pro Glu Ile
 185 190 195
 tac atc gaa cca aaa gaa atc gcc aac gca atc aga ttc gtg att gac 739
 Tyr Ile Glu Pro Lys Glu Ile Ala Asn Ala Ile Arg Phe Val Ile Asp
 200 205 210
 gct ggc gaa acc acc cag atc acc aac gtg gac gta cga cca cgt atc 787
 Ala Gly Glu Thr Thr Gln Ile Thr Asn Val Asp Val Arg Pro Arg Ile
 215 220 225
 gaa ctg gcg gac cgg aaa gat tagttctgagg gggcttcctg ggc 831
 Glu Leu Ala Asp Arg Lys Asp
 230 235

<210> 314

<211> 236

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 314

Met Lys Lys Lys Ile Ala Val Val Thr Gly Ala Thr Gly Gly Met Gly
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 Ile Glu Ile Val Lys Asp Leu Ser Arg Asp His Ile Val Tyr Ala Leu
 20 25 30
 Gly Arg Asn Pro Glu His Leu Ala Ala Leu Ala Glu Ile Glu Gly Val
 35 40 45
 Glu Pro Ile Glu Ser Asp Ile Val Lys Glu Val Leu Glu Glu Gly Gly
 50 55 60

Val Asp Lys Leu Lys Asn Leu Asp His Val Asp Thr Leu Val His Ala
 65 70 75 80
 Ala Ala Val Ala Arg Asp Thr Thr Ile Glu Ala Gly Ser Val Ala Glu
 85 90 95
 Trp His Ala His Leu Asp Leu Asn Val Ile Val Pro Ala Glu Leu Ser
 100 105 110
 Arg Gln Leu Leu Pro Ala Leu Arg Ala Ala Ser Gly Cys Val Ile Tyr
 115 120 125
 Ile Asn Ser Gly Ala Gly Asn Gly Pro His Pro Gly Asn Thr Ile Tyr
 130 135 140
 Ala Ala Ser Lys His Ala Leu Arg Gly Leu Ala Asp Ala Phe Arg Lys
 145 150 155 160
 Glu Glu Ala Asn Asn Gly Ile Arg Val Ser Thr Val Ser Pro Gly Pro
 165 170 175
 Thr Asn Thr Pro Met Leu Gln Gly Leu Met Asp Ser Gln Gly Thr Asn
 180 185 190
 Phe Arg Pro Glu Ile Tyr Ile Glu Pro Lys Glu Ile Ala Asn Ala Ile
 195 200 205
 Arg Phe Val Ile Asp Ala Gly Glu Thr Thr Gln Ile Thr Asn Val Asp
 210 215 220
 Val Arg Pro Arg Ile Glu Leu Ala Asp Arg Lys Asp
 225 230 235

<210> 315
 <211> 1008
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(985)
 <223> RXN02654

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 gaggtacggt agttcgttcg aggacaacgt cgagaaaggc atg att tca ttg cta 115
 Met Ile Ser Leu Leu
 1 5
 aat gat cca cgt acg cta ttc ccg aaa gtc gat ccc cca aag caa agc 163
 Asn Asp Pro Arg Thr Leu Phe Pro Lys Val Asp Pro Pro Lys Gln Ser
 10 15 20
 cag ccg gaa cca ggc cta gat ata aaa ctt tcc ccc caa gcc gat att 211
 Gln Pro Glu Pro Gly Leu Asp Ile Lys Leu Ser Pro Gln Ala Asp Ile
 25 30 35
 ggt ctc tcc agc tat caa gga agt gga agg ctt aag ggc cgc aag gct 259

Gly	Leu	Ser	Ser	Tyr	Gln	Gly	Ser	Gly	Arg	Leu	Lys	Gly	Arg	Lys	Ala		
		40					45					50					
ctt	att	act	ggt	ggc	gat	tct	ggg	att	gga	gct	gcc	gta	gca	atc	gct	307	
Leu	Ile	Thr	Gly	Gly	Asp	Ser	Gly	Ile	Gly	Ala	Ala	Val	Ala	Ile	Ala		
	55					60					65						
tat	gct	cgc	gag	ggg	gca	gat	gtt	gcg	atc	gct	tac	ttg	ccc	gaa	gaa	355	
Tyr	Ala	Arg	Glu	Gly	Ala	Asp	Val	Ala	Ile	Ala	Tyr	Leu	Pro	Glu	Glu		
70					75				80						85		
caa	gcc	gat	gct	gac	aga	gtg	ctc	caa	gca	atc	gag	gaa	aca	ggt	caa	403	
Gln	Ala	Asp	Ala	Asp	Arg	Val	Leu	Gln	Ala	Ile	Glu	Glu	Thr	Gly	Gln		
				90					95					100			
aaa	gct	ttt	tct	ttc	cct	ggt	gat	ctc	cgt	gat	cca	gaa	tac	tgt	cgc	451	
Lys	Ala	Phe	Ser	Phe	Pro	Gly	Asp	Leu	Arg	Asp	Pro	Glu	Tyr	Cys	Arg		
			105					110					115				
tcg	ctg	gtc	caa	gag	acg	gtg	aac	gct	tta	ggt	ggc	cta	gac	atc	ttg	499	
Ser	Leu	Val	Gln	Glu	Thr	Val	Asn	Ala	Leu	Gly	Gly	Leu	Asp	Ile	Leu		
		120					125					130					
gtc	aac	aac	gcg	tca	cgt	cag	gtg	tgg	gca	cct	ggt	ttg	acc	gaa	att	547	
Val	Asn	Asn	Ala	Ser	Arg	Gln	Val	Trp	Ala	Pro	Gly	Leu	Thr	Glu	Ile		
	135					140					145						
acc	gac	gaa	aac	ttc	gac	cag	act	ttg	cag	gtt	aac	ctc	tat	ggt	agt	595	
Thr	Asp	Glu	Asn	Phe	Asp	Gln	Thr	Leu	Gln	Val	Asn	Leu	Tyr	Gly	Ser		
150					155				160					165			
ttt	cgg	gtt	acc	aaa	gca	gct	ata	cct	cat	ctg	aag	ccc	gga	tca	tcg	643	
Phe	Arg	Val	Thr	Lys	Ala	Ala	Ile	Pro	His	Leu	Lys	Pro	Gly	Ser	Ser		
				170					175					180			
ata	atc	ttt	aca	tcg	tcc	att	cag	gcg	tac	caa	cct	tcg	gaa	acc	ctc	691	
Ile	Ile	Phe	Thr	Ser	Ser	Ile	Gln	Ala	Tyr	Gln	Pro	Ser	Glu	Thr	Leu		
			185					190					195				
ttg	gat	tac	gcc	atg	act	aag	gcg	gca	ttg	aac	aat	ttg	tca	aag	ggc	739	
Leu	Asp	Tyr	Ala	Met	Thr	Lys	Ala	Ala	Leu	Asn	Asn	Leu	Ser	Lys	Gly		
		200					205					210					
ttg	gca	agt	agt	ctg	ata	ggc	gat	ggc	att	cgg	gta	aat	tct	gta	gcc	787	
Leu	Ala	Ser	Ser	Leu	Ile	Gly	Asp	Gly	Ile	Arg	Val	Asn	Ser	Val	Ala		
	215					220				225							
cca	ggt	cct	ttc	tgg	acg	ccg	ttg	caa	ccc	agc	cat	ggt	cag	cca	caa	835	
Pro	Gly	Pro	Phe	Trp	Thr	Pro	Leu	Gln	Pro	Ser	His	Gly	Gln	Pro	Gln		
230					235					240					245		
gag	aaa	ata	gaa	gga	ttt	ggc	cag	cac	gct	ccg	att	gga	aga	gcg	ggt	883	
Glu	Lys	Ile	Glu	Gly	Phe	Gly	Gln	His	Ala	Pro	Ile	Gly	Arg	Ala	Gly		
				250					255					260			
cac	cct	gtt	gag	ttg	gca	ggt	gcg	tac	gtt	ttt	ctc	gct	tct	gac	gaa	931	
His	Pro	Val	Glu	Leu	Ala	Gly	Ala	Tyr	Val	Phe	Leu	Ala	Ser	Asp	Glu		
			265					270					275				
gcc	agc	tat	gtg	gta	gga	gaa	acc	ctg	gga	gtc	aca	ggt	ggg	acg	ccc	979	
Ala	Ser	Tyr	Val	Val	Gly	Glu	Thr	Leu	Gly	Val	Thr	Gly	Gly	Thr	Pro		

280 285 290 1008

acc cca tagtcggtac aagcgggaatc act
 Thr Pro
 295

<210> 316
 <211> 295
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 316
 Met Ile Ser Leu Leu Asn Asp Pro Arg Thr Leu Phe Pro Lys Val Asp
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 Pro Pro Lys Gln Ser Gln Pro Glu Pro Gly Leu Asp Ile Lys Leu Ser
 20 25 30
 Pro Gln Ala Asp Ile Gly Leu Ser Ser Tyr Gln Gly Ser Gly Arg Leu
 35 40 45
 Lys Gly Arg Lys Ala Leu Ile Thr Gly Gly Asp Ser Gly Ile Gly Ala
 50 55 60
 Ala Val Ala Ile Ala Tyr Ala Arg Glu Gly Ala Asp Val Ala Ile Ala
 65 70 75 80
 Tyr Leu Pro Glu Glu Gln Ala Asp Ala Asp Arg Val Leu Gln Ala Ile
 85 90 95
 Glu Glu Thr Gly Gln Lys Ala Phe Ser Phe Pro Gly Asp Leu Arg Asp
 100 105 110
 Pro Glu Tyr Cys Arg Ser Leu Val Gln Glu Thr Val Asn Ala Leu Gly
 115 120 125
 Gly Leu Asp Ile Leu Val Asn Asn Ala Ser Arg Gln Val Trp Ala Pro
 130 135 140
 Gly Leu Thr Glu Ile Thr Asp Glu Asn Phe Asp Gln Thr Leu Gln Val
 145 150 155 160
 Asn Leu Tyr Gly Ser Phe Arg Val Thr Lys Ala Ala Ile Pro His Leu
 165 170 175
 Lys Pro Gly Ser Ser Ile Ile Phe Thr Ser Ser Ile Gln Ala Tyr Gln
 180 185 190
 Pro Ser Glu Thr Leu Leu Asp Tyr Ala Met Thr Lys Ala Ala Leu Asn
 195 200 205
 Asn Leu Ser Lys Gly Leu Ala Ser Ser Leu Ile Gly Asp Gly Ile Arg
 210 215 220
 Val Asn Ser Val Ala Pro Gly Pro Phe Trp Thr Pro Leu Gln Pro Ser
 225 230 235 240
 His Gly Gln Pro Gln Glu Lys Ile Glu Gly Phe Gly Gln His Ala Pro
 245 250 255

Ile Gly Arg Ala Gly His Pro Val Glu Leu Ala Gly Ala Tyr Val Phe
 260 265 270

Leu Ala Ser Asp Glu Ala Ser Tyr Val Val Gly Glu Thr Leu Gly Val
 275 280 285

Thr Gly Gly Thr Pro Thr Pro
 290 295

<210> 317

<211> 1008

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(985)

<223> FRXA02654

<400> 317

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gaggtacggt agttcgttcg aggacaacgt cgagaaaggc atg att tca ttg cta 115
 Met Ile Ser Leu Leu
 1 5

aat gat cca cgt acg cta ttc ccg aaa gtc gat ccc cca aag caa agc 163
 Asn Asp Pro Arg Thr Leu Phe Pro Lys Val Asp Pro Pro Lys Gln Ser
 10 15 20

cag ccg gaa cca ggc cta gat ata aaa ctt tcc ccc caa gcc gat att 211
 Gln Pro Glu Pro Gly Leu Asp Ile Lys Leu Ser Pro Gln Ala Asp Ile
 25 30 35

ggt ctc tcc agc tat caa gga agt gga agg ctt aag ggc cgc aag gct 259
 Gly Leu Ser Ser Tyr Gln Gly Ser Gly Arg Leu Lys Gly Arg Lys Ala
 40 45 50

ctt att act ggt ggc gat tct ggg att gga gct gcc gta gca atc gct 307
 Leu Ile Thr Gly Gly Asp Ser Gly Ile Gly Ala Val Ala Ile Ala
 55 60 65

tat gct cgc gag ggg gca gat gtt gcg atc gct tac ttg ccc gaa gaa 355
 Tyr Ala Arg Glu Gly Ala Asp Val Ala Ile Ala Tyr Leu Pro Glu Glu
 70 75 80 85

caa gcc gat gct gac aga gtg ctc caa gca atc gag gaa aca ggt caa 403
 Gln Ala Asp Ala Asp Arg Val Leu Gln Ala Ile Glu Glu Thr Gly Gln
 90 95 100

aaa gct ttt tct ttc cct ggt gat ctc cgt gat cca gaa tac tgt cgc 451
 Lys Ala Phe Ser Phe Pro Gly Asp Leu Arg Asp Pro Glu Tyr Cys Arg
 105 110 115

tcg ctg gtc caa gag acg gtg aac gct tta ggt ggc cta gac atc ttg 499
 Ser Leu Val Gln Glu Thr Val Asn Ala Leu Gly Gly Leu Asp Ile Leu
 120 125 130

gtc aac aac gcg tca cgt cag gtg tgg gca cct ggt ttg acc gaa att 547
 Val Asn Asn Ala Ser Arg Gln Val Trp Ala Pro Gly Leu Thr Glu Ile

135	140	145	
acc gac gaa aac ttc gac cag act ttg cag gtt aac ctc tat ggt agt			595
Thr Asp Glu Asn Phe Asp Gln Thr Leu Gln Val Asn Leu Tyr Gly Ser			
150	155	160	165
ttt cgg gtt acc aaa gca gct ata cct cat ctg aag ccc gga tca tcg			643
Phe Arg Val Thr Lys Ala Ala Ile Pro His Leu Lys Pro Gly Ser Ser			
	170	175	180
ata atc ttt aca tcg tcc att cag gcg tac caa cct tcg gaa acc ctc			691
Ile Ile Phe Thr Ser Ser Ile Gln Ala Tyr Gln Pro Ser Glu Thr Leu			
	185	190	195
ttg gat tac gcc atg act aag gcg gca ttg aac aat ttg tca aag ggc			739
Leu Asp Tyr Ala Met Thr Lys Ala Ala Leu Asn Asn Leu Ser Lys Gly			
	200	205	210
ttg gca agt agt ctg ata ggc gat ggc att cgg gta aat tct gta gcc			787
Leu Ala Ser Ser Leu Ile Gly Asp Gly Ile Arg Val Asn Ser Val Ala			
	215	220	225
cca ggt cct ttc tgg acg ccg ttg caa ccc agc cat ggt cag cca caa			835
Pro Gly Pro Phe Trp Thr Pro Leu Gln Pro Ser His Gly Gln Pro Gln			
	230	235	240
gag aaa ata gaa gga ttt ggc cag cac gct ccg att gga aga gcg ggt			883
Glu Lys Ile Glu Gly Phe Gly Gln His Ala Pro Ile Gly Arg Ala Gly			
	250	255	260
cac cct gtt gag ttg gca ggt gcg tac gtt ttt ctc gct tct gac gaa			931
His Pro Val Glu Leu Ala Gly Ala Tyr Val Phe Leu Ala Ser Asp Glu			
	265	270	275
gcc agc tat gtg gta gga gaa acc ctg gga gtc aca ggt ggg acg ccc			979
Ala Ser Tyr Val Val Gly Glu Thr Leu Gly Val Thr Gly Gly Thr Pro			
	280	285	290
acc cca tagtcggtac aagcgggaatc act			1008
Thr Pro			
295			

<210> 318

<211> 295

<212> PRT

<213> Corynebacterium glutamicum

<400> 318

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Pro	Pro	Lys	Gln	Ser	Gln	Pro	Glu	Pro	Gly	Leu	Asp	Ile	Lys	Leu	Ser
			20					25					30		

Pro	Gln	Ala	Asp	Ile	Gly	Leu	Ser	Ser	Tyr	Gln	Gly	Ser	Gly	Arg	Leu
		35				40						45			

Lys	Gly	Arg	Lys	Ala	Leu	Ile	Thr	Gly	Gly	Asp	Ser	Gly	Ile	Gly	Ala
	50					55					60				

Ala Val Ala Ile Ala Tyr Ala Arg Glu Gly Ala Asp Val Ala Ile Ala
 65 70 75 80
 Tyr Leu Pro Glu Glu Gln Ala Asp Ala Asp Arg Val Leu Gln Ala Ile
 85 90 95
 Glu Glu Thr Gly Gln Lys Ala Phe Ser Phe Pro Gly Asp Leu Arg Asp
 100 105 110
 Pro Glu Tyr Cys Arg Ser Leu Val Gln Glu Thr Val Asn Ala Leu Gly
 115 120 125
 Gly Leu Asp Ile Leu Val Asn Asn Ala Ser Arg Gln Val Trp Ala Pro
 130 135 140
 Gly Leu Thr Glu Ile Thr Asp Glu Asn Phe Asp Gln Thr Leu Gln Val
 145 150 155 160
 Asn Leu Tyr Gly Ser Phe Arg Val Thr Lys Ala Ala Ile Pro His Leu
 165 170 175
 Lys Pro Gly Ser Ser Ile Ile Phe Thr Ser Ser Ile Gln Ala Tyr Gln
 180 185 190
 Pro Ser Glu Thr Leu Leu Asp Tyr Ala Met Thr Lys Ala Ala Leu Asn
 195 200 205
 Asn Leu Ser Lys Gly Leu Ala Ser Ser Leu Ile Gly Asp Gly Ile Arg
 210 215 220
 Val Asn Ser Val Ala Pro Gly Pro Phe Trp Thr Pro Leu Gln Pro Ser
 225 230 235 240
 His Gly Gln Pro Gln Glu Lys Ile Glu Gly Phe Gly Gln His Ala Pro
 245 250 255
 Ile Gly Arg Ala Gly His Pro Val Glu Leu Ala Gly Ala Tyr Val Phe
 260 265 270
 Leu Ala Ser Asp Glu Ala Ser Tyr Val Val Gly Glu Thr Leu Gly Val
 275 280 285
 Thr Gly Gly Thr Pro Thr Pro
 290 295

<210> 319

<211> 1605

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(1582)

<223> RXN01049

<400> 319

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 aagaatattc tttattagtc agacctttaa aggaaacctt atg gga tca att cca 115
 Met Gly Ser Ile Pro

	1	5	
aca atg tcc atc cct ttt gat gac tca cgt gga cct tat gtc ctt gct			163
Thr Met Ser Ile Pro Phe Asp Asp Ser Arg Gly Pro Tyr Val Leu Ala	10	20	
atg gat att ggt tcc act gca tca cga ggt gga ctt tat gat gct tcc			211
Met Asp Ile Gly Ser Thr Ala Ser Arg Gly Gly Leu Tyr Asp Ala Ser	25	35	
ggc tgc cca atc aaa ggc acc aag cag cgc gaa tcc cat gaa ttc acc			259
Gly Cys Pro Ile Lys Gly Thr Lys Gln Arg Glu Ser His Glu Phe Thr	40	50	
acc ggt gag ggc gtt tcc acc att gat gct gac cag gtg gtt tcg gag			307
Thr Gly Glu Gly Val Ser Thr Ile Asp Ala Asp Gln Val Val Ser Glu	55	65	
atc acc tca gtt att aat ggc att ttg aac gcg gct gat cat cac aac			355
Ile Thr Ser Val Ile Asn Gly Ile Leu Asn Ala Ala Asp His His Asn	70	85	
atc aaa gat cag atc gcc gct gtc gcg cta gat tct ttt gca tcc tca			403
Ile Lys Asp Gln Ile Ala Ala Val Ala Leu Asp Ser Phe Ala Ser Ser	90	100	
tta atc ttg gtc gat ggt gaa ggc aat gcg ctc acc ccg tgc att acc			451
Leu Ile Leu Val Asp Gly Glu Gly Asn Ala Leu Thr Pro Cys Ile Thr	105	115	
tac gcg gat tct cgt tct gca cag tat gtg gag cag ctg cgc gcg gaa			499
Tyr Ala Asp Ser Arg Ser Ala Gln Tyr Val Glu Gln Leu Arg Ala Glu	120	130	
atc gat gag aag gcc tac cac ggc cgc acc ggc gtc tgc ttg cac acc			547
Ile Asp Glu Lys Ala Tyr His Gly Arg Thr Gly Val Cys Leu His Thr	135	145	
tcc tac cac cca tcg cgc ttg ctg tgg ctg aaa act gag ttc gag aaa			595
Ser Tyr His Pro Ser Arg Leu Leu Trp Leu Lys Thr Glu Phe Glu Lys	150	165	
gag ttc aac aaa gcc aag tat gtg atg acc atc ggt gag tac gtc tac			643
Glu Phe Asn Lys Ala Lys Tyr Val Met Thr Ile Gly Glu Tyr Val Tyr	170	180	
ttc aaa ctt gca ggc atc acc gga atg gct act tcg att gcc gcg tgg			691
Phe Lys Leu Ala Gly Ile Thr Gly Met Ala Thr Ser Ile Ala Ala Trp	185	195	
agt ggc att ttg gac gcc cat acc ggc gaa ctt gat ctg act atc ttg			739
Ser Gly Ile Leu Asp Ala His Thr Gly Glu Leu Asp Leu Thr Ile Leu	200	210	
gag cac atc ggt gtt gat ccg gct ctg ttc ggt gag atc aga aac cct			787
Glu His Ile Gly Val Asp Pro Ala Leu Phe Gly Glu Ile Arg Asn Pro	215	225	
gat gaa cca gcc acc gat gcc aaa gtt gtc gac aaa aag tgg aag cac			835
Asp Glu Pro Ala Thr Asp Ala Lys Val Val Asp Lys Lys Trp Lys His	230	245	

ctg gaa gaa atc cct tgg ttc cat gcc att cca gac ggc tgg cct tcc	883
Leu Glu Glu Ile Pro Trp Phe His Ala Ile Pro Asp Gly Trp Pro Ser	
250 255 260	
aac att ggc cca ggc gcc gtg gat tct aaa acc gtc gca gtc gcc gcc	931
Asn Ile Gly Pro Gly Ala Val Asp Ser Lys Thr Val Ala Val Ala Ala	
265 270 275	
gct aca tcc ggc gcc atg cgc gtg atc ctt ccg agc gtt ccc gaa cag	979
Ala Thr Ser Gly Ala Met Arg Val Ile Leu Pro Ser Val Pro Glu Gln	
280 285 290	
atc ccc tct ggc ctg tgg tgt tac cgc gtt tcc cgc gac cag tgc atc	1027
Ile Pro Ser Gly Leu Trp Cys Tyr Arg Val Ser Arg Asp Gln Cys Ile	
295 300 305	
gtt ggt ggc gca ctc aac gac gtc gga cgc gcc gtc acc tgg ctg gaa	1075
Val Gly Gly Ala Leu Asn Asp Val Gly Arg Ala Val Thr Trp Leu Glu	
310 315 320 325	
cgc acc att atc aag cct gaa aac ctc gac gaa gtg ctg atc cgc gaa	1123
Arg Thr Ile Ile Lys Pro Glu Asn Leu Asp Glu Val Leu Ile Arg Glu	
330 335 340	
ccc ctc gaa ggc acc cca gct gtc ctg ccg ttc ttc tcc ggg gaa cgc	1171
Pro Leu Glu Gly Thr Pro Ala Val Leu Pro Phe Phe Ser Gly Glu Arg	
345 350 355	
tcc atc ggc tgg gca gcc tca gcg cag gcc acg atc acc aac att cag	1219
Ser Ile Gly Trp Ala Ala Ser Ala Gln Ala Thr Ile Thr Asn Ile Gln	
360 365 370	
gaa caa acc ggc cct gaa cac ttg tgg cgc ggc gtt ttc gaa gcc ctc	1267
Glu Gln Thr Gly Pro Glu His Leu Trp Arg Gly Val Phe Glu Ala Leu	
375 380 385	
gca ctc tcc tac cag cgc gtt tgg gaa cac atg ggg aaa gcc ggc gca	1315
Ala Leu Ser Tyr Gln Arg Val Trp Glu His Met Gly Lys Ala Gly Ala	
390 395 400 405	
gcc cct gaa cgg gtc atc gca tca gga cga gtc tcc acc gac cac cca	1363
Ala Pro Glu Arg Val Ile Ala Ser Gly Arg Val Ser Thr Asp His Pro	
410 415 420	
gaa ttc ctc gcg atg ctt tcc gac gcc ctc gac acc cca gtc atc cct	1411
Glu Phe Leu Ala Met Leu Ser Asp Ala Leu Asp Thr Pro Val Ile Pro	
425 430 435	
ctg gaa atg aag cgc gcc acc ctc cgc ggc acc gca ctt atc gtc ctt	1459
Leu Glu Met Lys Arg Ala Thr Leu Arg Gly Thr Ala Leu Ile Val Leu	
440 445 450	
gag cag ctc gaa cca ggc ggc acg cgc gcg acg cca cca ttc ggc acg	1507
Glu Gln Leu Glu Pro Gly Thr Arg Ala Thr Pro Pro Phe Gly Thr	
455 460 465	
acg cat cag ccg cgc ttt gcg cac cat tac tcc aag gca aga gag ctt	1555
Thr His Gln Pro Arg Phe Ala His His Tyr Ser Lys Ala Arg Glu Leu	
470 475 480 485	

ttc gac gcc ctc tac ctc aag ttg gtc tagcttttcg cagtgggaacg 1602
 Phe Asp Ala Leu Tyr Leu Lys Leu Val
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cgc 1605

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<211> 494

<212> PRT

<213> Corynebacterium glutamicum

<400> 320

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Pro Tyr Val Leu Ala Met Asp Ile Gly Ser Thr Ala Ser Arg Gly Gly
 20 25 30

Leu Tyr Asp Ala Ser Gly Cys Pro Ile Lys Gly Thr Lys Gln Arg Glu
 35 40 45

Ser His Glu Phe Thr Thr Gly Glu Gly Val Ser Thr Ile Asp Ala Asp
 50 55 60

Gln Val Val Ser Glu Ile Thr Ser Val Ile Asn Gly Ile Leu Asn Ala
 65 70 75 80

Ala Asp His His Asn Ile Lys Asp Gln Ile Ala Ala Val Ala Leu Asp
 85 90 95

Ser Phe Ala Ser Ser Leu Ile Leu Val Asp Gly Glu Gly Asn Ala Leu
 100 105 110

Thr Pro Cys Ile Thr Tyr Ala Asp Ser Arg Ser Ala Gln Tyr Val Glu
 115 120 125

Gln Leu Arg Ala Glu Ile Asp Glu Lys Ala Tyr His Gly Arg Thr Gly
 130 135 140

Val Cys Leu His Thr Ser Tyr His Pro Ser Arg Leu Leu Trp Leu Lys
 145 150 155 160

Thr Glu Phe Glu Lys Glu Phe Asn Lys Ala Lys Tyr Val Met Thr Ile
 165 170 175

Gly Glu Tyr Val Tyr Phe Lys Leu Ala Gly Ile Thr Gly Met Ala Thr
 180 185 190

Ser Ile Ala Ala Trp Ser Gly Ile Leu Asp Ala His Thr Gly Glu Leu
 195 200 205

Asp Leu Thr Ile Leu Glu His Ile Gly Val Asp Pro Ala Leu Phe Gly
 210 215 220

Glu Ile Arg Asn Pro Asp Glu Pro Ala Thr Asp Ala Lys Val Val Asp
 225 230 235 240

Lys Lys Trp Lys His Leu Glu Glu Ile Pro Trp Phe His Ala Ile Pro
 245 250 255

Asp Gly Trp Pro Ser Asn Ile Gly Pro Gly Ala Val Asp Ser Lys Thr
 260 265 270
 Val Ala Val Ala Ala Ala Thr Ser Gly Ala Met Arg Val Ile Leu Pro
 275 280 285
 Ser Val Pro Glu Gln Ile Pro Ser Gly Leu Trp Cys Tyr Arg Val Ser
 290 295 300
 Arg Asp Gln Cys Ile Val Gly Gly Ala Leu Asn Asp Val Gly Arg Ala
 305 310 315 320
 Val Thr Trp Leu Glu Arg Thr Ile Ile Lys Pro Glu Asn Leu Asp Glu
 325 330 335
 Val Leu Ile Arg Glu Pro Leu Glu Gly Thr Pro Ala Val Leu Pro Phe
 340 345 350
 Phe Ser Gly Glu Arg Ser Ile Gly Trp Ala Ala Ser Ala Gln Ala Thr
 355 360 365
 Ile Thr Asn Ile Gln Glu Gln Thr Gly Pro Glu His Leu Trp Arg Gly
 370 375 380
 Val Phe Glu Ala Leu Ala Leu Ser Tyr Gln Arg Val Trp Glu His Met
 385 390 395 400
 Gly Lys Ala Gly Ala Ala Pro Glu Arg Val Ile Ala Ser Gly Arg Val
 405 410 415
 Ser Thr Asp His Pro Glu Phe Leu Ala Met Leu Ser Asp Ala Leu Asp
 420 425 430
 Thr Pro Val Ile Pro Leu Glu Met Lys Arg Ala Thr Leu Arg Gly Thr
 435 440 445
 Ala Leu Ile Val Leu Glu Gln Leu Glu Pro Gly Gly Thr Arg Ala Thr
 450 455 460
 Pro Pro Phe Gly Thr Thr His Gln Pro Arg Phe Ala His His Tyr Ser
 465 470 475 480
 Lys Ala Arg Glu Leu Phe Asp Ala Leu Tyr Leu Lys Leu Val
 485 490

<210> 321

<211> 1134

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1111)

<223> FRXA01049

<400> 321

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 gcgtctgctt gcacacctcc taccacccat cgcgcttgct gtg gtg aaa act gag 115
 Val Val Lys Thr Glu

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ttc	gag	aaa	gag	ttc	aac	aaa	gcc	aag	tat	gtg	atg	acc	atc	ggt	gag	163															
Phe	Glu	Lys	Glu	Phe	Asn	Lys	Ala	Lys	Tyr	Val	Met	Thr	Ile	Gly	Glu																
				10					15					20																	
tac	gtc	tac	ttc	aaa	ctt	gca	ggc	atc	acc	gga	atg	gct	act	tcg	att	211															
Tyr	Val	Tyr	Phe	Lys	Leu	Ala	Gly	Ile	Thr	Gly	Met	Ala	Thr	Ser	Ile																
				25					30					35																	
gcc	gcg	tgg	agt	ggc	att	ttg	gac	gcc	cat	acc	ggc	gaa	ctt	gat	ctg	259															
Ala	Ala	Trp	Ser	Gly	Ile	Leu	Asp	Ala	His	Thr	Gly	Glu	Leu	Asp	Leu																
				40					45					50																	
act	atc	ttg	gag	cac	atc	ggt	gtt	gat	ccg	gct	ctg	ttc	ggt	gag	atc	307															
Thr	Ile	Leu	Glu	His	Ile	Gly	Val	Asp	Pro	Ala	Leu	Phe	Gly	Glu	Ile																
				55					60					65																	
aga	aac	cct	gat	gaa	cca	gcc	acc	gat	gcc	aaa	gtt	gtc	gac	aaa	aag	355															
Arg	Asn	Pro	Asp	Glu	Pro	Ala	Thr	Asp	Ala	Lys	Val	Val	Asp	Lys	Lys																
				70					75					80																	
tgg	aag	cac	ctg	gaa	gaa	atc	cct	tgg	ttc	cat	gcc	att	cca	gac	ggc	403															
Trp	Lys	His	Leu	Glu	Glu	Ile	Pro	Trp	Phe	His	Ala	Ile	Pro	Asp	Gly																
				90					95					100																	
tgg	cct	tcc	aac	att	ggc	cca	ggc	gcc	gtg	gat	tct	aaa	acc	gtc	gca	451															
Trp	Pro	Ser	Asn	Ile	Gly	Pro	Gly	Ala	Val	Asp	Ser	Lys	Thr	Val	Ala																
				105					110					115																	
gtc	gcc	gcc	gct	aca	tcc	ggc	gcc	atg	cgc	gtg	atc	ctt	ccg	agc	gtt	499															
Val	Ala	Ala	Ala	Thr	Ser	Gly	Ala	Met	Arg	Val	Ile	Leu	Pro	Ser	Val																
				120					125					130																	
ccc	gaa	cag	atc	ccc	tct	ggc	ctg	tgg	tgt	tac	cgc	gtt	tcc	cgc	gac	547															
Pro	Glu	Gln	Ile	Pro	Ser	Gly	Leu	Trp	Cys	Tyr	Arg	Val	Ser	Arg	Asp																
				135					140					145																	
cag	tgc	atc	gtt	ggt	ggc	gca	ctc	aac	gac	gtc	gga	cgc	gcc	gtc	acc	595															
Gln	Cys	Ile	Val	Gly	Gly	Ala	Leu	Asn	Asp	Val	Gly	Arg	Ala	Val	Thr																
				150					155					160																	
tgg	ctg	gaa	cgc	acc	att	atc	aag	cct	gaa	aac	ctc	gac	gaa	gtg	ctg	643															
Trp	Leu	Glu	Arg	Thr	Ile	Ile	Lys	Pro	Glu	Asn	Leu	Asp	Glu	Val	Leu																
				170					175					180																	
atc	cgc	gaa	ccc	ctc	gaa	ggc	acc	cca	gct	gtc	ctg	ccg	ttc	ttc	tcc	691															
Ile	Arg	Glu	Pro	Leu	Glu	Gly	Thr	Pro	Ala	Val	Leu	Pro	Phe	Phe	Ser																
				185					190					195																	
ggg	gaa	cgc	tcc	atc	ggc	tgg	gca	gcc	tca	gcg	cag	gcc	acg	atc	acc	739															
Gly	Glu	Arg	Ser	Ile	Gly	Trp	Ala	Ala	Ser	Ala	Gln	Ala	Thr	Ile	Thr																
				200					205					210																	
aac	att	cag	gaa	caa	acc	ggc	cct	gaa	cac	ttg	tgg	cgc	ggc	gtt	ttc	787															
Asn	Ile	Gln	Glu	Gln	Thr	Gly	Pro	Glu	His	Leu	Trp	Arg	Gly	Val	Phe																
				215					220					225																	
gaa	gcc	ctc	gca	ctc	tcc	tac	cag	cgc	gtt	tgg	gaa	cac	atg	ggg	aaa	835															
Glu	Ala	Leu	Ala	Leu	Ser	Tyr	Gln	Arg	Val	Trp	Glu	His	Met	Gly	Lys																
				230					235					240																	

gcc ggc gca gcc cct gaa cgg gtc atc gca tca gga cga gtc tcc acc 883
 Ala Gly Ala Ala Pro Glu Arg Val Ile Ala Ser Gly Arg Val Ser Thr
 250 255 260

gac cac cca gaa ttc ctc gcg atg ctt tcc gac gcc ctc gac acc cca 931
 Asp His Pro Glu Phe Leu Ala Met Leu Ser Asp Ala Leu Asp Thr Pro
 265 270 275

gtc atc cct ctg gaa atg aag cgc gcc acc ctc cgc ggc acc gca ctt 979
 Val Ile Pro Leu Glu Met Lys Arg Ala Thr Leu Arg Gly Thr Ala Leu
 280 285 290

atc gtc ctt gag cag ctc gaa cca ggc ggc acg cgc gcg acg cca cca 1027
 Ile Val Leu Glu Gln Leu Glu Pro Gly Gly Thr Arg Ala Thr Pro Pro
 295 300 305

ttc ggc acg acg cat cag ccg cgc ttt gcg cac cat tac tcc aag gca 1075
 Phe Gly Thr Thr His Gln Pro Arg Phe Ala His His Tyr Ser Lys Ala
 310 315 320 325

aga gag ctt ttc gac gcc ctc tac ctc aag ttg gtc tagcttttcg 1121
 Arg Glu Leu Phe Asp Ala Leu Tyr Leu Lys Leu Val
 330 335

cagtggaacg cgc 1134

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 <211> 337
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 322
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 Met Thr Ile Gly Glu Tyr Val Tyr Phe Lys Leu Ala Gly Ile Thr Gly
 20 25 30
 Met Ala Thr Ser Ile Ala Ala Trp Ser Gly Ile Leu Asp Ala His Thr
 35 40 45
 Gly Glu Leu Asp Leu Thr Ile Leu Glu His Ile Gly Val Asp Pro Ala
 50 55 60
 Leu Phe Gly Glu Ile Arg Asn Pro Asp Glu Pro Ala Thr Asp Ala Lys
 65 70 75 80
 Val Val Asp Lys Lys Trp Lys His Leu Glu Glu Ile Pro Trp Phe His
 85 90 95
 Ala Ile Pro Asp Gly Trp Pro Ser Asn Ile Gly Pro Gly Ala Val Asp
 100 105 110
 Ser Lys Thr Val Ala Val Ala Ala Thr Ser Gly Ala Met Arg Val
 115 120 125
 Ile Leu Pro Ser Val Pro Glu Gln Ile Pro Ser Gly Leu Trp Cys Tyr
 130 135 140

Arg Val Ser Arg Asp Gln Cys Ile Val Gly Gly Ala Leu Asn Asp Val
 145 150 155 160
 Gly Arg Ala Val Thr Trp Leu Glu Arg Thr Ile Ile Lys Pro Glu Asn
 165 170 175
 Leu Asp Glu Val Leu Ile Arg Glu Pro Leu Glu Gly Thr Pro Ala Val
 180 185 190
 Leu Pro Phe Phe Ser Gly Glu Arg Ser Ile Gly Trp Ala Ala Ser Ala
 195 200 205
 Gln Ala Thr Ile Thr Asn Ile Gln Glu Gln Thr Gly Pro Glu His Leu
 210 215 220
 Trp Arg Gly Val Phe Glu Ala Leu Ala Leu Ser Tyr Gln Arg Val Trp
 225 230 235 240
 Glu His Met Gly Lys Ala Gly Ala Ala Pro Glu Arg Val Ile Ala Ser
 245 250 255
 Gly Arg Val Ser Thr Asp His Pro Glu Phe Leu Ala Met Leu Ser Asp
 260 265 270
 Ala Leu Asp Thr Pro Val Ile Pro Leu Glu Met Lys Arg Ala Thr Leu
 275 280 285
 Arg Gly Thr Ala Leu Ile Val Leu Glu Gln Leu Glu Pro Gly Gly Thr
 290 295 300
 Arg Ala Thr Pro Pro Phe Gly Thr Thr His Gln Pro Arg Phe Ala His
 305 310 315 320
 His Tyr Ser Lys Ala Arg Glu Leu Phe Asp Ala Leu Tyr Leu Lys Leu
 325 330 335
 Val

<210> 323
 <211> 597
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
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 <222> (101)..(574)
 <223> FRXA01050

<400> 323
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 aagaatattc tttattagtc agacctttaa aggaaacott atg gga tca att cca 115
 Met Gly Ser Ile Pro
 1 5
 aca atg tcc atc cct ttt gat gac tca cgt gga cct tat gtc ctt gct 163
 Thr Met Ser Ile Pro Phe Asp Asp Ser Arg Gly Pro Tyr Val Leu Ala
 10 15 20

atg gat att ggt tcc act gca tca cga ggt gga ctt tat gat gct tcc 211
 Met Asp Ile Gly Ser Thr Ala Ser Arg Gly Gly Leu Tyr Asp Ala Ser
 25 30 35
 ggc tgc cca atc aaa ggc acc aag cag cgc gaa tcc cat gaa ttc acc 259
 Gly Cys Pro Ile Lys Gly Thr Lys Gln Arg Glu Ser His Glu Phe Thr
 40 45 50
 acc ggt gag ggc gtt tcc acc att gat gct gac cag gtg gtt tcg gag 307
 Thr Gly Glu Gly Val Ser Thr Ile Asp Ala Asp Gln Val Val Ser Glu
 55 60 65
 atc acc tca gtt att aat ggc att ttg aac gcg gct gat cat cac aac 355
 Ile Thr Ser Val Ile Asn Gly Ile Leu Asn Ala Ala Asp His His Asn
 70 75 80 85
 atc aaa gat cag atc gcc gct gtc gcg cta gat tct ttt gca tcc tca 403
 Ile Lys Asp Gln Ile Ala Ala Val Ala Leu Asp Ser Phe Ala Ser Ser
 90 95 100
 tta atc ttg gtc gat ggt gaa ggc aat gcg ctc acc ccg tgc att acc 451
 Leu Ile Leu Val Asp Gly Glu Gly Asn Ala Leu Thr Pro Cys Ile Thr
 105 110 115
 tac gcg gat tct cgt tct gca cag tat gtg gag cag ctg cgc gcg gaa 499
 Tyr Ala Asp Ser Arg Ser Ala Gln Tyr Val Glu Gln Leu Arg Ala Glu
 120 125 130
 atc gat gag aag gcc tac cac ggc cgc acc ggc gtc tgc ttg cac acc 547
 Ile Asp Glu Lys Ala Tyr His Gly Arg Thr Gly Val Cys Leu His Thr
 135 140 145
 tcc tac cac cca tcg cgc ttg ctg tgg tgaaaactga gttcgagaaa 594
 Ser Tyr His Pro Ser Arg Leu Leu Trp
 150 155
 gag 597

<210> 324
 <211> 158
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 324
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 Pro Tyr Val Leu Ala Met Asp Ile Gly Ser Thr Ala Ser Arg Gly Gly
 20 25 30
 Leu Tyr Asp Ala Ser Gly Cys Pro Ile Lys Gly Thr Lys Gln Arg Glu
 35 40 45
 Ser His Glu Phe Thr Thr Gly Glu Gly Val Ser Thr Ile Asp Ala Asp
 50 55 60
 Gln Val Val Ser Glu Ile Thr Ser Val Ile Asn Gly Ile Leu Asn Ala
 65 70 75 80
 Ala Asp His His Asn Ile Lys Asp Gln Ile Ala Ala Val Ala Leu Asp

	85	90	95
Ser Phe Ala Ser Ser Leu Ile Leu Val Asp Gly Glu Gly Asn Ala Leu	100	105	110
Thr Pro Cys Ile Thr Tyr Ala Asp Ser Arg Ser Ala Gln Tyr Val Glu	115	120	125
Gln Leu Arg Ala Glu Ile Asp Glu Lys Ala Tyr His Gly Arg Thr Gly	130	135	140
Val Cys Leu His Thr Ser Tyr His Pro Ser Arg Leu Leu Trp	145	150	155
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		Met Tyr Ala Arg Lys	
		1 5	
ctt att gct ctg tcc gct tct gtc gtt ttg gct ttc agc ttg tct gct			163
Leu Ile Ala Leu Ser Ala Ser Val Val Leu Ala Phe Ser Leu Ser Ala	10	15	20
tgc aac cgt gaa tct tct ggc acc agc gca gac ggc ggt tct gcg gat			211
Cys Asn Arg Glu Ser Ser Gly Thr Ser Ala Asp Gly Gly Ser Ala Asp	25	30	35
ggg tcg atc acc ttg gct ctg tct acc cag acc aac ccg ttc ttt gtg			259
Gly Ser Ile Thr Leu Ala Leu Ser Thr Gln Thr Asn Pro Phe Phe Val	40	45	50
cag ctt cgt gat ggt gcc cag gaa aag gct gat gaa ttg ggc gtg acc			307
Gln Leu Arg Asp Gly Ala Gln Glu Lys Ala Asp Glu Leu Gly Val Thr	55	60	65
ctc aat gtt cag gat gct tcc gat gac gct gca acg cag gcc aac cag			355
Leu Asn Val Gln Asp Ala Ser Asp Asp Ala Ala Thr Gln Ala Asn Gln	70	75	80 85
ctc aac aac gct gtc acc acc ggt gct ggc gtg gtg att gtc aac cca			403
Leu Asn Asn Ala Val Thr Thr Gly Ala Gly Val Val Ile Val Asn Pro	90	95	100
act gat tct gat gct gtg gtg ccg tcg gtg gaa gct ctc aac cag gct			451
Thr Asp Ser Asp Ala Val Val Pro Ser Val Glu Ala Leu Asn Gln Ala	105	110	115
gac att cct gtt gtg gct gtc gac cgt tcc tcc aat ggt ggc gag gtg			499

Asp Ile Pro Val Val Ala Val Asp Arg Ser Ser Asn Gly Gly Glu Val
 120 125 130
 gcg tcc ttc gtg gca tct gac aac gtt gct ggc ggc gcg cag gct gct 547
 Ala Ser Phe Val Ala Ser Asp Asn Val Ala Gly Gly Ala Gln Ala Ala
 135 140 145
 gca gcc ctg gca gag gcg atc ggt ggc gaa ggt gaa atc ctc atg ctg 595
 Ala Ala Leu Ala Glu Ala Ile Gly Gly Glu Gly Glu Ile Leu Met Leu
 150 155 160 165
 caa ggc att gcg gga tcc tct gca tca cgt gat cgt gga cag gga ttt 643
 Gln Gly Ile Ala Gly Ser Ser Ala Ser Arg Asp Arg Gly Gln Gly Phe
 170 175 180
 gaa gag gag atc gct aag cat gag ggc att tcc att gtg gct aag cag 691
 Glu Glu Glu Ile Ala Lys His Glu Gly Ile Ser Ile Val Ala Lys Gln
 185 190 195
 acc gcc aac ttt gac cgc ggt gag ggc ctg gac gtg gca act aac ctg 739
 Thr Ala Asn Phe Asp Arg Gly Glu Gly Leu Asp Val Ala Thr Asn Leu
 200 205 210
 ctg cag gca cac ccc aat gtg aag gcg atc ttc gcg gaa aac gat gag 787
 Leu Gln Ala His Pro Asn Val Lys Ala Ile Phe Ala Glu Asn Asp Glu
 215 220 225
 atg gcg ttg ggc gca atc gaa gcc ctg ggt gct cgt gct ggt gaa gat 835
 Met Ala Leu Gly Ala Ile Glu Ala Leu Gly Ala Arg Ala Gly Glu Asp
 230 235 240 245
 gtc atc gtt gtc ggt ttc gat ggc acc aat gat ggt ctg gca gcg gtt 883
 Val Ile Val Val Gly Phe Asp Gly Thr Asn Asp Gly Leu Ala Ala Val
 250 255 260
 gaa gat gga cgc atg ttg gcc acc gtt gct cag cag cca gaa gag ctg 931
 Glu Asp Gly Arg Met Leu Ala Thr Val Ala Gln Gln Pro Glu Glu Leu
 265 270 275
 gga gca aag gct gtg gaa gaa gca gct aag ctc ctg cgc ggt gag gac 979
 Gly Ala Lys Ala Val Glu Glu Ala Ala Lys Leu Leu Arg Gly Glu Asp
 280 285 290
 gct gaa aca gag gta cca gtt gag gtt gtc act gtg aag ctc gac aac 1027
 Ala Glu Thr Glu Val Pro Val Glu Val Val Thr Val Lys Leu Asp Asn
 295 300 305
 gtc gcg gac ttc aag tagtcggcga tgaaaaagtc cgt 1065
 Val Ala Asp Phe Lys
 310

<210> 326

<211> 314

<212> PRT

<213> Corynebacterium glutamicum

<400> 326

Met Tyr Ala Arg Lys Leu Ile Ala Leu Ser Ala Ser Val Val Leu Ala
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Phe Ser Leu Ser Ala Cys Asn Arg Glu Ser Ser Gly Thr Ser Ala Asp
 20 25 30
 Gly Gly Ser Ala Asp Gly Ser Ile Thr Leu Ala Leu Ser Thr Gln Thr
 35 40 45
 Asn Pro Phe Phe Val Gln Leu Arg Asp Gly Ala Gln Glu Lys Ala Asp
 50 55 60
 Glu Leu Gly Val Thr Leu Asn Val Gln Asp Ala Ser Asp Asp Ala Ala
 65 70 75 80
 Thr Gln Ala Asn Gln Leu Asn Asn Ala Val Thr Thr Gly Ala Gly Val
 85 90 95
 Val Ile Val Asn Pro Thr Asp Ser Asp Ala Val Val Pro Ser Val Glu
 100 105 110
 Ala Leu Asn Gln Ala Asp Ile Pro Val Val Ala Val Asp Arg Ser Ser
 115 120 125
 Asn Gly Gly Glu Val Ala Ser Phe Val Ala Ser Asp Asn Val Ala Gly
 130 135 140
 Gly Ala Gln Ala Ala Ala Ala Leu Ala Glu Ala Ile Gly Gly Glu Gly
 145 150 155 160
 Glu Ile Leu Met Leu Gln Gly Ile Ala Gly Ser Ser Ala Ser Arg Asp
 165 170 175
 Arg Gly Gln Gly Phe Glu Glu Glu Ile Ala Lys His Glu Gly Ile Ser
 180 185 190
 Ile Val Ala Lys Gln Thr Ala Asn Phe Asp Arg Gly Glu Gly Leu Asp
 195 200 205
 Val Ala Thr Asn Leu Leu Gln Ala His Pro Asn Val Lys Ala Ile Phe
 210 215 220
 Ala Glu Asn Asp Glu Met Ala Leu Gly Ala Ile Glu Ala Leu Gly Ala
 225 230 235 240
 Arg Ala Gly Glu Asp Val Ile Val Val Gly Phe Asp Gly Thr Asn Asp
 245 250 255
 Gly Leu Ala Ala Val Glu Asp Gly Arg Met Leu Ala Thr Val Ala Gln
 260 265 270
 Gln Pro Glu Glu Leu Gly Ala Lys Ala Val Glu Glu Ala Ala Lys Leu
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 Val Lys Leu Asp Asn Val Ala Asp Phe Lys
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 <212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1054)

<223> RXN00872

<400> 327

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              Met Thr Asn Leu Thr
              1 5

agc act cac gaa gtc cta gct atc ggc cgc ttg ggc gta gat att tac 163
Ser Thr His Glu Val Leu Ala Ile Gly Arg Leu Gly Val Asp Ile Tyr
              10 15 20

cca ctt caa agt gga gta gga ctg gcc gat gtt caa tct ttc ggc aag 211
Pro Leu Gln Ser Gly Val Gly Leu Ala Asp Val Gln Ser Phe Gly Lys
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tac ctc ggc gga agc gca gca aac gtt tct gtt gca gcc gcc cgc cat 259
Tyr Leu Gly Gly Ser Ala Ala Asn Val Ser Val Ala Ala Ala Arg His
              40 45 50

gga cac aat tcc gca ctg ctg tcc cgt gtg gga aat gat cct ttc ggc 307
Gly His Asn Ser Ala Leu Leu Ser Arg Val Gly Asn Asp Pro Phe Gly
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Glu Tyr Leu Leu Ala Glu Leu Glu Arg Leu Gly Val Asp Asn Gln Tyr
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gtt gcc acc gat cag act ttt aag acc cca gtg acc ttc tgt gaa att 403
Val Ala Thr Asp Gln Thr Phe Lys Thr Pro Val Thr Phe Cys Glu Ile
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Phe Pro Pro Asp Asp Phe Pro Leu Tyr Phe Tyr Arg Glu Pro Lys Ala
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ccg gat ctc aat att gaa tcc gca gac gtc agc ctg gac gat gtg cgc 499
Pro Asp Leu Asn Ile Glu Ser Ala Asp Val Ser Leu Asp Asp Val Arg
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Glu Ala Asp Ile Leu Trp Phe Thr Leu Thr Gly Phe Ser Glu Glu Pro
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Ser Arg Gly Thr His Arg Glu Ile Leu Thr Thr Arg Ala Asn Arg Arg
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cac acc atc ttt gat ctg gac tac cga cca atg ttc tgg gaa tcc cca 643
His Thr Ile Phe Asp Leu Asp Tyr Arg Pro Met Phe Trp Glu Ser Pro
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Glu Glu Ala Thr Lys Gln Ala Glu Trp Ala Leu Gln His Ser Thr Val
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cca gag cgc gcg ggc cga gca ctg ttg gaa cgc ggt gtg gag ttg gcc 787
 Pro Glu Arg Ala Gly Arg Ala Leu Leu Glu Arg Gly Val Glu Leu Ala
 215 220 225

atc gtc aag cag gga cct aag ggt gtc atg gcg atg acc aag gac gaa 835
 Ile Val Lys Gln Gly Pro Lys Gly Val Met Ala Met Thr Lys Asp Glu
 230 235 240 245

acc gta gaa gtt cct ccg ttc ttc gtc gat gtc atc aac ggt ctt ggt 883
 Thr Val Glu Val Pro Pro Phe Phe Val Asp Val Ile Asn Gly Leu Gly
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gcc ggc gat gca ttc ggc ggc gcg ctg tgc cac ggt ctg ctc tct gaa 931
 Ala Gly Asp Ala Phe Gly Gly Ala Leu Cys His Gly Leu Leu Ser Glu
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tgg ccg ttg gaa aag gtt ctc cgt ttt gcc aac acc gcg ggt gcg ctt 979
 Trp Pro Leu Glu Lys Val Leu Arg Phe Ala Asn Thr Ala Gly Ala Leu
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 Val Ala Ser Arg Leu Glu Cys Ser Thr Ala Met Pro Thr Thr Asp Glu
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gtg gaa gcc tcc ctc aac cag aaa gtc tgatatgact cctccgatta 1074
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tct 1077

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<211> 318

<212> PRT

<213> Corynebacterium glutamicum

<400> 328

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Gln Ser Phe Gly Lys Tyr Leu Gly Gly Ser Ala Ala Asn Val Ser Val
 35 40 45

Ala Ala Ala Arg His Gly His Asn Ser Ala Leu Leu Ser Arg Val Gly
 50 55 60

Asn Asp Pro Phe Gly Glu Tyr Leu Leu Ala Glu Leu Glu Arg Leu Gly
 65 70 75 80

Val Asp Asn Gln Tyr Val Ala Thr Asp Gln Thr Phe Lys Thr Pro Val
 85 90 95

Thr Phe Cys Glu Ile Phe Pro Pro Asp Asp Phe Pro Leu Tyr Phe Tyr

100 105 110
 Arg Glu Pro Lys Ala Pro Asp Leu Asn Ile Glu Ser Ala Asp Val Ser
 115 120 125
 Leu Asp Asp Val Arg Glu Ala Asp Ile Leu Trp Phe Thr Leu Thr Gly
 130 135 140
 Phe Ser Glu Glu Pro Ser Arg Gly Thr His Arg Glu Ile Leu Thr Thr
 145 150 155 160
 Arg Ala Asn Arg Arg His Thr Ile Phe Asp Leu Asp Tyr Arg Pro Met
 165 170 175
 Phe Trp Glu Ser Pro Glu Glu Ala Thr Lys Gln Ala Glu Trp Ala Leu
 180 185 190
 Gln His Ser Thr Val Ala Val Gly Asn Lys Glu Glu Cys Glu Ile Ala
 195 200 205
 Val Gly Glu Thr Glu Pro Glu Arg Ala Gly Arg Ala Leu Leu Glu Arg
 210 215 220
 Gly Val Glu Leu Ala Ile Val Lys Gln Gly Pro Lys Gly Val Met Ala
 225 230 235 240
 Met Thr Lys Asp Glu Thr Val Glu Val Pro Pro Phe Phe Val Asp Val
 245 250 255
 Ile Asn Gly Leu Gly Ala Gly Asp Ala Phe Gly Gly Ala Leu Cys His
 260 265 270
 Gly Leu Leu Ser Glu Trp Pro Leu Glu Lys Val Leu Arg Phe Ala Asn
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<211> 622

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(622)

<223> FRXA00872

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 Met Thr Asn Leu Thr
 1 5

agc act cac gaa gtc cta gct atc ggc cgc ttg ggc gta gat att tac 163
 Ser Thr His Glu Val Leu Ala Ile Gly Arg Leu Gly Val Asp Ile Tyr

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cca ctt caa agt gga gta gga ctg gcc gat gtt caa tct ttc ggc aag				211
Pro Leu Gln Ser Gly Val Gly Leu Ala Asp Val Gln Ser Phe Gly Lys				
	25	30	35	
tac ctc ggc gga agc gca gca aac gtt tct gtt gca gcc gcc cgc cat				259
Tyr Leu Gly Gly Ser Ala Ala Asn Val Ser Val Ala Ala Ala Arg His				
	40	45	50	
gga cac aat tcc gca ctg ctg tcc cgt gtg gga aat gat cct ttc ggc				307
Gly His Asn Ser Ala Leu Leu Ser Arg Val Gly Asn Asp Pro Phe Gly				
	55	60	65	
gag tac ctg ctt gct gag ctg gag cgt ttg ggc gtg gac aac cag tac				355
Glu Tyr Leu Leu Ala Glu Leu Glu Arg Leu Gly Val Asp Asn Gln Tyr				
	70	75	80	85
gtt gcc acc gat cag act ttt aag acc cca gtg acc ttc tgt gaa att				403
Val Ala Thr Asp Gln Thr Phe Lys Thr Pro Val Thr Phe Cys Glu Ile				
	90	95	100	
ttc cca ccg gat gat ttc cca ctg tac ttc tac cgc gaa cca aag gct				451
Phe Pro Pro Asp Asp Phe Pro Leu Tyr Phe Tyr Arg Glu Pro Lys Ala				
	105	110	115	
ccg gat ctc aat att gaa tcc gca gac gtc agc ctg gac gat gtg cgc				499
Pro Asp Leu Asn Ile Glu Ser Ala Asp Val Ser Leu Asp Asp Val Arg				
	120	125	130	
gaa gcc gat att ttg tgg ttc aca ctc act ggt ttc agt gaa gag cca				547
Glu Ala Asp Ile Leu Trp Phe Thr Leu Thr Gly Phe Ser Glu Glu Pro				
	135	140	145	
agc cgc ggc aca cac cgc gag atc ttg act act cgt gcg aac cgt cgc				595
Ser Arg Gly Thr His Arg Glu Ile Leu Thr Thr Arg Ala Asn Arg Arg				
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cac acc atc ttt gat ctg gac tac cga				622
His Thr Ile Phe Asp Leu Asp Tyr Arg				
	170			

<210> 330

<211> 174

<212> PRT

<213> Corynebacterium glutamicum

<400> 330

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Gly Val Asp Ile Tyr Pro Leu Gln Ser Gly Val Gly Leu Ala Asp Val				
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Gln Ser Phe Gly Lys Tyr Leu Gly Gly Ser Ala Ala Asn Val Ser Val				
35	40	45		
Ala Ala Ala Arg His Gly His Asn Ser Ala Leu Leu Ser Arg Val Gly				
50	55	60		

Asn Asp Pro Phe Gly Glu Tyr Leu Leu Ala Glu Leu Glu Arg Leu Gly
 65 70 75 80
 Val Asp Asn Gln Tyr Val Ala Thr Asp Gln Thr Phe Lys Thr Pro Val
 85 90 95
 Thr Phe Cys Glu Ile Phe Pro Pro Asp Asp Phe Pro Leu Tyr Phe Tyr
 100 105 110
 Arg Glu Pro Lys Ala Pro Asp Leu Asn Ile Glu Ser Ala Asp Val Ser
 115 120 125
 Leu Asp Asp Val Arg Glu Ala Asp Ile Leu Trp Phe Thr Leu Thr Gly
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 Phe Ser Glu Glu Pro Ser Arg Gly Thr His Arg Glu Ile Leu Thr Thr
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<210> 331
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 <212> DNA
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<220>
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 <223> RXN00799

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 Met Ser Gln Glu Arg
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 cct caa atc ggc tcc cgc ctc tct cgt gtc att gaa caa gac ggc cta 163
 Pro Gln Ile Gly Ser Arg Leu Ser Arg Val Ile Glu Gln Asp Gly Leu
 10 15 20
 caa ttc cgc gat ctc gac ggc gac ggc gta ctt gca cct tat gaa gat 211
 Gln Phe Arg Asp Leu Asp Gly Asp Gly Val Leu Ala Pro Tyr Glu Asp
 25 30 35
 tgg cgt cta acc cca gca gag cgt gcc gct gac ctg gtg aaa cgt atg 259
 Trp Arg Leu Thr Pro Ala Glu Arg Ala Ala Asp Leu Val Lys Arg Met
 40 45 50
 aat gtg gaa gaa aaa gcg ggc ctg atg atc atc ggt tcg cac tac ccc 307
 Asn Val Glu Glu Lys Ala Gly Leu Met Ile Ile Gly Ser His Tyr Pro
 55 60 65
 gga tac tcg cct ttg gcg ccg gag agt gaa ggc aaa gac gcg gaa aag 355
 Gly Tyr Ser Pro Leu Ala Pro Glu Ser Glu Gly Lys Asp Ala Glu Lys
 70 75 80 85
 tgc gag cct ttg ctg aac cct gtc gat atg tgg cgt gag gat aac ccg 403
 Cys Glu Pro Leu Leu Asn Pro Val Asp Met Trp Arg Glu Asp Asn Pro

465

cag ctg tgg caa aac ccg acc acg cag ttc gaa gag gtt gcg ttt gcc 1171
 Gln Leu Trp Gln Asn Pro Thr Thr Gln Phe Glu Glu Val Ala Phe Ala
 345 350 355
 tac aac cgc acc ttc att cag gat ttg ctt cgc gac gcc atg ggc cac 1219
 Tyr Asn Arg Thr Phe Ile Gln Asp Leu Leu Arg Asp Ala Met Gly His
 360 365 370
 cgt ggg tac gtc aac tcc gac tcc ggc gtc atc gac gcc atg atg tgg 1267
 Arg Gly Tyr Val Asn Ser Asp Ser Gly Val Ile Asp Ala Met Met Trp
 375 380 385
 ggc gtg gag gaa ctc agc gag cca gaa cgc ttc gcc gca gca gtg cgt 1315
 Gly Val Glu Glu Leu Ser Glu Pro Glu Arg Phe Ala Ala Ala Val Arg
 390 395 400 405
 gca ggc acc gac att ttc tcc gac atg gct aac cca cgt cga ctg ctc 1363
 Ala Gly Thr Asp Ile Phe Ser Asp Met Ala Asn Pro Arg Arg Leu Leu
 410 415 420
 gaa gca gtt gct gag gga cac ctt gat gag tca gag ctg aat cag cca 1411
 Glu Ala Val Ala Glu Gly His Leu Asp Glu Ser Glu Leu Asn Gln Pro
 425 430 435
 gtc cag cga ctc ctg gag gaa atc ttc cag ctt ggt ctg ttt gag aac 1459
 Val Gln Arg Leu Leu Glu Glu Ile Phe Gln Leu Gly Leu Phe Glu Asn
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 cca tat gtc tct gaa gat gaa gca gaa aag atc att ggt gcg cca gag 1507
 Pro Tyr Val Ser Glu Asp Glu Ala Glu Lys Ile Ile Gly Ala Pro Glu
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 Val Ser Ala Leu Gly Asn Lys Ala Gln Leu Asp Ser Val Thr Leu Leu
 470 475 480 485
 cgt aac aac ccc atc cgt gct gcc act gga tcc tgc agc aag cct gaa 1603
 Arg Asn Asn Pro Ile Arg Ala Ala Thr Gly Ser Cys Ser Lys Pro Glu
 490 495 500
 gat cta ccc att ggt tac tgg ccg tac caa gat cga cga ggt tca act 1651
 Asp Leu Pro Ile Gly Tyr Trp Pro Tyr Gln Asp Arg Arg Gly Ser Thr
 505 510 515
 aca gct gga agc agc cat tcg cgc aga act ccc agg ggt aac ctt ggt 1699
 Thr Ala Gly Ser Ser His Ser Arg Arg Thr Pro Arg Gly Asn Leu Gly
 520 525 530
 gtc ttc cga gtc aga agc aga tct tgc aat cgt gtg ggc tcg ccc 1744
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<211> 548

<212> PRT

<213> Corynebacterium glutamicum

<400> 332

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Ala Pro Tyr Glu Asp Trp Arg Leu Thr Pro Ala Glu Arg Ala Ala Asp
      35              40              45

Leu Val Lys Arg Met Asn Val Glu Glu Lys Ala Gly Leu Met Ile Ile
      50              55              60

Gly Ser His Tyr Pro Gly Tyr Ser Pro Leu Ala Pro Glu Ser Glu Gly
      65              70              75              80

Lys Asp Ala Glu Lys Cys Glu Pro Leu Leu Asn Pro Val Asp Met Trp
      85              90              95

Arg Glu Asp Asn Pro Ile Thr Gly Val Pro Phe Thr Glu Pro Val Leu
      100              105              110

Ala Thr Ser Ser Thr Glu Asn Ala Ile Asn Leu Arg Asn Gln Arg Tyr
      115              120              125

Leu Ile Val Arg Asp Asn Leu Pro Ala Arg Gly Leu Ala Thr Trp Thr
      130              135              140

Asn Ala Val Gln Glu Val Ala Glu Arg Ser Arg Leu Gly Ile Pro Val
      145              150              155              160

Ala Phe Ala Ser Asn Pro Arg Asn His Val Ala Leu Val Ala Gln Phe
      165              170              175

Gly Val Asn Glu Ser Ala Gly Val Phe Ser Glu Trp Pro Gly Glu Leu
      180              185              190

Gly Leu Ala Ala Leu Arg Asp Ala Glu Leu Met Glu Thr Phe Gly Thr
      195              200              205

Glu Ala Ala Lys Glu Trp Arg Ala Gly Gly Val His Lys Leu Tyr Gly
      210              215              220

Tyr Met Ala Asp Leu Ala Ser Glu Pro Arg Trp Ser Arg Phe Asn Gly
      225              230              235              240

Thr Phe Gly Glu Asp Pro Glu Leu Ile Ser Asp Tyr Ile Ala Ala Val
      245              250              255

Val Arg Gly Leu Gln Gly Pro Glu Leu Ser Lys Asn Ser Val Ser Thr
      260              265              270

Thr Ile Lys His Phe Pro Gly Gly Gly Val Arg Leu Asp Gly His Asp
      275              280              285

Pro His Phe His Trp Gly Gln Thr Asn Glu Tyr Pro Thr Glu Asp Ala
      290              295              300

Leu Gly Lys Tyr His Leu Pro Pro Phe Gln Ala Ala Ile Asp Ala Gly
      305              310              315              320

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Cys Ala Ser Ile Met Pro Tyr Tyr Ala Arg Pro Met Asn Asn Ser Ala
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 Asn Gln Leu Asp Gln Gln Leu Trp Gln Asn Pro Thr Thr Gln Phe Glu
 340 345 350
 Glu Val Ala Phe Ala Tyr Asn Arg Thr Phe Ile Gln Asp Leu Leu Arg
 355 360 365
 Asp Ala Met Gly His Arg Gly Tyr Val Asn Ser Asp Ser Gly Val Ile
 370 375 380
 Asp Ala Met Met Trp Gly Val Glu Glu Leu Ser Glu Pro Glu Arg Phe
 385 390 395 400
 Ala Ala Ala Val Arg Ala Gly Thr Asp Ile Phe Ser Asp Met Ala Asn
 405 410 415
 Pro Arg Arg Leu Leu Glu Ala Val Ala Glu Gly His Leu Asp Glu Ser
 420 425 430
 Glu Leu Asn Gln Pro Val Gln Arg Leu Leu Glu Glu Ile Phe Gln Leu
 435 440 445
 Gly Leu Phe Glu Asn Pro Tyr Val Ser Glu Asp Glu Ala Glu Lys Ile
 450 455 460
 Ile Gly Ala Pro Glu Val Ser Ala Leu Gly Asn Lys Ala Gln Leu Asp
 465 470 475 480
 Ser Val Thr Leu Leu Arg Asn Asn Pro Ile Arg Ala Ala Thr Gly Ser
 485 490 495
 Cys Ser Lys Pro Glu Asp Leu Pro Ile Gly Tyr Trp Pro Tyr Gln Asp
 500 505 510
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 Val Gly Ser Pro
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 <212> DNA
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<220>
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Asp Trp Arg Leu Thr Pro Ala Glu Arg Ala Ala Asp Leu Val Lys Arg	
20 25 30	
atg aat gtg gaa gaa aaa gcg ggc ctg atg atc atc ggt tcg cac tac	144
Met Asn Val Glu Glu Lys Ala Gly Leu Met Ile Ile Gly Ser His Tyr	
35 40 45	
ccc gga tac tcg cct ttg gcg ccg gag agt gaa ggc aaa gac gcg gaa	192
Pro Gly Tyr Ser Pro Leu Ala Pro Glu Ser Glu Gly Lys Asp Ala Glu	
50 55 60	
aag tgc gag cct ttg ctg aac cct gtc gat atg tgg cgt gag gat aac	240
Lys Cys Glu Pro Leu Asn Pro Val Asp Met Trp Arg Glu Asp Asn	
65 70 75 80	
ccg atc acg ggt gtt cct ttc acc gag cct gtg ctg gca act tct tcc	288
Pro Ile Thr Gly Val Pro Phe Thr Glu Pro Val Leu Ala Thr Ser Ser	
85 90 95	
act gaa aat gcc att aac ctg cgc aat cag cgt tac tta att gtt cgt	336
Thr Glu Asn Ala Ile Asn Leu Arg Asn Gln Arg Tyr Leu Ile Val Arg	
100 105 110	
gac aac ctg cca gct cgt ggg ctt gct act tgg acc aat gct gtt cag	384
Asp Asn Leu Pro Ala Arg Gly Leu Ala Thr Trp Thr Asn Ala Val Gln	
115 120 125	
gaa gtc gcg gag cga tcc cgt ttg ggt att cct gtt gcg ttt gcg tcg	432
Glu Val Ala Glu Arg Ser Arg Leu Gly Ile Pro Val Ala Phe Ala Ser	
130 135 140	
aat cct cgt aac cac gtc gcg ctc gtt gcg cag ttc ggt gtg aac gag	480
Asn Pro Arg Asn His Val Ala Leu Val Ala Gln Phe Gly Val Asn Glu	
145 150 155 160	
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Ser Ala Gly Val Phe Ser Glu Trp Pro Gly Glu Leu Gly Leu Ala Ala	
165 170 175	
ctt cgc gat gct gaa ctg atg gag act ttc ggt acc gag gct gct aaa	576
Leu Arg Asp Ala Glu Leu Met Glu Thr Phe Gly Thr Glu Ala Ala Lys	
180 185 190	
gaa tgg cgt gcc ggt ggt gtg cac aag ctg tac ggt tac atg gct gac	624
Glu Trp Arg Ala Gly Gly Val His Lys Leu Tyr Gly Tyr Met Ala Asp	
195 200 205	
ctc gct tct gag cct cgt tgg tcc cgc ttc aac ggt act ttt ggt gag	672
Leu Ala Ser Glu Pro Arg Trp Ser Arg Phe Asn Gly Thr Phe Gly Glu	
210 215 220	
gat ccg gag ttg atc tct gat tac atc gct gct gtt gtg cgt ggt ttg	720
Asp Pro Glu Leu Ile Ser Asp Tyr Ile Ala Ala Val Val Arg Gly Leu	
225 230 235 240	
cag ggc cct gag ctg tcc aag aat tcc gtg tcg acc acc att aag cac	768
Gln Gly Pro Glu Leu Ser Lys Asn Ser Val Ser Thr Thr Ile Lys His	
245 250 255	
ttc cca ggt ggc ggc gtg cgc ctc gac ggc cac gat cct cac ttc cac	816

Phe	Pro	Gly	Gly	Gly	Val	Arg	Leu	Asp	Gly	His	Asp	Pro	His	Phe	His	
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tgg	ggt	cag	acc	aat	gag	tac	cca	acc	gaa	gat	gcg	ctg	ggc	aag	tac	864
Trp	Gly	Gln	Thr	Asn	Glu	Tyr	Pro	Thr	Glu	Asp	Ala	Leu	Gly	Lys	Tyr	
		275					280					285				
cat	ctg	cct	cct	ttc	cag	gca	gct	atc	gac	gct	ggc	tgc	gcc	tcg	atc	912
His	Leu	Pro	Pro	Phe	Gln	Ala	Ala	Ile	Asp	Ala	Gly	Cys	Ala	Ser	Ile	
	290					295					300					
atg	cct	tac	tac	gca	cgg	cca	atg	aac	aac	tcc	gcc	aac	cag	ctc	gat	960
Met	Pro	Tyr	Tyr	Ala	Arg	Pro	Met	Asn	Asn	Ser	Ala	Asn	Gln	Leu	Asp	
305					310					315					320	
cag	cag	ctg	tgg	caa	aac	ccg	acc	acg	cag	ttc	gaa	gag	gtt	gcg	ttt	1008
Gln	Gln	Leu	Trp	Gln	Asn	Pro	Thr	Thr	Gln	Phe	Glu	Glu	Val	Ala	Phe	
				325					330					335		
gcc	tac	aac	cgc	acc	ttc	att	cag	gat	ttg	ctt	cgc	gac	gcc	atg	ggc	1056
Ala	Tyr	Asn	Arg	Thr	Phe	Ile	Gln	Asp	Leu	Leu	Arg	Asp	Ala	Met	Gly	
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cac	cgt	ggg	tac	gtc	aac	tcc	gac	tcc	ggc	gtc	atc	gac	gcc	atg	atg	1104
His	Arg	Gly	Tyr	Val	Asn	Ser	Asp	Ser	Gly	Val	Ile	Asp	Ala	Met	Met	
		355					360					365				
tgg	ggc	gtg	gag	gaa	ctc	agc	gag	cca	gaa	cgc	ttc	gcc	gca	gca	gtg	1152
Trp	Gly	Val	Glu	Glu	Leu	Ser	Glu	Pro	Glu	Arg	Phe	Ala	Ala	Ala	Val	
	370					375					380					
cgt	gca	ggc	acc	gac	att	ttc	tcc	gac	atg	gct	aac	cca	cgt	cga	ctg	1200
Arg	Ala	Gly	Thr	Asp	Ile	Phe	Ser	Asp	Met	Ala	Asn	Pro	Arg	Arg	Leu	
385					390					395					400	
ctc	gaa	gca	gtt	gct	gag	gga	cac	ctt	gat	gag	tca	gag	ctg	aat	cag	1248
Leu	Glu	Ala	Val	Ala	Glu	Gly	His	Leu	Asp	Glu	Ser	Glu	Leu	Asn	Gln	
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cca	gtc	cag	cga	ctc	ctg	gag	gaa	atc	ttc	cag	ctt	ggt	ctg	ttt	gag	1296
Pro	Val	Gln	Arg	Leu	Leu	Glu	Glu	Ile	Phe	Gln	Leu	Gly	Leu	Phe	Glu	
			420					425					430			
aac	cca	tat	gtc	tct	gaa	gat	gaa	gca	gaa	aag	atc	att	ggt	gcg	cca	1344
Asn	Pro	Tyr	Val	Ser	Glu	Asp	Glu	Ala	Glu	Lys	Ile	Ile	Gly	Ala	Pro	
		435				440						445				
gag	gtt	tct	gca	ttg	ggc	aac	aaa	gca	cag	ctt	gat	tcc	gtc	acc	ttg	1392
Glu	Val	Ser	Ala	Leu	Gly	Asn	Lys	Ala	Gln	Leu	Asp	Ser	Val	Thr	Leu	
	450					455					460					
ctg	cgt	aac	aac	ccc	atc	cgt	gct	gcc	act	gga	tcc	tgc	agc	aag	cct	1440
Leu	Arg	Asn	Asn	Pro	Ile	Arg	Ala	Ala	Thr	Gly	Ser	Cys	Ser	Lys	Pro	
465					470					475					480	
gaa	gat	cta	ccc	att	ggt	tac	tgg	ccg	tac	caa	gat	cga	cga	ggt	tca	1488
Glu	Asp	Leu	Pro	Ile	Gly	Tyr	Trp	Pro	Tyr	Gln	Asp	Arg	Arg	Gly	Ser	
				485				490						495		
act	aca	gct	gga	agc	agc	cat	tcg	cgc	aga	act	ccc	agg	ggt	aac	ctt	1536
Thr	Thr	Ala	Gly	Ser	Ser	His	Ser	Arg	Arg	Thr	Pro	Arg	Gly	Asn	Leu	

500 505 510
 ggt gtc ttc cga gtc aga agc aga tct tgc aat cgt gtg ggc tcg ccc 1584
 Gly Val Phe Arg Val Arg Ser Arg Ser Cys Asn Arg Val Gly Ser Pro
 515 520 525
 tgaaattgca ctgtttgaag atg 1607

 <210> 334
 <211> 528
 <212> PRT
 <213> Corynebacterium glutamicum

 <400> 334
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 35 40 45
 Pro Gly Tyr Ser Pro Leu Ala Pro Glu Ser Glu Gly Lys Asp Ala Glu
 50 55 60
 Lys Cys Glu Pro Leu Leu Asn Pro Val Asp Met Trp Arg Glu Asp Asn
 65 70 75 80
 Pro Ile Thr Gly Val Pro Phe Thr Glu Pro Val Leu Ala Thr Ser Ser
 85 90 95
 Thr Glu Asn Ala Ile Asn Leu Arg Asn Gln Arg Tyr Leu Ile Val Arg
 100 105 110
 Asp Asn Leu Pro Ala Arg Gly Leu Ala Thr Trp Thr Asn Ala Val Gln
 115 120 125
 Glu Val Ala Glu Arg Ser Arg Leu Gly Ile Pro Val Ala Phe Ala Ser
 130 135 140
 Asn Pro Arg Asn His Val Ala Leu Val Ala Gln Phe Gly Val Asn Glu
 145 150 155 160
 Ser Ala Gly Val Phe Ser Glu Trp Pro Gly Glu Leu Gly Leu Ala Ala
 165 170 175
 Leu Arg Asp Ala Glu Leu Met Glu Thr Phe Gly Thr Glu Ala Ala Lys
 180 185 190
 Glu Trp Arg Ala Gly Gly Val His Lys Leu Tyr Gly Tyr Met Ala Asp
 195 200 205
 Leu Ala Ser Glu Pro Arg Trp Ser Arg Phe Asn Gly Thr Phe Gly Glu
 210 215 220
 Asp Pro Glu Leu Ile Ser Asp Tyr Ile Ala Ala Val Val Arg Gly Leu
 225 230 235 240
 Gln Gly Pro Glu Leu Ser Lys Asn Ser Val Ser Thr Thr Ile Lys His

245										250					255				
Phe	Pro	Gly	Gly	Gly	Val	Arg	Leu	Asp	Gly	His	Asp	Pro	His	Phe	His				
260										265					270				
Trp	Gly	Gln	Thr	Asn	Glu	Tyr	Pro	Thr	Glu	Asp	Ala	Leu	Gly	Lys	Tyr				
275										280					285				
His	Leu	Pro	Pro	Phe	Gln	Ala	Ala	Ile	Asp	Ala	Gly	Cys	Ala	Ser	Ile				
290										295					300				
Met	Pro	Tyr	Tyr	Ala	Arg	Pro	Met	Asn	Asn	Ser	Ala	Asn	Gln	Leu	Asp				
305										310					315				
Gln	Gln	Leu	Trp	Gln	Asn	Pro	Thr	Thr	Gln	Phe	Glu	Glu	Val	Ala	Phe				
325										330					335				
Ala	Tyr	Asn	Arg	Thr	Phe	Ile	Gln	Asp	Leu	Leu	Arg	Asp	Ala	Met	Gly				
340										345					350				
His	Arg	Gly	Tyr	Val	Asn	Ser	Asp	Ser	Gly	Val	Ile	Asp	Ala	Met	Met				
355										360					365				
Trp	Gly	Val	Glu	Glu	Leu	Ser	Glu	Pro	Glu	Arg	Phe	Ala	Ala	Ala	Val				
370										375					380				
Arg	Ala	Gly	Thr	Asp	Ile	Phe	Ser	Asp	Met	Ala	Asn	Pro	Arg	Arg	Leu				
385										390					395				
Leu	Glu	Ala	Val	Ala	Glu	Gly	His	Leu	Asp	Glu	Ser	Glu	Leu	Asn	Gln				
405										410					415				
Pro	Val	Gln	Arg	Leu	Leu	Glu	Glu	Ile	Phe	Gln	Leu	Gly	Leu	Phe	Glu				
420										425					430				
Asn	Pro	Tyr	Val	Ser	Glu	Asp	Glu	Ala	Glu	Lys	Ile	Ile	Gly	Ala	Pro				
435										440					445				
Glu	Val	Ser	Ala	Leu	Gly	Asn	Lys	Ala	Gln	Leu	Asp	Ser	Val	Thr	Leu				
450										455					460				
Leu	Arg	Asn	Asn	Pro	Ile	Arg	Ala	Ala	Thr	Gly	Ser	Cys	Ser	Lys	Pro				
465										470					475				
Glu	Asp	Leu	Pro	Ile	Gly	Tyr	Trp	Pro	Tyr	Gln	Asp	Arg	Arg	Gly	Ser				
485										490					495				
Thr	Thr	Ala	Gly	Ser	Ser	His	Ser	Arg	Arg	Thr	Pro	Arg	Gly	Asn	Leu				
500										505					510				
Gly	Val	Phe	Arg	Val	Arg	Ser	Arg	Ser	Cys	Asn	Arg	Val	Gly	Ser	Pro				
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<210> 335

<211> 1632

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1609)

<223> RXA00032

<400> 335

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ttttcgagct aaacccatcc ttgaaaggat cttttccacc atg aac acc cca ctc 115
          *                               Met Asn Thr Pro Leu
                                   1                               5

cag ctc aac act gaa aac ctg cag gaa atc gct tcg act tcc gga gtg 163
Gln Leu Asn Thr Glu Asn Leu Gln Glu Ile Ala Ser Thr Ser Gly Val
          10                               15                               20

cag atc cca gcg ttc aac cgc gct gac gtc gcc ccg ggc att gtc cac 211
Gln Ile Pro Ala Phe Asn Arg Ala Asp Val Ala Pro Gly Ile Val His
          25                               30                               35

ttc ggt gtt ggc gga ttc cat cgc gct cac caa gcg atg tac ctc aat 259
Phe Gly Val Gly Gly Phe His Arg Ala His Gln Ala Met Tyr Leu Asn
          40                               45                               50

gaa ttg atg aat gag ggc aag gcc ttg gat tgg ggc atc atc ggc atg 307
Glu Leu Met Asn Glu Gly Lys Ala Leu Asp Trp Gly Ile Ile Gly Met
          55                               60                               65

ggt gtc atg cct tcc gat gtg cgc atg cgc gat gcc ctg gcc agc caa 355
Gly Val Met Pro Ser Asp Val Arg Met Arg Asp Ala Leu Ala Ser Gln
          70                               75                               80                               85

gat cac ctt tat acc ctg acc act aaa gct cct gat gga act ctt gat 403
Asp His Leu Tyr Thr Leu Thr Thr Lys Ala Pro Asp Gly Thr Leu Asp
          90                               95                               100

caa aaa atc atc gga tcc atc att gac tac gtg ttc gct ccc gag gac 451
Gln Lys Ile Ile Gly Ser Ile Ile Asp Tyr Val Phe Ala Pro Glu Asp
          105                               110                               115

cca gca cgg gcc gtt gca acc ctc gcg cag gac tcc atc cgc att gtt 499
Pro Ala Arg Ala Val Ala Thr Leu Ala Gln Asp Ser Ile Arg Ile Val
          120                               125                               130

tcc ctc acg gtg act gaa ggc gga tac aac atc gat ccg gcg aca gaa 547
Ser Leu Thr Val Thr Glu Gly Gly Tyr Asn Ile Asp Pro Ala Thr Glu
          135                               140                               145

gat ttc gac cac acc aac cct cga atc gtt gct gac cgc gaa gcc ctg 595
Asp Phe Asp His Thr Asn Pro Arg Ile Val Ala Asp Arg Glu Ala Leu
          150                               155                               160                               165

cag gcg ggc gat act tcc act ttg cag acc ttc ttt ggg ttg atc act 643
Gln Ala Gly Asp Thr Ser Thr Leu Gln Thr Phe Phe Gly Leu Ile Thr
          170                               175                               180

gcc gca ttg att tcc cga aaa gaa tca gga tct acg cca ttt acc atc 691
Ala Ala Leu Ile Ser Arg Lys Glu Ser Gly Ser Thr Pro Phe Thr Ile
          185                               190                               195

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atg agc tgc gat aac atc caa ggc aac ggc gat ctg gct aag cgt ttc	739
Met Ser Cys Asp Asn Ile Gln Gly Asn Gly Asp Leu Ala Lys Arg Phe	
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ttc ctc gcc ttc gca cat tcc gtg tct tct gag ctc ggc gaa tgg gtg	787
Phe Leu Ala Phe Ala His Ser Val Ser Ser Glu Leu Gly Glu Trp Val	
215 220 225	
gaa aac aac gtg gcc ttc ccc aac tcc atg gtg gac cgc atc acc cct	835
Glu Asn Asn Val Ala Phe Pro Asn Ser Met Val Asp Arg Ile Thr Pro	
230 235 240 245	
gaa acc acc gac ggc gac cgc gat gac atc aag gaa atc ggc tac atc	883
Glu Thr Thr Asp Gly Asp Arg Asp Asp Ile Lys Glu Ile Gly Tyr Ile	
250 255 260	
gat gcg tgg cca gtg gtt tct gaa gat ttc acc caa tgg gtc ctc gag	931
Asp Ala Trp Pro Val Val Ser Glu Asp Phe Thr Gln Trp Val Leu Glu	
265 270 275	
gat gcc ttc acc cag ggc cgc ccc gcg tac gag gag gtt ggc gtg cag	979
Asp Ala Phe Thr Gln Gly Arg Pro Ala Tyr Glu Glu Val Gly Val Gln	
280 285 290	
gtc gtc tcc gac gtg gag cct tat gaa tta atg aag ctg cgc ctg ctc	1027
Val Val Ser Asp Val Glu Pro Tyr Glu Leu Met Lys Leu Arg Leu Leu	
295 300 305	
aac gcc tcc cac cag gga ctt tgc tac ttc ggc cac ttg gct ggc cac	1075
Asn Ala Ser His Gln Gly Leu Cys Tyr Phe Gly His Leu Ala Gly His	
310 315 320 325	
cac atg gtc cac gac gtc atg gcg gat acc cgc ttc cag gat ttc ctc	1123
His Met Val His Asp Val Met Ala Asp Thr Arg Phe Gln Asp Phe Leu	
330 335 340	
ctg gct tac atg gag cgc gaa gcc acc cct acc ctc aag gaa ctt cca	1171
Leu Ala Tyr Met Glu Arg Glu Ala Thr Pro Thr Leu Lys Glu Leu Pro	
345 350 355	
ggt gtc gat cta gat gct tat cga cgc caa ctc atc gcg cga ttc ggc	1219
Gly Val Asp Leu Asp Ala Tyr Arg Arg Gln Leu Ile Ala Arg Phe Gly	
360 365 370	
aac gcc gca gtc aaa gac acc gta ccg cgc ctg tgt gcg gaa tcc tcc	1267
Asn Ala Ala Val Lys Asp Thr Val Pro Arg Leu Cys Ala Glu Ser Ser	
375 380 385	
gac cgc att cca aag tgg ctg ttg cca gtc gta cgc gaa aac ctc gca	1315
Asp Arg Ile Pro Lys Trp Leu Leu Pro Val Val Arg Glu Asn Leu Ala	
390 395 400 405	
gca ggc cgc gac gtc aca ctt tct gca gcc atc gtc gca tcc tgg gcg	1363
Ala Gly Arg Asp Val Thr Leu Ser Ala Ala Ile Val Ala Ser Trp Ala	
410 415 420	
cgc tac gca gaa ggc acc gac gag cag ggc aac cca ata aag att gtt	1411
Arg Tyr Ala Glu Gly Thr Asp Glu Gln Gly Asn Pro Ile Lys Ile Val	
425 430 435	
gac cgt ttg agt gag cgc gtc caa gaa aac gca tca gga aat cgc acc	1459

Asp Arg Leu Ser Glu Arg Val Gln Glu Asn Ala Ser Gly Asn Arg Thr
 440 445 450
 gat att ttg tca ttc atc cgc gac cgt gga atc ttc gga gac ttg gtc 1507
 Asp Ile Leu Ser Phe Ile Arg Asp Arg Gly Ile Phe Gly Asp Leu Val
 455 460 465
 gat gct gaa cca ttc acc aag gca tac tcc gag aca ctg tcc tcc ctt 1555
 Asp Ala Glu Pro Phe Thr Lys Ala Tyr Ser Glu Thr Leu Ser Ser Leu
 470 475 480 485
 cat gac cgt ggc gcg gaa gca acc atc gat gca ctt ctt acg cag gta 1603
 His Asp Arg Gly Ala Glu Ala Thr Ile Asp Ala Leu Leu Thr Gln Val
 490 495 500
 act gtc taaatccggtt gcgcgctagg gtt 1632
 Thr Val

<210> 336
 <211> 503
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 336
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 Pro Gly Ile Val His Phe Gly Val Gly Gly Phe His Arg Ala His Gln
 35 40 45
 Ala Met Tyr Leu Asn Glu Leu Met Asn Glu Gly Lys Ala Leu Asp Trp
 50 55 60
 Gly Ile Ile Gly Met Gly Val Met Pro Ser Asp Val Arg Met Arg Asp
 65 70 75 80
 Ala Leu Ala Ser Gln Asp His Leu Tyr Thr Leu Thr Thr Lys Ala Pro
 85 90 95
 Asp Gly Thr Leu Asp Gln Lys Ile Ile Gly Ser Ile Ile Asp Tyr Val
 100 105 110
 Phe Ala Pro Glu Asp Pro Ala Arg Ala Val Ala Thr Leu Ala Gln Asp
 115 120 125
 Ser Ile Arg Ile Val Ser Leu Thr Val Thr Glu Gly Gly Tyr Asn Ile
 130 135 140
 Asp Pro Ala Thr Glu Asp Phe Asp His Thr Asn Pro Arg Ile Val Ala
 145 150 155 160
 Asp Arg Glu Ala Leu Gln Ala Gly Asp Thr Ser Thr Leu Gln Thr Phe
 165 170 175
 Phe Gly Leu Ile Thr Ala Ala Leu Ile Ser Arg Lys Glu Ser Gly Ser
 180 185 190

Thr Pro Phe Thr Ile Met Ser Cys Asp Asn Ile Gln Gly Asn Gly Asp
 195 200 205
 Leu Ala Lys Arg Phe Phe Leu Ala Phe Ala His Ser Val Ser Ser Glu
 210 215 220
 Leu Gly Glu Trp Val Glu Asn Asn Val Ala Phe Pro Asn Ser Met Val
 225 230 235 240
 Asp Arg Ile Thr Pro Glu Thr Thr Asp Gly Asp Arg Asp Asp Ile Lys
 245 250 255
 Glu Ile Gly Tyr Ile Asp Ala Trp Pro Val Val Ser Glu Asp Phe Thr
 260 265 270
 Gln Trp Val Leu Glu Asp Ala Phe Thr Gln Gly Arg Pro Ala Tyr Glu
 275 280 285
 Glu Val Gly Val Gln Val Val Ser Asp Val Glu Pro Tyr Glu Leu Met
 290 295 300
 Lys Leu Arg Leu Leu Asn Ala Ser His Gln Gly Leu Cys Tyr Phe Gly
 305 310 315 320
 His Leu Ala Gly His His Met Val His Asp Val Met Ala Asp Thr Arg
 325 330 335
 Phe Gln Asp Phe Leu Leu Ala Tyr Met Glu Arg Glu Ala Thr Pro Thr
 340 345 350
 Leu Lys Glu Leu Pro Gly Val Asp Leu Asp Ala Tyr Arg Arg Gln Leu
 355 360 365
 Ile Ala Arg Phe Gly Asn Ala Ala Val Lys Asp Thr Val Pro Arg Leu
 370 375 380
 Cys Ala Glu Ser Ser Asp Arg Ile Pro Lys Trp Leu Leu Pro Val Val
 385 390 395 400
 Arg Glu Asn Leu Ala Ala Gly Arg Asp Val Thr Leu Ser Ala Ala Ile
 405 410 415
 Val Ala Ser Trp Ala Arg Tyr Ala Glu Gly Thr Asp Glu Gln Gly Asn
 420 425 430
 Pro Ile Lys Ile Val Asp Arg Leu Ser Glu Arg Val Gln Glu Asn Ala
 435 440 445
 Ser Gly Asn Arg Thr Asp Ile Leu Ser Phe Ile Arg Asp Arg Gly Ile
 450 455 460
 Phe Gly Asp Leu Val Asp Ala Glu Pro Phe Thr Lys Ala Tyr Ser Glu
 465 470 475 480
 Thr Leu Ser Ser Leu His Asp Arg Gly Ala Glu Ala Thr Ile Asp Ala
 485 490 495
 Leu Leu Thr Gln Val Thr Val
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<210> 337
<211> 1098
<212> DNA
<213> Corynebacterium glutamicum
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<220>
<221> CDS
<222> (101)..(1075)
<223> RXA02528
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																	Met Ser Ala Lys Ser	
																	1 5	
agc ctc aag gaa gtt gct gag tta gct gga gtc ggt tat gcc aca gcc												163						
Ser Leu Lys Glu Val Ala Glu Leu Ala Gly Val Gly Tyr Ala Thr Ala																		
																	10 15 20	
tcg agg gca cta tct ggc aag ggg tat gtg tcc ccg cag acg cgg gag												211						
Ser Arg Ala Leu Ser Gly Lys Gly Tyr Val Ser Pro Gln Thr Arg Glu																		
																	25 30 35	
aaa gtt cag gcg gcg gct aaa gag ctg aac tat gta cca aat cag ctg												259						
Lys Val Gln Ala Ala Ala Lys Glu Leu Asn Tyr Val Pro Asn Gln Leu																		
																	40 45 50	
gcc aag gcg ttg cgg gaa cat cgc agt gcc ttg gtg ggg gtc att gtt												307						
Ala Lys Ala Leu Arg Glu His Arg Ser Ala Leu Val Gly Val Ile Val																		
																	55 60 65	
ccg gat ttg tcc aat gag tat tat tcg gaa tcg ctg cag act att cag												355						
Pro Asp Leu Ser Asn Glu Tyr Tyr Ser Glu Ser Leu Gln Thr Ile Gln																		
																	70 75 80 85	
cag gat ctg aaa gct gct ggc tat caa atg ctg gtt gcg gag gcc aac												403						
Gln Asp Leu Lys Ala Ala Gly Tyr Gln Met Leu Val Ala Glu Ala Asn																		
																	90 95 100	
agt gtg cag gcg cag gac gtg gtg atg gaa tcg ttg atc tcg att caa												451						
Ser Val Gln Ala Gln Asp Val Val Met Glu Ser Leu Ile Ser Ile Gln																		
																	105 110 115	
gct gca gga att atc cac gtt cca gtg gtc ggc tca att gct cct gaa												499						
Ala Ala Gly Ile Ile His Val Pro Val Val Gly Ser Ile Ala Pro Glu																		
																	120 125 130	
gga atc ccc atg gtg cag ttg act cgt ggt gaa ttg ggt cct ggt ttc												547						
Gly Ile Pro Met Val Gln Leu Thr Arg Gly Glu Leu Gly Pro Gly Phe																		
																	135 140 145	
cct cgg gtg ttg tgt gat gat gag gct ggg ttt ttt cag ctg acc gag												595						
Pro Arg Val Leu Cys Asp Asp Glu Ala Gly Phe Phe Gln Leu Thr Glu																		
																	150 155 160 165	
tcg gtg ctg ggc ggc agc gga atg aac att gct gct ttg gtt ggt gaa												643						
Ser Val Leu Gly Gly Ser Gly Met Asn Ile Ala Ala Leu Val Gly Glu																		
																	170 175 180	

gaa tca ctt tcc acc acg cag gaa cga atg cgc ggt att agt cat gcg 691
 Glu Ser Leu Ser Thr Thr Gln Glu Arg Met Arg Gly Ile Ser His Ala
 185 190 195

gcg tcg ata tat ggg gct gag gtg acg ttc cat ttt ggc cac tat tct 739
 Ala Ser Ile Tyr Gly Ala Glu Val Thr Phe His Phe Gly His Tyr Ser
 200 205 210

gtc gaa tct ggc gaa gag atg gct cag gtg gtg ttt aac aac ggc ctt 787
 Val Glu Ser Gly Glu Glu Met Ala Gln Val Val Phe Asn Asn Gly Leu
 215 220 225

ccc gat gca ttg att gtg gcg tct cct cgg ctg atg gct ggg gtg atg 835
 Pro Asp Ala Leu Ile Val Ala Ser Pro Arg Leu Met Ala Gly Val Met
 230 235 240 245

cgt gct ttt act cgc ctg aat gtc cgc gtt ccc cac gat gtg gtg att 883
 Arg Ala Phe Thr Arg Leu Asn Val Arg Val Pro His Asp Val Val Ile
 250 255 260

ggt ggt tat gac gat cct gag tgg tac agc ttt gtc ggc gcg ggg att 931
 Gly Gly Tyr Asp Asp Pro Glu Trp Tyr Ser Phe Val Gly Ala Gly Ile
 265 270 275

acc acg ttt gtt cca ccg cat gag gag atg ggg aaa gag gcc gtg cgc 979
 Thr Thr Phe Val Pro Pro His Glu Glu Met Gly Lys Glu Ala Val Arg
 280 285 290

ttg ttg gta gat ctg att gaa aat ccc gaa ctt ccc acc ggc gat gtg 1027
 Leu Leu Val Asp Leu Ile Glu Asn Pro Glu Leu Pro Thr Gly Asp Val
 295 300 305

gtt ttg cag ggg cag gtg atc ctt cgg ggg tcg agc aca cat tcc ggg 1075
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 310 315 320 325

tagaattgcc caaatgtcat caa 1098

<210> 338

<211> 325

<212> PRT

<213> Corynebacterium glutamicum

<400> 338

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Pro Gln Thr Arg Glu Lys Val Gln Ala Ala Ala Lys Glu Leu Asn Tyr
 35 40 45

Val Pro Asn Gln Leu Ala Lys Ala Leu Arg Glu His Arg Ser Ala Leu
 50 55 60

Val Gly Val Ile Val Pro Asp Leu Ser Asn Glu Tyr Tyr Ser Glu Ser
 65 70 75 80

Leu Gln Thr Ile Gln Gln Asp Leu Lys Ala Ala Gly Tyr Gln Met Leu
 85 90 95
 Val Ala Glu Ala Asn Ser Val Gln Ala Gln Asp Val Val Met Glu Ser
 100 105 110
 Leu Ile Ser Ile Gln Ala Ala Gly Ile Ile His Val Pro Val Val Gly
 115 120 125
 Ser Ile Ala Pro Glu Gly Ile Pro Met Val Gln Leu Thr Arg Gly Glu
 130 135 140
 Leu Gly Pro Gly Phe Pro Arg Val Leu Cys Asp Asp Glu Ala Gly Phe
 145 150 155 160
 Phe Gln Leu Thr Glu Ser Val Leu Gly Gly Ser Gly Met Asn Ile Ala
 165 170 175
 Ala Leu Val Gly Glu Glu Ser Leu Ser Thr Thr Gln Glu Arg Met Arg
 180 185 190
 Gly Ile Ser His Ala Ala Ser Ile Tyr Gly Ala Glu Val Thr Phe His
 195 200 205
 Phe Gly His Tyr Ser Val Glu Ser Gly Glu Glu Met Ala Gln Val Val
 210 215 220
 Phe Asn Asn Gly Leu Pro Asp Ala Leu Ile Val Ala Ser Pro Arg Leu
 225 230 235 240
 Met Ala Gly Val Met Arg Ala Phe Thr Arg Leu Asn Val Arg Val Pro
 245 250 255
 His Asp Val Val Ile Gly Gly Tyr Asp Asp Pro Glu Trp Tyr Ser Phe
 260 265 270
 Val Gly Ala Gly Ile Thr Thr Phe Val Pro Pro His Glu Glu Met Gly
 275 280 285
 Lys Glu Ala Val Arg Leu Leu Val Asp Leu Ile Glu Asn Pro Glu Leu
 290 295 300
 Pro Thr Gly Asp Val Val Leu Gln Gly Gln Val Ile Leu Arg Gly Ser
 305 310 315 320
 Ser Thr His Ser Gly
 325

<210> 339

<211> 1246

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1246)

<223> RXN00316

<400> 339

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gcttctggcc cgcggtcaa aaaatgaaaa aggagccgtc	atg ggc caa tgc acg	115
	Met Gly Gln Cys Thr	
	1 5	
gta gcg ctt tac cga gag cat tcc tat tac aca gca acc cca tgg cga		163
Val Ala Leu Tyr Arg Glu His Ser Tyr Tyr Thr Ala Thr Pro Trp Arg		
	10 15 20	
gga acc tgg gca gcc gat ggc ggt gga gtg ctc atg act caa gcc atc		211
Gly Thr Trp Ala Ala Asp Gly Gly Gly Val Leu Met Thr Gln Ala Ile		
	25 30 35	
cac tac atc gat ctt ttg tac tgg ctg ttg ggc gaa ccc gtg gaa gtt		259
His Tyr Ile Asp Leu Leu Tyr Trp Leu Leu Gly Glu Pro Val Glu Val		
	40 45 50	
ttc ggc tac acc aac tcc ttc aaa cac ggc gac aac atc gaa gtc gaa		307
Phe Gly Tyr Thr Asn Ser Phe Lys His Gly Asp Asn Ile Glu Val Glu		
	55 60 65	
gac agc gcc gtt gcc act gtg cgt ttt gaa tcg ggc gcg ttg gcc aca		355
Asp Ser Ala Val Ala Thr Val Arg Phe Glu Ser Gly Ala Leu Ala Thr		
	70 75 80 85	
att tca gcc acc acc gcc gca gag cca gca ctc ggc gca caa gtg cag		403
Ile Ser Ala Thr Thr Ala Ala Glu Pro Ala Leu Gly Ala Gln Val Gln		
	90 95 100	
gtg atg gga aca aag ggt gcc acc atg acg atc ctg gaa ttc cct gaa		451
Val Met Gly Thr Lys Gly Ala Thr Met Thr Ile Leu Glu Phe Pro Glu		
	105 110 115	
ggt acc gac ggc agg ctc att gtt cgc agt gaa aac gac acc cgt cga		499
Gly Thr Asp Gly Arg Leu Ile Val Arg Ser Glu Asn Asp Thr Arg Arg		
	120 125 130	
aac cac ccc att cca ccc cgc gga tct tta tcc caa tgc cga tct ttc		547
Asn His Pro Ile Pro Pro Arg Gly Ser Leu Ser Gln Cys Arg Ser Phe		
	135 140 145	
cat cat caa cgg tgc ttt gat ccc gta tca cac cgc cca gat cgc aga		595
His His Gln Arg Cys Phe Asp Pro Val Ser His Arg Pro Asp Arg Arg		
	150 155 160 165	
ctt tat cga tgc gct caa cga agg ccg ccc acc act gat cac cgg ccg		643
Leu Tyr Arg Cys Ala Gln Arg Arg Pro Pro Thr Thr Asp His Arg Pro		
	170 175 180	
cga tgc cac cag agc tct gaa agt tct cct tgg tgt cta cga atc agc		691
Arg Cys His Gln Ser Ser Glu Ser Ser Pro Trp Cys Leu Arg Ile Ser		
	185 190 195	
agc cac cca cca gcc ggt ctc ttt gat cta acg gaa gct ttt aaa acg		739
Ser His Pro Pro Ala Gly Leu Phe Asp Leu Thr Glu Ala Phe Lys Thr		
	200 205 210	
tca cgc caa atc ggt ctt gca cct tta tcc tcc ctg tcc aca cca cct		787
Ser Arg Gln Ile Gly Leu Ala Pro Leu Ser Ser Leu Ser Thr Pro Pro		
	215 220 225	

gat caa cta gtg cgc ctc gca gct gcc act ggt ttc tcc ttt gtc ggt 835
Asp Gln Leu Val Arg Leu Ala Ala Ala Thr Gly Phe Ser Phe Val Gly
230 235 240 245

ctg cgc gtc atc gca gta acc ccc aac gaa cgt gta tat gac ctt tcc 883
Leu Arg Val Ile Ala Val Thr Pro Asn Glu Arg Val Tyr Asp Leu Ser
250 255 260

cca gga tcc cca ctg ctg gct gca acc caa caa gcg ttg aaa gaa acc 931
Pro Gly Ser Pro Leu Leu Ala Ala Thr Gln Gln Ala Leu Lys Glu Thr
265 270 275

gcc ctg tat gtg ctc gac act gaa ttc cta cag gta aac gca gac acc 979
Ala Leu Tyr Val Leu Asp Thr Glu Phe Leu Gln Val Asn Ala Asp Thr
280 285 290

acc cgc gag gcc tgg ctt ccc gca cta gaa gcc gcc gga gca ctg gga 1027
Thr Arg Glu Ala Trp Leu Pro Ala Leu Glu Ala Ala Gly Ala Leu Gly
295 300 305

gct aaa acc ttc acc atc gcc gcc ggt gat gac aac att gcg ccc ctg 1075
Ala Lys Thr Phe Thr Ile Ala Ala Gly Asp Asp Asn Ile Ala Pro Leu
310 315 320 325

acc gac acg atc ggt gcc atg gtt gac gat gcc cgt gat ttc gga gtc 1123
Thr Asp Thr Ile Gly Ala Met Val Asp Asp Ala Arg Asp Phe Gly Val
330 335 340

acc cca gcc cta gag cca atc tct tac cgc agc gtg cat tcc att ccg 1171
Thr Pro Ala Leu Glu Pro Ile Ser Tyr Arg Ser Val His Ser Ile Pro
345 350 355

cag gca gca gca atc gcc aga gac tcc ggc gga aaa gtc gtg gcg gac 1219
Gln Ala Ala Ala Ile Ala Arg Asp Ser Gly Gly Lys Val Val Ala Asp
360 365 370

acc ttg cac atg gcc agg ttc gga gcc 1246
Thr Leu His Met Ala Arg Phe Gly Ala
375 380

<210> 340
<211> 382
<212> PRT
<213> Corynebacterium glutamicum

<400> 340
Met Gly Gln Cys Thr Val Ala Leu Tyr Arg Glu His Ser Tyr Tyr Thr
1 5 10 15
Ala Thr Pro Trp Arg Gly Thr Trp Ala Ala Asp Gly Gly Gly Val Leu
20 25 30
Met Thr Gln Ala Ile His Tyr Ile Asp Leu Leu Tyr Trp Leu Leu Gly
35 40 45
Glu Pro Val Glu Val Phe Gly Tyr Thr Asn Ser Phe Lys His Gly Asp
50 55 60
Asn Ile Glu Val Glu Asp Ser Ala Val Ala Thr Val Arg Phe Glu Ser
65 70 75 80

Gly Ala Leu Ala Thr Ile Ser Ala Thr Thr Ala Ala Glu Pro Ala Leu
 85 90 95
 Gly Ala Gln Val Gln Val Met Gly Thr Lys Gly Ala Thr Met Thr Ile
 100 105 110
 Leu Glu Phe Pro Glu Gly Thr Asp Gly Arg Leu Ile Val Arg Ser Glu
 115 120 125
 Asn Asp Thr Arg Arg Asn His His Gln Arg Cys Phe Asp Pro Val Ser His
 130 135 140
 Gln Cys Arg Ser Phe His His Gln Arg Cys Phe Asp Pro Val Ser His
 145 150 155 160
 Arg Pro Asp Arg Arg Leu Tyr Arg Cys Ala Gln Arg Arg Pro Pro Thr
 165 170 175
 Thr Asp His Arg Pro Arg Cys His Gln Ser Ser Glu Ser Ser Pro Trp
 180 185 190
 Cys Leu Arg Ile Ser Ser His Pro Pro Ala Gly Leu Phe Asp Leu Thr
 195 200 205
 Glu Ala Phe Lys Thr Ser Arg Gln Ile Gly Leu Ala Pro Leu Ser Ser
 210 215 220
 Leu Ser Thr Pro Pro Asp Gln Leu Val Arg Leu Ala Ala Ala Thr Gly
 225 230 235 240
 Phe Ser Phe Val Gly Leu Arg Val Ile Ala Val Thr Pro Asn Glu Arg
 245 250 255
 Val Tyr Asp Leu Ser Pro Gly Ser Pro Leu Leu Ala Ala Thr Gln Gln
 260 265 270
 Ala Leu Lys Glu Thr Ala Leu Tyr Val Leu Asp Thr Glu Phe Leu Gln
 275 280 285
 Val Asn Ala Asp Thr Thr Arg Glu Ala Trp Leu Pro Ala Leu Glu Ala
 290 295 300
 Ala Gly Ala Leu Gly Ala Lys Thr Phe Thr Ile Ala Ala Gly Asp Asp
 305 310 315 320
 Asn Ile Ala Pro Leu Thr Asp Thr Ile Gly Ala Met Val Asp Asp Ala
 325 330 335
 Arg Asp Phe Gly Val Thr Pro Ala Leu Glu Pro Ile Ser Tyr Arg Ser
 340 345 350
 Val His Ser Ile Pro Gln Ala Ala Ala Ile Ala Arg Asp Ser Gly Gly
 355 360 365
 Lys Val Val Ala Asp Thr Leu His Met Ala Arg Phe Gly Ala
 370 375 380

<210> 341

<211> 412

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(412)

<223> FRXA00309

<400> 341

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gcttctggcc cgcggctcaa aaaatgaaaa aggagccgctc atg ggc caa tgc acg 115
                                         Met Gly Gln Cys Thr
                                         1       5

gta gcg ctt tac cga gag cat tcc tat tac aca gca acc cca tgg cga 163
Val Ala Leu Tyr Arg Glu His Ser Tyr Tyr Thr Ala Thr Pro Trp Arg
                        10                        15                        20

gga acc tgg gca gcc gat ggc ggt gga gtg ctc atg act caa gcc atc 211
Gly Thr Trp Ala Ala Asp Gly Gly Gly Val Leu Met Thr Gln Ala Ile
                        25                        30                        35

cac tac atc gat ctt ttg tac tgg ctg ttg ggc gaa ccc gtg gaa gtt 259
His Tyr Ile Asp Leu Leu Tyr Trp Leu Leu Gly Glu Pro Val Glu Val
                        40                        45                        50

ttc ggc tac acc aac tcc ttc aaa cac ggc gac aac atc gaa gtc gaa 307
Phe Gly Tyr Thr Asn Ser Phe Lys His Gly Asp Asn Ile Glu Val Glu
                        55                        60                        65

gac agc gcc gtt gcc act gtg cgt ttt gaa tcg ggc gcg ttg gcc aca 355
Asp Ser Ala Val Ala Thr Val Arg Phe Glu Ser Gly Ala Leu Ala Thr
70                        75                        80                        85

att tca gcc acc acc gcc gca gag cca gca ctc ggc gca caa gtg cag 403
Ile Ser Ala Thr Thr Ala Ala Glu Pro Ala Leu Gly Ala Gln Val Gln
                        90                        95                        100

gtg atg gga 412
Val Met Gly

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<210> 342

<211> 104

<212> PRT

<213> Corynebacterium glutamicum

<400> 342

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Ala Thr Pro Trp Arg Gly Thr Trp Ala Ala Asp Gly Gly Gly Val Leu
      20              25              30

Met Thr Gln Ala Ile His Tyr Ile Asp Leu Leu Tyr Trp Leu Leu Gly
      35              40              45

Glu Pro Val Glu Val Phe Gly Tyr Thr Asn Ser Phe Lys His Gly Asp
      50              55              60

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Asn Ile Glu Val Glu Asp Ser Ala Val Ala Thr Val Arg Phe Glu Ser
65 70 75 80

Gly Ala Leu Ala Thr Ile Ser Ala Thr Thr Ala Ala Glu Pro Ala Leu
85 90 95

Gly Ala Gln Val Gln Val Met Gly
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<210> 343

<211> 558

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(535)

<223> RXN00310

<400> 343

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aaaccgcctt caccaagctt gaagatctag ggaagaaata atg tct gac aag atc 115
                                         Met Ser Asp Lys Ile
                                         1 5

tgg aaa gtc ggc atc atc ggt tgc ggt gca atc agc cga aac cat atc 163
Trp Lys Val Gly Ile Ile Gly Cys Gly Ala Ile Ser Arg Asn His Ile
                        10 15 20

gaa gca gtt cag gca atc ccc ggc gca gaa gtc agc gca gtc tgt gat 211
Glu Ala Val Gln Ala Ile Pro Gly Ala Glu Val Ser Ala Val Cys Asp
                        25 30 35

gtg gat ggt gcg aaa gca tcg gaa acc gca gcg aaa tat gga att tct 259
Val Asp Gly Ala Lys Ala Ser Glu Thr Ala Ala Lys Tyr Gly Ile Ser
                        40 45 50

ccc agt ttc acg tct gtc gat gag atc ctc gcc tcc ggg gtg gac att 307
Pro Ser Phe Thr Ser Val Asp Glu Ile Leu Ala Ser Gly Val Asp Ile
                        55 60 65

gtc gca gtc tgc acc cca cat cca acc cac gaa aca gtg gtc ctc gcc 355
Val Ala Val Cys Thr Pro His Pro Thr His Glu Thr Val Val Leu Ala
                        70 75 80 85

gct gct gcc gcc gga gtg cac gtg ctt tgt gag aag cca atc gcc atc 403
Ala Ala Ala Ala Gly Val His Val Leu Cys Glu Lys Pro Ile Ala Ile
                        90 95 100

gaa ctc gat tcc gca cag cgc atg atc gat gcc tgc gag tcc gca ggg 451
Glu Leu Asp Ser Ala Gln Arg Met Ile Asp Ala Cys Glu Ser Ala Gly
                        105 110 115

gtc caa ctt ggc gtg ctc ttc cag cgc cgc ttc tgg ccc gcg gct caa 499
Val Gln Leu Gly Val Leu Phe Gln Arg Arg Phe Trp Pro Ala Ala Gln
                        120 125 130

aaa atg aaa aag gag ccg tca tgg gcc aat gca cgg tagcgcttta 545

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Lys Met Lys Lys Glu Pro Ser Trp Ala Asn Ala Arg
 135 140 145

ccgagagcat tcc

558

<210> 344

<211> 145

<212> PRT

<213> Corynebacterium glutamicum

<400> 344

Met Ser Asp Lys Ile Trp Lys Val Gly Ile Ile Gly Cys Gly Ala Ile
 1 5 10 15

Ser Arg Asn His Ile Glu Ala Val Gln Ala Ile Pro Gly Ala Glu Val
 20 25 30

Ser Ala Val Cys Asp Val Asp Gly Ala Lys Ala Ser Glu Thr Ala Ala
 35 40 45

Lys Tyr Gly Ile Ser Pro Ser Phe Thr Ser Val Asp Glu Ile Leu Ala
 50 55 60

Ser Gly Val Asp Ile Val Ala Val Cys Thr Pro His Pro Thr His Glu
 65 70 75 80

Thr Val Val Leu Ala Ala Ala Ala Gly Val His Val Leu Cys Glu
 85 90 95

Lys Pro Ile Ala Ile Glu Leu Asp Ser Ala Gln Arg Met Ile Asp Ala
 100 105 110

Cys Glu Ser Ala Gly Val Gln Leu Gly Val Leu Phe Gln Arg Arg Phe
 115 120 125

Trp Pro Ala Ala Gln Lys Met Lys Lys Glu Pro Ser Trp Ala Asn Ala
 130 135 140

Arg
 145

<210> 345

<211> 558

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(535)

<223> FRXA00310

<400> 345

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aaaccgcctt caccaagctt gaagatctag ggaagaaata atg tct gac aag atc 115
 Met Ser Asp Lys Ile
 1 5

tgg aaa gtc ggc atc atc ggt tgc ggt gca atc agc cga aac cat atc 163

Trp Lys Val Gly Ile Ile Gly Cys Gly Ala Ile Ser Arg Asn His Ile
 10 15 20
 gaa gca gtt cag gca atc ccc ggc gca gaa gtc agc gca gtc tgt gat 211
 Glu Ala Val Gln Ala Ile Pro Gly Ala Glu Val Ser Ala Val Cys Asp
 25 30 35
 gtg gat ggt gcg aaa gca tcg gaa acc gca gcg aaa tat gga att tct 259
 Val Asp Gly Ala Lys Ala Ser Glu Thr Ala Ala Lys Tyr Gly Ile Ser
 40 45 50
 ccc agt ttc acg tct gtc gat gag atc ctc gcc tcc ggg gtg gac att 307
 Pro Ser Phe Thr Ser Val Asp Glu Ile Leu Ala Ser Gly Val Asp Ile
 55 60 65
 gtc gca gtc tgc acc cca cat cca acc cac gaa aca gtg gtc ctc gcc 355
 Val Ala Val Cys Thr Pro His Pro Thr His Glu Thr Val Val Leu Ala
 70 75 80 85
 gct gct gcc gcc gga gtg cac gtg ctt tgt gag aag cca atc gcc atc 403
 Ala Ala Ala Ala Gly Val His Val Leu Cys Glu Lys Pro Ile Ala Ile
 90 95 100
 gaa ctc gat tcc gca cag cgc atg atc gat gcc tgc gag tcc gca ggg 451
 Glu Leu Asp Ser Ala Gln Arg Met Ile Asp Ala Cys Glu Ser Ala Gly
 105 110 115
 gtc caa ctt ggc gtg ctc ttc cag cgc cgc ttc tgg ccc gcg gct caa 499
 Val Gln Leu Gly Val Leu Phe Gln Arg Arg Phe Trp Pro Ala Ala Gln
 120 125 130
 aaa atg aaa aag gag ccg tca tgg gcc aat gca cgg tagcgcttta 545
 Lys Met Lys Lys Glu Pro Ser Trp Ala Asn Ala Arg
 135 140 145
 ccgagagcat tcc 558

<210> 346

<211> 145

<212> PRT

<213> Corynebacterium glutamicum

<400> 346

Met Ser Asp Lys Ile Trp Lys Val Gly Ile Ile Gly Cys Gly Ala Ile
 1 5 10 15
 Ser Arg Asn His Ile Glu Ala Val Gln Ala Ile Pro Gly Ala Glu Val
 20 25 30
 Ser Ala Val Cys Asp Val Asp Gly Ala Lys Ala Ser Glu Thr Ala Ala
 35 40 45
 Lys Tyr Gly Ile Ser Pro Ser Phe Thr Ser Val Asp Glu Ile Leu Ala
 50 55 60
 Ser Gly Val Asp Ile Val Ala Val Cys Thr Pro His Pro Thr His Glu
 65 70 75 80
 Thr Val Val Leu Ala Ala Ala Ala Ala Gly Val His Val Leu Cys Glu
 85 90 95

Lys Pro Ile Ala Ile Glu Leu Asp Ser Ala Gln Arg Met Ile Asp Ala
 100 105 110

Cys Glu Ser Ala Gly Val Gln Leu Gly Val Leu Phe Gln Arg Arg Phe
 115 120 125

Trp Pro Ala Ala Gln Lys Met Lys Lys Glu Pro Ser Trp Ala Asn Ala
 130 135 140

Arg
 145

<210> 347

<211> 1342

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1342)

<223> RXA00041

<400> 347

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 agctgcgcta gaaacaaaaa ggaaagtagt gtgtggggct atg cac aca gaa ctt 115
 Met His Thr Glu Leu
 1 5
 tcc agt ttg cgc cct gcg tac cat gtg act cct ccg cag ggc agg ctc 163
 Ser Ser Leu Arg Pro Ala Tyr His Val Thr Pro Pro Gln Gly Arg Leu
 10 15 20
 aat gat ccc aac gga atg tac gtc gat ggc gat acc ctc cac gtc tac 211
 Asn Asp Pro Asn Gly Met Tyr Val Asp Gly Asp Thr Leu His Val Tyr
 25 30 35
 tac cag cac gat cca ggt ttc ccc ttc gca cca aag cgc acc ggc tgg 259
 Tyr Gln His Asp Pro Gly Phe Pro Phe Ala Pro Lys Arg Thr Gly Trp
 40 45 50
 gct cac acc acc acg ccg ttg acc gga ccg cag cga ttg cag tgg acg 307
 Ala His Thr Thr Thr Pro Leu Thr Gly Pro Gln Arg Leu Gln Trp Thr
 55 60 65
 cac ctg ccc gac gct ctt tac ccg gat gca tcc tat gac ctg gat gga 355
 His Leu Pro Asp Ala Leu Tyr Pro Asp Ala Ser Tyr Asp Leu Asp Gly
 70 75 80 85
 tgc tat tcc ggt gga gcc gta ttt act gac ggc aca ctt aaa ctt ttc 403
 Cys Tyr Ser Gly Gly Ala Val Phe Thr Asp Gly Thr Leu Lys Leu Phe
 90 95 100
 tac acc ggc aac cta aaa att gac ggc aag cgc cgc gcc acc caa aac 451
 Tyr Thr Gly Asn Leu Lys Ile Asp Gly Lys Arg Arg Ala Thr Gln Asn
 105 110 115
 ctc gtc gaa gtc gag gac cca act ggg ctg atg ggc ggc att cat cgc 499
 Leu Val Glu Val Glu Asp Pro Thr Gly Leu Met Gly Gly Ile His Arg

120					125					130						
cgt	tcg	cct	aaa	aat	ccg	ctt	atc	gac	gga	ccc	gcc	agc	ggg	ttc	aca	547
Arg	Ser	Pro	Lys	Asn	Pro	Leu	Ile	Asp	Gly	Pro	Ala	Ser	Gly	Phe	Thr	
135						140				145						
ccc	cat	tac	cgc	gat	ccc	atg	atc	agc	cct	gat	ggg	gat	ggg	tgg	aaa	595
Pro	His	Tyr	Arg	Asp	Pro	Met	Ile	Ser	Pro	Asp	Gly	Asp	Gly	Trp	Lys	
150				155						160				165		
atg	gtt	ctt	ggg	gcc	caa	cgc	gaa	aac	ctc	acc	ggg	gca	gcg	gtt	cta	643
Met	Val	Leu	Gly	Ala	Gln	Arg	Glu	Asn	Leu	Thr	Gly	Ala	Ala	Val	Leu	
				170				175						180		
tac	cgc	tcg	aca	gat	ctt	gaa	aac	tgg	gaa	ttc	tcc	ggg	gaa	atc	acc	691
Tyr	Arg	Ser	Thr	Asp	Leu	Glu	Asn	Trp	Glu	Phe	Ser	Gly	Glu	Ile	Thr	
		185						190				195				
ttt	gac	ctc	agt	gat	gca	caa	cct	ggg	tct	gct	cct	gat	ctc	gtt	ccc	739
Phe	Asp	Leu	Ser	Asp	Ala	Gln	Pro	Gly	Ser	Ala	Pro	Asp	Leu	Val	Pro	
		200				205						210				
ggg	ggc	tac	atg	tgg	gaa	tgc	ccc	aac	ctt	ttt	acg	ctt	cgc	gat	gaa	787
Gly	Gly	Tyr	Met	Trp	Glu	Cys	Pro	Asn	Leu	Phe	Thr	Leu	Arg	Asp	Glu	
215						220				225						
gaa	act	ggc	gaa	gat	ctc	gac	gtg	ctg	att	ttc	tgt	cca	caa	gga	ttg	835
Glu	Thr	Gly	Glu	Asp	Leu	Asp	Val	Leu	Ile	Phe	Cys	Pro	Gln	Gly	Leu	
230				235						240				245		
gac	cga	atc	cac	gat	gag	gtt	act	cac	tac	gca	agc	tct	gac	cag	tgc	883
Asp	Arg	Ile	His	Asp	Glu	Val	Thr	His	Tyr	Ala	Ser	Ser	Asp	Gln	Cys	
				250				255						260		
gga	tat	gtc	gtc	ggc	aag	ctt	gaa	gga	acg	acc	ttc	cgc	gtc	ttg	cga	931
Gly	Tyr	Val	Val	Gly	Lys	Leu	Glu	Gly	Thr	Thr	Phe	Arg	Val	Leu	Arg	
		265						270				275				
gga	ttc	agc	gag	ctg	gat	ttc	ggc	cat	gaa	ttc	tac	gca	ccg	cag	gtt	979
Gly	Phe	Ser	Glu	Leu	Asp	Phe	Gly	His	Glu	Phe	Tyr	Ala	Pro	Gln	Val	
		280				285						290				
gca	gta	aac	ggg	tct	gat	gcc	tgg	ctc	gtg	ggc	tgg	atg	ggg	ctg	ccc	1027
Ala	Val	Asn	Gly	Ser	Asp	Ala	Trp	Leu	Val	Gly	Trp	Met	Gly	Leu	Pro	
295						300				305						
gcg	cag	gat	gat	cac	cca	aca	gtt	gca	cgg	gaa	gga	tgg	gtg	cac	tgc	1075
Ala	Gln	Asp	Asp	His	Pro	Thr	Val	Ala	Arg	Glu	Gly	Trp	Val	His	Cys	
310				315						320				325		
ctg	act	gtg	ccc	cgc	aag	ctt	cat	ttg	cgc	aac	cac	gcg	atc	tat	caa	1123
Leu	Thr	Val	Pro	Arg	Lys	Leu	His	Leu	Arg	Asn	His	Ala	Ile	Tyr	Gln	
				330				335						340		
gag	ctt	ctt	ctc	cca	gag	ggg	gag	tca	ggg	gta	atc	aga	tct	gta	tta	1171
Glu	Leu	Leu	Leu	Pro	Glu	Gly	Glu	Ser	Gly	Val	Ile	Arg	Ser	Val	Leu	
		345						350				355				
ggg	tct	gaa	cct	gtc	cga	gta	gac	atc	cga	ggc	aat	att	tcc	ctc	gag	1219
Gly	Ser	Glu	Pro	Val	Arg	Val	Asp	Ile	Arg	Gly	Asn	Ile	Ser	Leu	Glu	
		360				365						370				

tgg gat ggt gtc cgt ttg tct gtg gat cgt ggt ggt gat cgt cgc gta 1267
 Trp Asp Gly Val Arg Leu Ser Val Asp Arg Gly Gly Asp Arg Arg Val
 375 380 385

gct gag gta aaa cct ggc gaa tta gtg atc gcg gac gat aat aca gcc 1315
 Ala Glu Val Lys Pro Gly Glu Leu Val Ile Ala Asp Asp Asn Thr Ala
 390 395 400 405

att gag ata act gca ggt gat gga cag 1342
 Ile Glu Ile Thr Ala Gly Asp Gly Gln
 410

<210> 348

<211> 414

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 348

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 20 25 30

Thr Leu His Val Tyr Tyr Gln His Asp Pro Gly Phe Pro Phe Ala Pro
 35 40 45

Lys Arg Thr Gly Trp Ala His Thr Thr Thr Pro Leu Thr Gly Pro Gln
 50 55 60

Arg Leu Gln Trp Thr His Leu Pro Asp Ala Leu Tyr Pro Asp Ala Ser
 65 70 75 80

Tyr Asp Leu Asp Gly Cys Tyr Ser Gly Gly Ala Val Phe Thr Asp Gly
 85 90 95

Thr Leu Lys Leu Phe Tyr Thr Gly Asn Leu Lys Ile Asp Gly Lys Arg
 100 105 110

Arg Ala Thr Gln Asn Leu Val Glu Val Glu Asp Pro Thr Gly Leu Met
 115 120 125

Gly Gly Ile His Arg Arg Ser Pro Lys Asn Pro Leu Ile Asp Gly Pro
 130 135 140

Ala Ser Gly Phe Thr Pro His Tyr Arg Asp Pro Met Ile Ser Pro Asp
 145 150 155 160

Gly Asp Gly Trp Lys Met Val Leu Gly Ala Gln Arg Glu Asn Leu Thr
 165 170 175

Gly Ala Ala Val Leu Tyr Arg Ser Thr Asp Leu Glu Asn Trp Glu Phe
 180 185 190

Ser Gly Glu Ile Thr Phe Asp Leu Ser Asp Ala Gln Pro Gly Ser Ala
 195 200 205

Pro Asp Leu Val Pro Gly Gly Tyr Met Trp Glu Cys Pro Asn Leu Phe
 210 215 220

Thr Leu Arg Asp Glu Glu Thr Gly Glu Asp Leu Asp Val Leu Ile Phe
 225 230 235 240
 Cys Pro Gln Gly Leu Asp Arg Ile His Asp Glu Val Thr His Tyr Ala
 245 250 255
 Ser Ser Asp Gln Cys Gly Tyr Val Val Gly Lys Leu Glu Gly Thr Thr
 260 265 270
 Phe Arg Val Leu Arg Gly Phe Ser Glu Leu Asp Phe Gly His Glu Phe
 275 280 285
 Tyr Ala Pro Gln Val Ala Val Asn Gly Ser Asp Ala Trp Leu Val Gly
 290 295 300
 Trp Met Gly Leu Pro Ala Gln Asp Asp His Pro Thr Val Ala Arg Glu
 305 310 315 320
 Gly Trp Val His Cys Leu Thr Val Pro Arg Lys Leu His Leu Arg Asn
 325 330 335
 His Ala Ile Tyr Gln Glu Leu Leu Leu Pro Glu Gly Glu Ser Gly Val
 340 345 350
 Ile Arg Ser Val Leu Gly Ser Glu Pro Val Arg Val Asp Ile Arg Gly
 355 360 365
 Asn Ile Ser Leu Glu Trp Asp Gly Val Arg Leu Ser Val Asp Arg Gly
 370 375 380
 Gly Asp Arg Arg Val Ala Glu Val Lys Pro Gly Glu Leu Val Ile Ala
 385 390 395 400
 Asp Asp Asn Thr Ala Ile Glu Ile Thr Ala Gly Asp Gly Gln
 405 410

<210> 349
 <211> 720
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (1)..(720)
 <223> RXA02026

<400> 349
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 Pro Phe His Ile Gln Pro Glu Thr Gly Leu Leu Asn Asp Pro Asn Gly
 1 5 10 15
 ctt att ttt tat aaa ggg aag tat tat gtt tca cat caa tgg ttc cca 96
 Leu Ile Phe Tyr Lys Gly Lys Tyr Tyr Val Ser His Gln Trp Phe Pro
 20 25 30
 tta ggc gca gta cat ggc tta aag tat tgg tat aac tac acg agt gat 144
 Leu Gly Ala Val His Gly Leu Lys Tyr Trp Tyr Asn Tyr Thr Ser Asp
 35 40 45

gac tta ata aac ttt aaa cct gaa ggg cca ata tta aat cca gat act 192
 Asp Leu Ile Asn Phe Lys Pro Glu Gly Pro Ile Leu Asn Pro Asp Thr
 50 55 60

aaa tat gac agc cat ggt gtt tat agc ggt agc gct ttt gaa tat aac 240
 Lys Tyr Asp Ser His Gly Val Tyr Ser Gly Ser Ala Phe Glu Tyr Asn
 65 70 75 80

ggg cat tta tat tat atg tac aca gga aat cat cga gat aat cat tgg 288
 Gly His Leu Tyr Tyr Met Tyr Thr Gly Asn His Arg Asp Asn His Trp
 85 90 95

caa cga cat gcg agt cag atg atc gca cga ttg aaa gaa gac ggt tca 336
 Gln Arg His Ala Ser Gln Met Ile Ala Arg Leu Lys Glu Asp Gly Ser
 100 105 110

gtt gaa aag ttt cca aag cca gta att agc cag caa cca gaa gga tat 384
 Val Glu Lys Phe Pro Lys Pro Val Ile Ser Gln Gln Pro Glu Gly Tyr
 115 120 125

aca agt cat ttt aga gat cct aaa gtt ttt aaa tat ggt gag aaa tat 432
 Thr Ser His Phe Arg Asp Pro Lys Val Phe Lys Tyr Gly Glu Lys Tyr
 130 135 140

tat gca atc att ggc gca caa aat aat gat cag caa ggt cga tta tta 480
 Tyr Ala Ile Ile Gly Ala Gln Asn Asn Asp Gln Gln Gly Arg Leu Leu
 145 150 155 160

ctt tat aat act gaa gat ata att aat tgg cat tat tta ggt gaa ata 528
 Leu Tyr Asn Thr Glu Asp Ile Ile Asn Trp His Tyr Leu Gly Glu Ile
 165 170 175

aat aca gag tta gat gat ttt gga tat atg tgg gaa tgc cca gat tac 576
 Asn Thr Glu Leu Asp Asp Phe Gly Tyr Met Trp Glu Cys Pro Asp Tyr
 180 185 190

ttt aat tta gat aat caa gat gtc ata ctt att tgt cca caa ggt att 624
 Phe Asn Leu Asp Asn Gln Asp Val Ile Leu Ile Cys Pro Gln Gly Ile
 195 200 205

gaa cca aaa ggc aat cag ttc aaa aat att tat caa agt ggt tat ata 672
 Glu Pro Lys Gly Asn Gln Phe Lys Asn Ile Tyr Gln Ser Gly Tyr Ile
 210 215 220

ctt gga aag ttt gat att gaa aag tta aca tat gaa cat gaa aat ttt 720
 Leu Gly Lys Phe Asp Ile Glu Lys Leu Thr Tyr Glu His Glu Asn Phe
 225 230 235 240

<210> 350

<211> 240

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 350

Pro Phe His Ile Gln Pro Glu Thr Gly Leu Leu Asn Asp Pro Asn Gly
 1 5 10 15

Leu Ile Phe Tyr Lys Gly Lys Tyr Tyr Val Ser His Gln Trp Phe Pro
 20 25 30

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<400> 351
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agacactggc gtaattgagt gaaggcagga caataaagag atg acg aac gtt tcc 115
                                     Met Thr Asn Val Ser
                                     1                               5

ggg tat cac cga cca gag ctg cac atc acc gct gaa agt ggt gtt ttg 163

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Gly	Tyr	His	Arg	Pro	Glu	Leu	His	Ile	Thr	Ala	Glu	Ser	Gly	Val	Leu		
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ttt	gca	cct	gca	ggc	gtt	ctg	ttg	gat	gac	gac	acg	tgg	cat	ttc	ttc	211	
Phe	Ala	Pro	Ala	Gly	Val	Leu	Leu	Asp	Asp	Asp	Thr	Trp	His	Phe	Phe		
			25					30					35				
cac	cag	tac	cgt	ccc	tca	cca	gat	cac	ggc	ccc	agg	tgg	gcg	cac	caa	259	
His	Gln	Tyr	Arg	Pro	Ser	Pro	Asp	His	Gly	Pro	Arg	Trp	Ala	His	Gln		
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ttc	gca	gag	cgc	act	cca	ttt	gtg	tgg	gat	atc	tgc	gat	gac	gtg	cta	307	
Phe	Ala	Glu	Arg	Thr	Pro	Phe	Val	Trp	Asp	Ile	Cys	Asp	Asp	Val	Leu		
	55					60					65						
gcc	cct	gaa	ggc	gat	gaa	acc	cag	gtt	cgc	gct	ggc	tca	gtg	gtg	tcc	355	
Ala	Pro	Glu	Gly	Asp	Glu	Thr	Gln	Val	Arg	Ala	Gly	Ser	Val	Val	Ser		
70					75				80						85		
aac	aac	ggt	ggc	gtt	gat	ctg	tac	ttc	acc	tgc	gtt	gtt	ggc	ccc	act	403	
Asn	Asn	Gly	Gly	Val	Asp	Leu	Tyr	Phe	Thr	Ser	Val	Val	Gly	Pro	Thr		
				90					95					100			
tcc	act	atc	cag	ttg	gca	cac	atc	aac	aac	atc	cgt	ggc	acc	acc	gaa	451	
Ser	Thr	Ile	Gln	Leu	Ala	His	Ile	Asn	Asn	Ile	Arg	Gly	Thr	Thr	Glu		
			105					110					115				
ctg	atc	aat	gag	gac	gag	ctg	ggg	ctc	gat	cca	gat	gtc	tcc	cga	atc	499	
Leu	Ile	Asn	Glu	Asp	Glu	Leu	Gly	Leu	Asp	Pro	Asp	Val	Ser	Arg	Ile		
		120					125					130					
ggc	gaa	gtg	gtt	ggc	aac	act	gat	ggt	tat	gta	aag	ttc	cgc	tca	ccg	547	
Gly	Glu	Val	Val	Gly	Asn	Thr	Asp	Gly	Tyr	Val	Lys	Phe	Arg	Ser	Pro		
	135					140					145						
tgc	gtt	atc	cca	ggt	tgg	gaa	gac	caa	gga	aac	cgc	gat	gaa	ggc	cac	595	
Cys	Val	Ile	Pro	Gly	Trp	Glu	Asp	Gln	Gly	Asn	Arg	Asp	Glu	Gly	His		
150					155				160						165		
tca	gga	tgg	ttg	atg	ctc	gca	gtt	act	ggc	cca	gtt	gaa	gcc	cca	aca	643	
Ser	Gly	Trp	Leu	Met	Leu	Ala	Val	Thr	Gly	Pro	Val	Glu	Ala	Pro	Thr		
				170					175					180			
gta	gtg	gtc	ctc	gac	tgc	cca	gat	gga	aga	gaa	tgg	tcc	att	aca	ggt	691	
Val	Val	Val	Leu	Asp	Ser	Pro	Asp	Gly	Arg	Glu	Trp	Ser	Ile	Thr	Gly		
			185					190					195				
ccc	ctg	tct	ctc	aac	ggc	ctc	tct	gga	tta	gag	tca	gac	gaa	gtt	cta	739	
Pro	Leu	Ser	Leu	Asn	Gly	Leu	Ser	Gly	Leu	Glu	Ser	Asp	Glu	Val	Leu		
		200					205					210					
gtt	gct	cct	cgc	atg	att	cgt	ctg	cgc	gat	gaa	gtg	gat	cat	gaa	atc	787	
Val	Ala	Pro	Arg	Met	Ile	Arg	Leu	Arg	Asp	Glu	Val	Asp	His	Glu	Ile		
	215					220					225						
tac	gat	gtc	ctc	att	gtc	acc	att	gaa	caa	gac	ggg	att	gac	att	tgc	835	
Tyr	Asp	Val	Leu	Ile	Val	Thr	Ile	Glu	Gln	Asp	Gly	Ile	Asp	Ile	Ser		
230					235					240					245		
gga	tac	ctg	gta	ggc	cag	ctc	aac	ggc	tca	gaa	ttc	gat	gtg	aag	act	883	
Gly	Tyr	Leu	Val	Gly	Gln	Leu	Asn	Gly	Ser	Glu	Phe	Asp	Val	Lys	Thr		

494

atgcgttcca gcc

1617

<210> 352

<211> 498

<212> PRT

<213> Corynebacterium glutamicum

<400> 352

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Glu Ser Gly Val Leu Phe Ala Pro Ala Gly Val Leu Leu Asp Asp Asp
 20 25 30

Thr Trp His Phe Phe His Gln Tyr Arg Pro Ser Pro Asp His Gly Pro
 35 40 45

Arg Trp Ala His Gln Phe Ala Glu Arg Thr Pro Phe Val Trp Asp Ile
 50 55 60

Cys Asp Asp Val Leu Ala Pro Glu Gly Asp Glu Thr Gln Val Arg Ala
 65 70 75 80

Gly Ser Val Val Ser Asn Asn Gly Gly Val Asp Leu Tyr Phe Thr Ser
 85 90 95

Val Val Gly Pro Thr Ser Thr Ile Gln Leu Ala His Ile Asn Asn Ile
 100 105 110

Arg Gly Thr Thr Glu Leu Ile Asn Glu Asp Glu Leu Gly Leu Asp Pro
 115 120 125

Asp Val Ser Arg Ile Gly Glu Val Val Gly Asn Thr Asp Gly Tyr Val
 130 135 140

Lys Phe Arg Ser Pro Cys Val Ile Pro Gly Trp Glu Asp Gln Gly Asn
 145 150 155 160

Arg Asp Glu Gly His Ser Gly Trp Leu Met Leu Ala Val Thr Gly Pro
 165 170 175

Val Glu Ala Pro Thr Val Val Val Leu Asp Ser Pro Asp Gly Arg Glu
 180 185 190

Trp Ser Ile Thr Gly Pro Leu Ser Leu Asn Gly Leu Ser Gly Leu Glu
 195 200 205

Ser Asp Glu Val Leu Val Ala Pro Arg Met Ile Arg Leu Arg Asp Glu
 210 215 220

Val Asp His Glu Ile Tyr Asp Val Leu Ile Val Thr Ile Glu Gln Asp
 225 230 235 240

Gly Ile Asp Ile Ser Gly Tyr Leu Val Gly Gln Leu Asn Gly Ser Glu
 245 250 255

Phe Asp Val Lys Thr Pro Phe Thr Arg Ile Asp Phe Gly His Asp Phe
 260 265 270

Ser Arg Pro Arg Asn Thr Asn Tyr Ala Glu Thr Thr Ile Gly Tyr Asp
 275 280 285
 Phe Ala His Ile Phe Gly Leu Met Asn Gly Val Gly Arg Leu Asp Ser
 290 295 300
 Pro Thr Glu His Leu Ser Trp Lys Glu Glu Gly Trp Ala Asn Ala Ile
 305 310 315 320
 Ser Phe Pro Arg Ile Val Thr Leu Gln Asp Gly Thr Val Phe Gln Thr
 325 330 335
 Pro Pro Glu Gly Leu Leu Asp Ala Ile His Glu Ser Glu Ala Ala Ala
 340 345 350
 Gly Trp Thr Gly Leu Cys Glu Ile Pro Ser Asn Ser Ala Val Glu Val
 355 360 365
 Ala Leu Lys Asp Gln Glu Gly Glu Ile Ala Ala Thr Ile Thr His Arg
 370 375 380
 His Asn Gln Leu Val Val Asp Arg Ser Met Asn Pro Asn His Ala Gly
 385 390 395 400
 Asp Pro His Ala Ile Ala Pro Leu Thr Asp Asp Glu Thr Asp Ser Leu
 405 410 415
 Phe Ile Val Val Asp Gly Ser Thr Val Glu Val Phe Ala Asp Gly Gly
 420 425 430
 Tyr Val Ser Met Ala Ser Arg Val Tyr Phe Asn Asn Gly Pro Phe Ser
 435 440 445
 Glu Phe Glu Val Thr Thr Thr Gly Asp Ala Ser Ile Ile Arg Gln Glu
 450 455 460
 Ser His Phe Pro Val Asp Phe Ser Ser Val Ser Leu Asp Ile Asp Asp
 465 470 475 480
 Leu Thr Ala Leu Met Gln Phe Asp Glu Asn Glu Pro His Glu Gly Pro
 485 490 495
 Val Arg

<210> 353
 <211> 1305
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
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 <222> (101)..(1282)
 <223> RXN01369

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 gtcagccacg acctattcca ttgaagaaaa ggacttgtaa atg gag cta ttg gaa 115
 Met Glu Leu Leu Glu

1														5
ggc tca ctg cgc acc tac cca tgg ggt tca aga aca ctg atc gct gat	163													
Gly Ser Leu Arg Thr Tyr Pro Trp Gly Ser Arg Thr Leu Ile Ala Asp														
10					15					20				
ctc aaa ggc gaa gaa tca cca tcg tct cgc cca gag gcc gaa gtc tgg	211													
Leu Lys Gly Glu Glu Ser Pro Ser Ser Arg Pro Glu Ala Glu Val Trp														
25					30					35				
ttc ggt gcc cac cca gga tca cca tca acc atc ggt gga aac gca ctc	259													
Phe Gly Ala His Pro Gly Ser Pro Ser Thr Ile Gly Gly Asn Ala Leu														
40					45					50				
aac gaa gtc atc gca gcg aac ccc gaa gaa gca ttg ggc acg cgt gtt	307													
Asn Glu Val Ile Ala Ala Asn Pro Glu Glu Ala Leu Gly Thr Arg Val														
55					60					65				
gcc gaa gcg ttt gaa aat gag ctt cca ttc ctc ctc aaa atc ctc gca	355													
Ala Glu Ala Phe Glu Asn Glu Leu Pro Phe Leu Leu Lys Ile Leu Ala														
70					75					80				85
gcg gga gca ccc cta tca ctg cag gcc cac cca tcg ctg gaa cag gcc	403													
Ala Gly Ala Pro Leu Ser Leu Gln Ala His Pro Ser Leu Glu Gln Ala														
90					95					100				
cgt gaa gga ttc gcc cgc gaa aac tca gca gga att gac ctc ggc gca	451													
Arg Glu Gly Phe Ala Arg Glu Asn Ser Ala Gly Ile Asp Leu Gly Ala														
105					110					115				
ccg aac cgc aac tac cgc gac cca aac cac aag cca gag ctg atc gtt	499													
Pro Asn Arg Asn Tyr Arg Asp Pro Asn His Lys Pro Glu Leu Ile Val														
120					125					130				
gct ctc acg gaa ttc atc gcg atg gca ggc ttc cgc cca ctg cgg aac	547													
Ala Leu Thr Glu Phe Ile Ala Met Ala Gly Phe Arg Pro Leu Arg Asn														
135					140					145				
acc ctc acc att ttc gac gcc ctc gcc tgc gaa ccc ctc gac cgc tac	595													
Thr Leu Thr Ile Phe Asp Ala Leu Ala Cys Glu Pro Leu Asp Arg Tyr														
150					155					160				165
cgc agc atg ctc acc gtc gac aac gag gaa gaa tcc ctc cgc gca ctg	643													
Arg Ser Met Leu Thr Val Asp Asn Glu Glu Glu Ser Leu Arg Ala Leu														
170					175					180				
ttt acc acc tgg atc acc atc ccc atc ggt aaa cga cac gaa ctc atc	691													
Phe Thr Thr Trp Ile Thr Ile Pro Ile Gly Lys Arg His Glu Leu Ile														
185					190					195				
gat gcc ctc atc agc aac gcc cac acc tac ctt gag gca agc gat cgt	739													
Asp Ala Leu Ile Ser Asn Ala His Thr Tyr Leu Glu Ala Ser Asp Arg														
200					205					210				
gac gag gac atc gca ttc gtg ctc tca cac atc atc gag ctc aac gaa	787													
Asp Glu Asp Ile Ala Phe Val Leu Ser His Ile Ile Glu Leu Asn Glu														
215					220					225				
cag tac ccc ggc gat gtc ggc gtt ctg ggt gct ctg ctg ttg aac ttc	835													
Gln Tyr Pro Gly Asp Val Gly Val Leu Gly Ala Leu Leu Leu Asn Phe														
230					235					240				245

tac aaa ctt gcc cca ggc gaa gcc ctc tac ctc gac gcc gca aac ctt 883
 Tyr Lys Leu Ala Pro Gly Glu Ala Leu Tyr Leu Asp Ala Ala Asn Leu
 250 255 260

cac gca tac atc agc ggc ctc ggc gta gag atc atg gcg aac tcc gac 931
 His Ala Tyr Ile Ser Gly Leu Gly Val Glu Ile Met Ala Asn Ser Asp
 265 270 275

aac gtg ctc cgc ggt gga ctg aca tcc aaa tac gtc gac gtc ccg gag 979
 Asn Val Leu Arg Gly Gly Leu Thr Ser Lys Tyr Val Asp Val Pro Glu
 280 285 290

ctt gtg cgc gtg ttg gat ttc aac tct ttg gaa aac gct cgc gtg gac 1027
 Leu Val Arg Val Leu Asp Phe Asn Ser Leu Glu Asn Ala Arg Val Asp
 295 300 305

gtt gaa gaa gac ggt gca acg acc cac tac cca gtt cca atc aac gaa 1075
 Val Glu Glu Asp Gly Ala Thr Thr His Tyr Pro Val Pro Ile Asn Glu
 310 315 320 325

ttc caa ctc gat cgc gtt gca gtt cag ggc gaa gca gaa gcc aac cac 1123
 Phe Gln Leu Asp Arg Val Ala Val Gln Gly Glu Ala Glu Ala Asn His
 330 335 340

gat ggt ccc atg att gtt ctg tgc acc tcc gga act gtt tcc ttg gaa 1171
 Asp Gly Pro Met Ile Val Leu Cys Thr Ser Gly Thr Val Ser Leu Glu
 345 350 355

gca ggg gag aag acc ctc gaa gta gca gca ggt cac gcc gca tgg gtt 1219
 Ala Gly Glu Lys Thr Leu Glu Val Ala Ala Gly His Ala Ala Trp Val
 360 365 370

cca gca aac gac cca acc att gcg atg cgt tct gag gac gca gaa gta 1267
 Pro Ala Asn Asp Pro Thr Ile Ala Met Arg Ser Glu Asp Ala Glu Val
 375 380 385

ttc ctc gct agg gtt tagatctttt tagattaaaa tca 1305
 Phe Leu Ala Arg Val
 390

<210> 354
 <211> 394
 <212> PRT
 <213> *Corynebacterium glutamicum*

<400> 354
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 Thr Leu Ile Ala Asp Leu Lys Gly Glu Glu Ser Pro Ser Ser Arg Pro
 20 25 30
 Glu Ala Glu Val Trp Phe Gly Ala His Pro Gly Ser Pro Ser Thr Ile
 35 40 45
 Gly Gly Asn Ala Leu Asn Glu Val Ile Ala Ala Asn Pro Glu Glu Ala
 50 55 60
 Leu Gly Thr Arg Val Ala Glu Ala Phe Glu Asn Glu Leu Pro Phe Leu

65	70	75	80
Leu Lys Ile Leu	Ala Gly Ala Pro	Leu Ser Leu Gln	Ala His Pro
	85	90	95
Ser Leu Glu Gln	Ala Arg Glu Gly	Phe Ala Arg Glu	Asn Ser Ala Gly
	100	105	110
Ile Asp Leu Gly	Ala Pro Asn Arg	Asn Tyr Arg Asp	Pro Asn His Lys
	115	120	125
Pro Glu Leu Ile	Val Ala Leu Thr	Glu Phe Ile Ala	Met Ala Gly Phe
	130	135	140
Arg Pro Leu Arg	Asn Thr Leu Thr	Ile Phe Asp Ala	Leu Ala Cys Glu
	145	150	155
Pro Leu Asp Arg	Tyr Arg Ser Met	Leu Thr Val Asp	Asn Glu Glu Glu
	165	170	175
Ser Leu Arg Ala	Leu Phe Thr Thr	Trp Ile Thr Ile	Pro Ile Gly Lys
	180	185	190
Arg His Glu Leu	Ile Asp Ala Leu	Ile Ser Asn Ala	His Thr Tyr Leu
	195	200	205
Glu Ala Ser Asp	Arg Asp Glu Asp	Ile Ala Phe Val	Leu Ser His Ile
	210	215	220
Ile Glu Leu Asn	Glu Gln Tyr Pro	Gly Asp Val Gly	Val Leu Gly Ala
	225	230	240
Leu Leu Leu Asn	Phe Tyr Lys Leu	Ala Pro Gly Glu	Ala Leu Tyr Leu
	245	250	255
Asp Ala Ala Asn	Leu His Ala Tyr	Ile Ser Gly Leu	Gly Val Glu Ile
	260	265	270
Met Ala Asn Ser	Asp Asn Val Leu	Arg Gly Gly Leu	Thr Ser Lys Tyr
	275	280	285
Val Asp Val Pro	Glu Leu Val Arg	Val Leu Asp Phe	Asn Ser Leu Glu
	290	295	300
Asn Ala Arg Val	Asp Val Glu Glu	Asp Gly Ala Thr	Thr His Tyr Pro
	305	310	315
Val Pro Ile Asn	Glu Phe Gln Leu	Asp Arg Val Ala	Val Gln Gly Glu
	325	330	335
Ala Glu Ala Asn	His Asp Gly Pro	Met Ile Val Leu	Cys Thr Ser Gly
	340	345	350
Thr Val Ser Leu	Glu Ala Gly Glu	Lys Thr Leu Glu	Val Ala Ala Gly
	355	360	365
His Ala Ala Trp	Val Pro Ala Asn	Asp Pro Thr Ile	Ala Met Arg Ser
	370	375	380
Glu Asp Ala Glu	Val Phe Leu Ala	Arg Val	
	385	390	

<210> 355
 <211> 524
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (1)..(501)
 <223> FRXA01369

<400> 355
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 1 5 10 15
 aac ttc tac aaa ctt gcc cca ggc gaa gcc ctc tac ctc gac gcc gca 96
 Asn Phe Tyr Lys Leu Ala Pro Gly Glu Ala Leu Tyr Leu Asp Ala Ala
 20 25 30
 aac ctt cac gca tac atc agc ggc ctc ggc gta gag atc atg gcg aac 144
 Asn Leu His Ala Tyr Ile Ser Gly Leu Gly Val Glu Ile Met Ala Asn
 35 40 45
 tcc gac aac gtg ctc cgc ggt gga ctg aca tcc aaa tac gtc gac gtc 192
 Ser Asp Asn Val Leu Arg Gly Gly Leu Thr Ser Lys Tyr Val Asp Val
 50 55 60
 ccg gag ctt gtg cgc gtg ttg gat ttc aac tct ttg gaa aac gct cgc 240
 Pro Glu Leu Val Arg Val Leu Asp Phe Asn Ser Leu Glu Asn Ala Arg
 65 70 75 80
 gtg gac gtt gaa gaa gac ggt gca acg acc cac tac cca gtt cca atc 288
 Val Asp Val Glu Glu Asp Gly Ala Thr Thr His Tyr Pro Val Pro Ile
 85 90 95
 aac gaa ttc caa ctc gat cgc gtt gca gtt cag ggc gaa gca gaa gcc 336
 Asn Glu Phe Gln Leu Asp Arg Val Ala Val Gln Gly Glu Ala Glu Ala
 100 105 110
 aac cac gat ggt ccc atg att gtt ctg tgc acc tcc gga act gtt tcc 384
 Asn His Asp Gly Pro Met Ile Val Leu Cys Thr Ser Gly Thr Val Ser
 115 120 125
 ttg gaa gca ggg gag aag acc ctc gaa gta gca gca ggt cac gcc gca 432
 Leu Glu Ala Gly Glu Lys Thr Leu Glu Val Ala Ala Gly His Ala Ala
 130 135 140
 tgg gtt cca gca aac gac cca acc att gcg atg cgt tct gag gac gca 480
 Trp Val Pro Ala Asn Asp Pro Thr Ile Ala Met Arg Ser Glu Asp Ala
 145 150 155 160
 gaa gta ttc ctc gct agg gtt tagatctttt tagattaaaa tca 524
 Glu Val Phe Leu Ala Arg Val
 165

<210> 356
 <211> 167
 <212> PRT

<213> Corynebacterium glutamicum

<400> 356

Asn Glu Gln Cys Leu Gly Asp Val Gly Val Leu Gly Ala Leu Leu Leu
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 Asn Phe Tyr Lys Leu Ala Pro Gly Glu Ala Leu Tyr Leu Asp Ala Ala
 20 25 30
 Asn Leu His Ala Tyr Ile Ser Gly Leu Gly Val Glu Ile Met Ala Asn
 35 40 45
 Ser Asp Asn Val Leu Arg Gly Gly Leu Thr Ser Lys Tyr Val Asp Val
 50 55 60
 Pro Glu Leu Val Arg Val Leu Asp Phe Asn Ser Leu Glu Asn Ala Arg
 65 70 75 80
 Val Asp Val Glu Glu Asp Gly Ala Thr Thr His Tyr Pro Val Pro Ile
 85 90 95
 Asn Glu Phe Gln Leu Asp Arg Val Ala Val Gln Gly Glu Ala Glu Ala
 100 105 110
 Asn His Asp Gly Pro Met Ile Val Leu Cys Thr Ser Gly Thr Val Ser
 115 120 125
 Leu Glu Ala Gly Glu Lys Thr Leu Glu Val Ala Ala Gly His Ala Ala
 130 135 140
 Trp Val Pro Ala Asn Asp Pro Thr Ile Ala Met Arg Ser Glu Asp Ala
 145 150 155 160
 Glu Val Phe Leu Ala Arg Val
 165

<210> 357

<211> 808

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(808)

<223> FRXA01373

<400> 357

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 gtcagccacg acctattcca ttgaagaaaa ggacttgtaa atg gag cta ttg gaa 115
 Met Glu Leu Leu Glu
 1 5
 ggc tca ctg cgc acc tac cca tgg ggt tca aga aca ctg atc gct gat 163
 Gly Ser Leu Arg Thr Tyr Pro Trp Gly Ser Arg Thr Leu Ile Ala Asp
 10 15 20
 ctc aaa ggc gaa gaa tca cca tcg tct cgc cca gag gcc gaa gtc tgg 211
 Leu Lys Gly Glu Glu Ser Pro Ser Ser Arg Pro Glu Ala Glu Val Trp
 25 30 35

ttc ggt gcc cac cca gga tca cca tca acc atc ggt gga aac gca ctc Phe Gly Ala His Pro Gly Ser Pro Ser Thr Ile Gly Gly Asn Ala Leu 40 45 50	259
aac gaa gtc atc gca gcg aac ccc gaa gaa gca ttg ggc acg cgt gtt Asn Glu Val Ile Ala Ala Asn Pro Glu Glu Ala Leu Gly Thr Arg Val 55 60 65	307
gcc gaa gcg ttt gaa aat gag ctt cca ttc ctc ctc aaa atc ctc gca Ala Glu Ala Phe Glu Asn Glu Leu Pro Phe Leu Leu Lys Ile Leu Ala 70 75 80 85	355
gcg gga gca ccc cta tca ctg cag gcc cac cca tcg ctg gaa cag gcc Ala Gly Ala Pro Leu Ser Leu Gln Ala His Pro Ser Leu Glu Gln Ala 90 95 100	403
cgt gaa gga ttc gcc cgc gaa aac tca gca gga att gac ctc ggc gca Arg Glu Gly Phe Ala Arg Glu Asn Ser Ala Gly Ile Asp Leu Gly Ala 105 110 115	451
ccg aac cgc aac tac cgc gac cca aac cac aag cca gag ctg atc gtt Pro Asn Arg Asn Tyr Arg Asp Pro Asn His Lys Pro Glu Leu Ile Val 120 125 130	499
gct ctc acg gaa ttc atc gcg atg gca ggc ttc cgc cca ctg cgg aac Ala Leu Thr Glu Phe Ile Ala Met Ala Gly Phe Arg Pro Leu Arg Asn 135 140 145	547
acc ctc acc att ttc gac gcc ctc gcc tgc gaa ccc ctc gac cgc tac Thr Leu Thr Ile Phe Asp Ala Leu Ala Cys Glu Pro Leu Asp Arg Tyr 150 155 160 165	595
cgc agc atg ctc acc gtc gac aac gag gaa gaa tcc ctc cgc gca ctg Arg Ser Met Leu Thr Val Asp Asn Glu Glu Glu Ser Leu Arg Ala Leu 170 175 180	643
ttt acc acc tgg atc acc atc ccc atc ggt aaa cga cac gaa ctc atc Phe Thr Thr Trp Ile Thr Ile Pro Ile Gly Lys Arg His Glu Leu Ile 185 190 195	691
gat gcc ctc atc agc aac gcc cac acc tac ctt gag gca agc gat cgt Asp Ala Leu Ile Ser Asn Ala His Thr Tyr Leu Glu Ala Ser Asp Arg 200 205 210	739
gac gag gac atc gca ttc gtg ctc tca cac atc atc gag ctc aac gaa Asp Glu Asp Ile Ala Phe Val Leu Ser His Ile Ile Glu Leu Asn Glu 215 220 225	787
cag tac ccc ggc gat gtc ggc Gln Tyr Pro Gly Asp Val Gly 230 235	808

<210> 358

<211> 236

<212> PRT

<213> Corynebacterium glutamicum

<400> 358

Met Glu Leu Leu Glu Gly Ser Leu Arg Thr Tyr Pro Trp Gly Ser Arg


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<400> 359
gat gcg tgg tcg gat cct atg gct acg tgg cgt cat gcg att acc act 48
Asp Ala Trp Ser Asp Pro Met Ala Thr Trp Arg His Ala Ile Thr Thr
  1             5             10             15
aag att gag gcc ggc cag ggt tcg gat gag ttg tat aac gac ttt gag 96

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Lys	Ile	Glu	Ala	Gly	Gln	Gly	Ser	Asp	Glu	Leu	Tyr	Asn	Asp	Phe	Glu		
			20					25					30				
cac	ggg	gct	cag	ctg	ttt	gag	cgt	gct	gcg	gag	aat	ttg	tct	aaa	gag	144	
His	Gly	Ala	Gln	Leu	Phe	Glu	Arg	Ala	Ala	Glu	Asn	Leu	Ser	Lys	Glu		
			35				40					45					
gat	agg	act	gcg	ctt	ttc	gac	gtc	gcc	tcc	tct	ctg	cgg	cgc	ggc	ggc	192	
Asp	Arg	Thr	Ala	Leu	Phe	Asp	Val	Ala	Ser	Ser	Leu	Arg	Arg	Gly	Gly		
		50					55				60						
gat	gta	cgc	gca	cgt	ctc	gcc	cca	gcg	ctc	acc	gcg	agt	gtc	act	cat	240	
Asp	Val	Arg	Ala	Arg	Leu	Ala	Pro	Ala	Leu	Thr	Ala	Ser	Val	Thr	His		
	65				70				75						80		
ctt	tta	gaa	ctt	aac	ccg	ttg	cgt	gag	ttg	gtc	acg	atg	ggg	gaa	aac	288	
Leu	Leu	Glu	Leu	Asn	Pro	Leu	Arg	Glu	Leu	Val	Thr	Met	Gly	Glu	Asn		
				85					90					95			
ctg	cag	gtt	cgt	gtc	gag	cgt	cgt	gcc	gct	ttg	gtc	aac	tct	tgg	tat	336	
Leu	Gln	Val	Arg	Val	Glu	Arg	Arg	Ala	Ala	Leu	Val	Asn	Ser	Trp	Tyr		
			100					105					110				
gag	ctt	ttc	cct	cgt	tcc	aca	ggg	ggg	tgg	gat	gag	tcc	ggc	acc	ccc	384	
Glu	Leu	Phe	Pro	Arg	Ser	Thr	Gly	Gly	Trp	Asp	Glu	Ser	Gly	Thr	Pro		
		115					120					125					
gtt	cat	ggc	act	ttc	gct	acc	act	gct	cag	gcg	ttg	gag	cgt	gtc	gcg	432	
Val	His	Gly	Thr	Phe	Ala	Thr	Thr	Ala	Gln	Ala	Leu	Glu	Arg	Val	Ala		
	130					135					140						
aag	atg	ggc	ttc	gat	act	gtt	tac	ttc	ccg	ccg	atc	cat	ccg	att	ggc	480	
Lys	Met	Gly	Phe	Asp	Thr	Val	Tyr	Phe	Pro	Pro	Ile	His	Pro	Ile	Gly		
	145				150					155					160		
gag	gtc	aac	cgc	aag	ggc	cgc	aat	aat	acg	ctg	acc	ccg	gaa	cct	cat	528	
Glu	Val	Asn	Arg	Lys	Gly	Arg	Asn	Asn	Thr	Leu	Thr	Pro	Glu	Pro	His		
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Asp	Val	Gly	Ser	Pro	Trp	Ala	Ile	Gly	Ser	Lys	Asp	Gly	Gly	His	Asp		
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gca	acg	cat	ccg	cgg	ttg	ggc	acc	att	gaa	gat	ttc	cag	gcg	ttg	ttg	624	
Ala	Thr	His	Pro	Arg	Leu	Gly	Thr	Ile	Glu	Asp	Phe	Gln	Ala	Leu	Leu		
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gct	cgc	gca	cgg	gaa	ctc	aat	ttg	gaa	gtt	gca	ctc	gat	cta	gct	ctg	672	
Ala	Arg	Ala	Arg	Glu	Leu	Asn	Leu	Glu	Val	Ala	Leu	Asp	Leu	Ala	Leu		
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cag	gct	gcc	cct	gat	cat	cca	tgg	gcg	cag	gaa	cac	cgc	gag	ttt	ttc	720	
Gln	Ala	Ala	Pro	Asp	His	Pro	Trp	Ala	Gln	Glu	His	Arg	Glu	Phe	Phe		
	225				230					235					240		
acg	gtg	ttg	gct	gat	ggc	acc	att	gcg	tat	gca	gaa	aac	cca	ccg	aag	768	
Thr	Val	Leu	Ala	Asp	Gly	Thr	Ile	Ala	Tyr	Ala	Glu	Asn	Pro	Pro	Lys		
				245				250					255				
aag	tac	cag	gat	att	tat	ccc	atc	aac	ttt	gat	aat	gat	gct	ccg	aag	816	
Lys	Tyr	Gln	Asp	Ile	Tyr	Pro	Ile	Asn	Phe	Asp	Asn	Asp	Ala	Pro	Lys		

260					265					270						
atc	tac	gaa	gag	gtc	tat	cgt	gtg	gtg	aag	ttc	tgg	gtg	gat	ttg	ggg	864
Ile	Tyr	Glu	Glu	Val	Tyr	Arg	Val	Val	Lys	Phe	Trp	Val	Asp	Leu	Gly	
		275					280					285				
gtg	acc	aca	ttc	cgc	gtg	gat	aac	ccg	cac	act	aag	ccc	gct	aat	ttc	912
Val	Thr	Thr	Phe	Arg	Val	Asp	Asn	Pro	His	Thr	Lys	Pro	Ala	Asn	Phe	
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tgg	cag	tgg	ctt	att	tct	gcc	atc	cat	aaa	tca	aac	cct	gag	gtc	att	960
Trp	Gln	Trp	Leu	Ile	Ser	Ala	Ile	His	Lys	Ser	Asn	Pro	Glu	Val	Ile	
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ttc	cta	gcg	gag	gcg	tct	act	cgc	ccg	gca	cgt	ctg	tat	ttc	ttg	tcc	1008
Phe	Leu	Ala	Glu	Ala	Ser	Thr	Arg	Pro	Ala	Arg	Leu	Tyr	Phe	Leu	Ser	
				325					330					335		
aag	att	ggg	ttc	tcc	cag	tct	tac	acc	tac	ttc	acc	tgg	aag	gtc	acc	1056
Lys	Ile	Gly	Phe	Ser	Gln	Ser	Tyr	Thr	Tyr	Phe	Thr	Trp	Lys	Val	Thr	
			340					345					350			
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Asn	Glu	Glu	Leu	Thr	Glu	Phe	Ala	Thr	Glu	Ile	Ala	Pro	Met	Ala	Asp	
		355					360					365				
att	tct	cgt	ccg	aac	ctg	ttt	gtg	aac	act	ccc	gac	att	ttg	cat	gcg	1152
Ile	Ser	Arg	Pro	Asn	Leu	Phe	Val	Asn	Thr	Pro	Asp	Ile	Leu	His	Ala	
		370				375					380					
tct	ctg	cag	cat	ggg	gga	cgc	gcc	atg	ttc	gct	atc	cgc	gcc	gca	ttg	1200
Ser	Leu	Gln	His	Gly	Gly	Arg	Ala	Met	Phe	Ala	Ile	Arg	Ala	Ala	Leu	
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gcc	gcc	acg	atg	tct	cct	gtg	tgg	ggc	gta	tat	tcc	gga	tat	gag	ctc	1248
Ala	Ala	Thr	Met	Ser	Pro	Val	Trp	Gly	Val	Tyr	Ser	Gly	Tyr	Glu	Leu	
				405					410					415		
ttt	gag	cac	gag	gcc	gtc	aag	cct	ggg	tcg	gaa	gag	tac	ttg	gat	tct	1296
Phe	Glu	His	Glu	Ala	Val	Lys	Pro	Gly	Ser	Glu	Glu	Tyr	Leu	Asp	Ser	
			420					425					430			
gag	aag	tac	gag	ctg	cgt	ccc	cgc	gat	ttc	gag	ggg	gct	ctg	gaa	cgt	1344
Glu	Lys	Tyr	Glu	Leu	Arg	Pro	Arg	Asp	Phe	Glu	Gly	Ala	Leu	Glu	Arg	
		435					440					445				
ggc	gat	tct	ctc	gag	gat	tac	atc	gct	ctg	ctc	aac	cag	atc	cgt	cgc	1392
Gly	Asp	Ser	Leu	Glu	Asp	Tyr	Ile	Ala	Leu	Leu	Asn	Gln	Ile	Arg	Arg	
		450				455					460					
gcg	aac	cct	gcc	ttg	cag	caa	cta	cgc	aac	atc	cac	ttc	cac	gaa	gcg	1440
Ala	Asn	Pro	Ala	Leu	Gln	Gln	Leu	Arg	Asn	Ile	His	Phe	His	Glu	Ala	
465					470					475					480	
gac	aat	gat	cag	atc	atc	gcc	tac	tcc	aag	gtt	gat	gct	ttg	acc	gga	1488
Asp	Asn	Asp	Gln	Ile	Ile	Ala	Tyr	Ser	Lys	Val	Asp	Ala	Leu	Thr	Gly	
				485					490				495			
aat	acc	gtg	ttg	att	gtg	gtc	aac	ttg	gat	cca	cgt	agt	gct	cgt	gag	1536
Asn	Thr	Val	Leu	Ile	Val	Val	Asn	Leu	Asp	Pro	Arg	Ser	Ala	Arg	Glu	
		500						505					510			

gct act gtt cgc ctt gat ctt gga gcg ctt ggc tta gaa gcg ggt gca 1584
 Ala Thr Val Arg Leu Asp Leu Gly Ala Leu Gly Leu Glu Ala Gly Ala
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cag ttt gag gtg cgc gat gcg atc acc ggc tcc cgt tac ctg tgg tca 1632
 Gln Phe Glu Val Arg Asp Ala Ile Thr Gly Ser Arg Tyr Leu Trp Ser
 530 535 540

gag acg aac ttt gtc cgc ctc gag ccc cta cgc gat gtc gcc cac atc 1680
 Glu Thr Asn Phe Val Arg Leu Glu Pro Leu Arg Asp Val Ala His Ile
 545 550 555 560

ttt gtt ctt cct gaa ctt cca gcg tct cgc cgt gag cgt ctc gcg tgg 1728
 Phe Val Leu Pro Glu Leu Pro Ala Ser Arg Arg Glu Arg Leu Ala Trp
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<211> 584

<212> PRT

<213> Corynebacterium glutamicum

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His Gly Ala Gln Leu Phe Glu Arg Ala Ala Glu Asn Leu Ser Lys Glu
 35 40 45

Asp Arg Thr Ala Leu Phe Asp Val Ala Ser Ser Leu Arg Arg Gly Gly
 50 55 60

Asp Val Arg Ala Arg Leu Ala Pro Ala Leu Thr Ala Ser Val Thr His
 65 70 75 80

Leu Leu Glu Leu Asn Pro Leu Arg Glu Leu Val Thr Met Gly Glu Asn
 85 90 95

Leu Gln Val Arg Val Glu Arg Arg Ala Ala Leu Val Asn Ser Trp Tyr
 100 105 110

Glu Leu Phe Pro Arg Ser Thr Gly Gly Trp Asp Glu Ser Gly Thr Pro
 115 120 125

Val His Gly Thr Phe Ala Thr Thr Ala Gln Ala Leu Glu Arg Val Ala
 130 135 140

Lys Met Gly Phe Asp Thr Val Tyr Phe Pro Pro Ile His Pro Ile Gly
 145 150 155 160

Glu Val Asn Arg Lys Gly Arg Asn Asn Thr Leu Thr Pro Glu Pro His
 165 170 175

Asp Val Gly Ser Pro Trp Ala Ile Gly Ser Lys Asp Gly Gly His Asp
 180 185 190
 Ala Thr His Pro Arg Leu Gly Thr Ile Glu Asp Phe Gln Ala Leu Leu
 195 200 205
 Ala Arg Ala Arg Glu Leu Asn Leu Glu Val Ala Leu Asp Leu Ala Leu
 210 215 220
 Gln Ala Ala Pro Asp His Pro Trp Ala Gln Glu His Arg Glu Phe Phe
 225 230 235 240
 Thr Val Leu Ala Asp Gly Thr Ile Ala Tyr Ala Glu Asn Pro Pro Lys
 245 250 255
 Lys Tyr Gln Asp Ile Tyr Pro Ile Asn Phe Asp Asn Asp Ala Pro Lys
 260 265 270
 Ile Tyr Glu Glu Val Tyr Arg Val Val Lys Phe Trp Val Asp Leu Gly
 275 280 285
 Val Thr Thr Phe Arg Val Asp Asn Pro His Thr Lys Pro Ala Asn Phe
 290 295 300
 Trp Gln Trp Leu Ile Ser Ala Ile His Lys Ser Asn Pro Glu Val Ile
 305 310 315 320
 Phe Leu Ala Glu Ala Ser Thr Arg Pro Ala Arg Leu Tyr Phe Leu Ser
 325 330 335
 Lys Ile Gly Phe Ser Gln Ser Tyr Thr Tyr Phe Thr Trp Lys Val Thr
 340 345 350
 Asn Glu Glu Leu Thr Glu Phe Ala Thr Glu Ile Ala Pro Met Ala Asp
 355 360 365
 Ile Ser Arg Pro Asn Leu Phe Val Asn Thr Pro Asp Ile Leu His Ala
 370 375 380
 Ser Leu Gln His Gly Gly Arg Ala Met Phe Ala Ile Arg Ala Ala Leu
 385 390 395 400
 Ala Ala Thr Met Ser Pro Val Trp Gly Val Tyr Ser Gly Tyr Glu Leu
 405 410 415
 Phe Glu His Glu Ala Val Lys Pro Gly Ser Glu Glu Tyr Leu Asp Ser
 420 425 430
 Glu Lys Tyr Glu Leu Arg Pro Arg Asp Phe Glu Gly Ala Leu Glu Arg
 435 440 445
 Gly Asp Ser Leu Glu Asp Tyr Ile Ala Leu Leu Asn Gln Ile Arg Arg
 450 455 460
 Ala Asn Pro Ala Leu Gln Gln Leu Arg Asn Ile His Phe His Glu Ala
 465 470 475 480
 Asp Asn Asp Gln Ile Ile Ala Tyr Ser Lys Val Asp Ala Leu Thr Gly
 485 490 495
 Asn Thr Val Leu Ile Val Val Asn Leu Asp Pro Arg Ser Ala Arg Glu

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Ala Thr Val Arg Leu Asp Leu Gly Ala Leu Gly Leu Glu Ala Gly Ala		
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Gln Phe Glu Val Arg Asp Ala Ile Thr Gly Ser Arg Tyr Leu Trp Ser		
530	535	540
Glu Thr Asn Phe Val Arg Leu Glu Pro Leu Arg Asp Val Ala His Ile		
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Phe Val Leu Pro Glu Leu Pro Ala Ser Arg Arg Glu Arg Leu Ala Trp		
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 Met Thr Val Asp Pro
 1 5
 gcg agc cac atc acc atc cct gaa gca gat ctg gcc cgc ctg cgc cac 163
 Ala Ser His Ile Thr Ile Pro Glu Ala Asp Leu Ala Arg Leu Arg His
 10 15 20
 tgc aac cat cac gat cct cat gga ttt tat ggt tgg cat gag acc gaa 211
 Cys Asn His His Asp Pro His Gly Phe Tyr Gly Trp His Glu Thr Glu
 25 30 35
 gct ggt tcg gtt atc cgc acg cgc cag gtc ggc gcg acg cag gtt aat 259
 Ala Gly Ser Val Ile Arg Thr Arg Gln Val Gly Ala Thr Gln Val Asn
 40 45 50
 ttg ctt atc gac gac acc tcc cac gtc atg acc cct atc ggc gac gac 307
 Leu Leu Ile Asp Asp Thr Ser His Val Met Thr Pro Ile Gly Asp Asp
 55 60 65
 att ttc gca att gac tta ggt cac cgc gag cgc gct gac tat cgc ttg 355
 Ile Phe Ala Ile Asp Leu Gly His Arg Glu Arg Ala Asp Tyr Arg Leu
 70 75 80 85
 gaa gtc acc tgg cct gat caa gaa ccg cag gtc aag gct gat cca tac 403
 Glu Val Thr Trp Pro Asp Gln Glu Pro Gln Val Lys Ala Asp Pro Tyr
 90 95 100
 tac ttc ctc ccc acc gta ggc gag atg gat att tac ctc ttc tct gag 451
 Tyr Phe Leu Pro Thr Val Gly Glu Met Asp Ile Tyr Leu Phe Ser Glu

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gct cca aac gca att ggc tgc gca gtg gtc ggt ggc ttc aac ggt tgg Ala Pro Asn Ala Ile Gly Cys Ala Val Val Gly Gly Phe Asn Gly Trp 150 155 160 165			595
aat gca tcc cag cat ccg atg cgt tct atg ggt ggt tcc ggt ctg tgg Asn Ala Ser Gln His Pro Met Arg Ser Met Gly Gly Ser Gly Leu Trp 170 175 180			643
gag ctg ttc atc cca ggc ata gag gaa ggc gaa gtg tac aaa ttc gcc Glu Leu Phe Ile Pro Gly Ile Glu Glu Gly Glu Val Tyr Lys Phe Ala 185 190 195			691
gtc caa acc agg gaa ggc caa cgt cgt gat aag gcc gat ccg atg gct Val Gln Thr Arg Glu Gly Gln Arg Arg Asp Lys Ala Asp Pro Met Ala 200 205 210			739
cgt cgc gca gaa ctg gcg ccg gca acc gga tct att gtc gct tcc tct Arg Arg Ala Glu Leu Ala Pro Ala Thr Gly Ser Ile Val Ala Ser Ser 215 220 225			787
gag tac cag tgg cag gat tcc gag tgg ctg cgc gag cgt tcc caa act Glu Tyr Gln Trp Gln Asp Ser Glu Trp Leu Arg Glu Arg Ser Gln Thr 230 235 240 245			835
gat ctc gca tcc aag cca atg agt gtc tac gag gtc cac ctc ggt tct Asp Leu Ala Ser Lys Pro Met Ser Val Tyr Glu Val His Leu Gly Ser 250 255 260			883
tgg cgc tgg ggt aag aac tat gag gat ttg gct act gag ctg gtt gat Trp Arg Trp Gly Lys Asn Tyr Glu Asp Leu Ala Thr Glu Leu Val Asp 265 270 275			931
tac gtc gca gat ctt ggc tac acc cac gtg gaa ttc ctc cct gtc gca Tyr Val Ala Asp Leu Gly Tyr Thr His Val Glu Phe Leu Pro Val Ala 280 285 290			979
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gca ccg acc tct cgt tgg ggt act cca gat cag ttc cgt gcg cta gtc Ala Pro Thr Ser Arg Trp Gly Thr Pro Asp Gln Phe Arg Ala Leu Val 310 315 320 325			1075
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gcc cac ttc cct aag gat gat tgg gct ctt gcc cgc ttt gat ggc gaa Ala His Phe Pro Lys Asp Asp Trp Ala Leu Ala Arg Phe Asp Gly Glu 345 350 355			1171

gcc ctc tat gaa cac cct gac tgg agg cgc ggc gaa caa aag gat tgg	1219
Ala Leu Tyr Glu His Pro Asp Trp Arg Arg Gly Glu Gln Lys Asp Trp	
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Gly Thr Leu Val Phe Asp Phe Gly Arg Asn Glu Val Arg Asn Phe Leu	
375 380 385	
gtc gct aat gcg ttg tac tgg att gaa gaa ttc cac atc gat ggt ctg	1315
Val Ala Asn Ala Leu Tyr Trp Ile Glu Glu Phe His Ile Asp Gly Leu	
390 395 400 405	
cgc gtc gac gcc gtg gcc tcc atg ctg tac ctc gat tac tcc cgt gag	1363
Arg Val Asp Ala Val Ala Ser Met Leu Tyr Leu Asp Tyr Ser Arg Glu	
410 415 420	
cac ggc gaa tgg gaa cca aac atc tac ggt ggt cgc gag aac ctc gag	1411
His Gly Glu Trp Glu Pro Asn Ile Tyr Gly Gly Arg Glu Asn Leu Glu	
425 430 435	
gca gtg cag ttc ctg cag gaa atg aac gcc acg gtg ctg cga ctg cac	1459
Ala Val Gln Phe Leu Gln Glu Met Asn Ala Thr Val Leu Arg Leu His	
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Pro Gly Ala Leu Thr Ile Ala Glu Glu Ser Thr Ser Trp Pro Gly Val	
455 460 465	
acc gca cca acg tgg gac ggc ggc ttg gga ttc tcc ctc aag tgg aac	1555
Thr Ala Pro Thr Trp Asp Gly Gly Leu Gly Phe Ser Leu Lys Trp Asn	
470 475 480 485	
atg ggc tgg atg cac gac acc tta gag tac ttc tcc aaa aac cct gtg	1603
Met Gly Trp Met His Asp Thr Leu Glu Tyr Phe Ser Lys Asn Pro Val	
490 495 500	
cac cgc gca ttc cac cac agt gag ctc act ttc tcc ttg gtg tac gca	1651
His Arg Ala Phe His His Ser Glu Leu Thr Phe Ser Leu Val Tyr Ala	
505 510 515	
ttc tct gag cgt ttt gta ctt ccg atc tct cac gat gaa gtc gtc cac	1699
Phe Ser Glu Arg Phe Val Leu Pro Ile Ser His Asp Glu Val Val His	
520 525 530	
ggc aag ggt tcc ctg tgg gac cgt atg cct ggc gat acg tgg aac aag	1747
Gly Lys Gly Ser Leu Trp Asp Arg Met Pro Gly Asp Thr Trp Asn Lys	
535 540 545	
gcc gct ggt ctt cgc acc ttc ctt gcg tac atg tgg tca cac cca ggc	1795
Ala Ala Gly Leu Arg Thr Phe Leu Ala Tyr Met Trp Ser His Pro Gly	
550 555 560 565	
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Lys Lys Leu Leu Phe Met Gly Gln Glu Phe Gly Gln Arg Glu Glu Trp	
570 575 580	
gct gaa ggc cag gga ctg cca tgg gat att gtc gac ggc tgg caa ggc	1891
Ala Glu Gly Gln Gly Leu Pro Trp Asp Ile Val Asp Gly Trp Gln Gly	
585 590 595	

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 Glu Tyr His Glu Ala Ile Arg Thr Leu Thr Arg Ser Leu Asn Gly Val
 600 605 610
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 Tyr Ser Asp Ser Pro Ala Leu His Thr Gln Asp Phe Thr Gly Glu Gly
 615 620 625
 ttc aca tgg aat aag ggc gac gac gcc acc aac aac att ttg gcg ttc 2035
 Phe Thr Trp Asn Lys Gly Asp Asp Ala Thr Asn Asn Ile Leu Ala Phe
 630 635 640 645
 act cgt ttc ggc agc gac ggc tcc cag atg ctg tgt gta ttc aac ctg 2083
 Thr Arg Phe Gly Ser Asp Gly Ser Gln Met Leu Cys Val Phe Asn Leu
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 Ser Gly Thr Ser Gln Pro Glu Tyr Gln Leu Gly Val Ala Ala Gly Gly
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 Glu Trp Lys Leu Val Leu Asn Thr Asp Asp Ala Glu Phe Leu Gly Ala
 680 685 690
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 Glu Asn Asp Ile Ala Thr Ser Val Gln Ala Ala Ala Thr Pro Arg Asp
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 aat ttc gcc tac tca ctc tca ctg cat gtc cca gcg atg agt gct cag 2275
 Asn Phe Ala Tyr Ser Leu Ser Leu His Val Pro Ala Met Ser Ala Gln
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 730

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<212> PRT

<213> *Corynebacterium glutamicum*

<400> 362

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 Trp His Glu Thr Glu Ala Gly Ser Val Ile Arg Thr Arg Gln Val Gly
 35 40 45
 Ala Thr Gln Val Asn Leu Leu Ile Asp Asp Thr Ser His Val Met Thr
 50 55 60
 Pro Ile Gly Asp Asp Ile Phe Ala Ile Asp Leu Gly His Arg Glu Arg
 65 70 75 80
 Ala Asp Tyr Arg Leu Glu Val Thr Trp Pro Asp Gln Glu Pro Gln Val
 85 90 95

Lys Ala Asp Pro Tyr Tyr Phe Leu Pro Thr Val Gly Glu Met Asp Ile
 100 105 110
 Tyr Leu Phe Ser Glu Gly Arg His Glu Arg Leu Trp Glu Ile Leu Gly
 115 120 125
 Ala Asn Ile Lys Thr Tyr Gln Thr Ala Leu Gly Thr Val Arg Gly Thr
 130 135 140
 Ala Phe Thr Val Trp Ala Pro Asn Ala Ile Gly Cys Ala Val Val Gly
 145 150 155 160
 Gly Phe Asn Gly Trp Asn Ala Ser Gln His Pro Met Arg Ser Met Gly
 165 170 175
 Gly Ser Gly Leu Trp Glu Leu Phe Ile Pro Gly Ile Glu Glu Gly Glu
 180 185 190
 Val Tyr Lys Phe Ala Val Gln Thr Arg Glu Gly Gln Arg Arg Asp Lys
 195 200 205
 Ala Asp Pro Met Ala Arg Arg Ala Glu Leu Ala Pro Ala Thr Gly Ser
 210 215 220
 Ile Val Ala Ser Ser Glu Tyr Gln Trp Gln Asp Ser Glu Trp Leu Arg
 225 230 235 240
 Glu Arg Ser Gln Thr Asp Leu Ala Ser Lys Pro Met Ser Val Tyr Glu
 245 250 255
 Val His Leu Gly Ser Trp Arg Trp Gly Lys Asn Tyr Glu Asp Leu Ala
 260 265 270
 Thr Glu Leu Val Asp Tyr Val Ala Asp Leu Gly Tyr Thr His Val Glu
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 Phe Leu Pro Val Ala Glu His Pro Phe Gly Gly Ser Trp Gly Tyr Gln
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 Val Thr Gly Tyr Tyr Ala Pro Thr Ser Arg Trp Gly Thr Pro Asp Gln
 305 310 315 320
 Phe Arg Ala Leu Val Asp Ala Phe His Ala Arg Gly Ile Gly Val Ile
 325 330 335
 Met Asp Trp Val Pro Ala His Phe Pro Lys Asp Asp Trp Ala Leu Ala
 340 345 350
 Arg Phe Asp Gly Glu Ala Leu Tyr Glu His Pro Asp Trp Arg Arg Gly
 355 360 365
 Glu Gln Lys Asp Trp Gly Thr Leu Val Phe Asp Phe Gly Arg Asn Glu
 370 375 380
 Val Arg Asn Phe Leu Val Ala Asn Ala Leu Tyr Trp Ile Glu Glu Phe
 385 390 395 400
 His Ile Asp Gly Leu Arg Val Asp Ala Val Ala Ser Met Leu Tyr Leu
 405 410 415
 Asp Tyr Ser Arg Glu His Gly Glu Trp Glu Pro Asn Ile Tyr Gly Gly

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Arg	Glu	Asn	Leu	Glu	Ala	Val	Gln	Phe	Leu	Gln	Glu	Met	Asn	Ala	Thr
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Val	Leu	Arg	Leu	His	Pro	Gly	Ala	Leu	Thr	Ile	Ala	Glu	Glu	Ser	Thr
	450					455					460				
Ser	Trp	Pro	Gly	Val	Thr	Ala	Pro	Thr	Trp	Asp	Gly	Gly	Leu	Gly	Phe
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Ser	Leu	Lys	Trp	Asn	Met	Gly	Trp	Met	His	Asp	Thr	Leu	Glu	Tyr	Phe
				485					490					495	
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Trp	Ser	His	Pro	Gly	Lys	Lys	Leu	Leu	Phe	Met	Gly	Gln	Glu	Phe	Gly
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Asp	Gly	Trp	Gln	Gly	Glu	Tyr	His	Glu	Ala	Ile	Arg	Thr	Leu	Thr	Arg
		595					600					605			
Ser	Leu	Asn	Gly	Val	Tyr	Ser	Asp	Ser	Pro	Ala	Leu	His	Thr	Gln	Asp
	610					615					620				
Phe	Thr	Gly	Glu	Gly	Phe	Thr	Trp	Asn	Lys	Gly	Asp	Asp	Ala	Thr	Asn
625					630					635					640
Asn	Ile	Leu	Ala	Phe	Thr	Arg	Phe	Gly	Ser	Asp	Gly	Ser	Gln	Met	Leu
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Cys	Val	Phe	Asn	Leu	Ser	Gly	Thr	Ser	Gln	Pro	Glu	Tyr	Gln	Leu	Gly
			660					665					670		
Val	Ala	Ala	Gly	Gly	Glu	Trp	Lys	Leu	Val	Leu	Asn	Thr	Asp	Asp	Ala
		675					680					685			
Glu	Phe	Leu	Gly	Ala	Glu	Asn	Asp	Ile	Ala	Thr	Ser	Val	Gln	Ala	Ala
	690					695					700				
Ala	Thr	Pro	Arg	Asp	Asn	Phe	Ala	Tyr	Ser	Leu	Ser	Leu	His	Val	Pro
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<211> 1913

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(1890)

<223> RXN01884

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cgt ctc cgc gac cta gga atg cgc aac tac tgg ggc tac aac tct ttc	96
Arg Leu Arg Asp Leu Gly Met Arg Asn Tyr Trp Gly Tyr Asn Ser Phe	
20 25 30	
ggc ttc ttt gcg ccc tac aac gat tac gct gcc aac aag aac ccc ggt	144
Gly Phe Phe Ala Pro Tyr Asn Asp Tyr Ala Ala Asn Lys Asn Pro Gly	
35 40 45	
ggc gcc gtg gcc gag ttc aaa ggc ttg gtg cgc agc tac cac gaa gcg	192
Gly Ala Val Ala Glu Phe Lys Gly Leu Val Arg Ser Tyr His Glu Ala	
50 55 60	
ggc ctc gaa gta att ttg gat gtg gtc tac aac cac acc gcc gag ggc	240
Gly Leu Glu Val Ile Leu Asp Val Val Tyr Asn His Thr Ala Glu Gly	
65 70 75 80	
aac cac atg ggc ccc acc atc gcg ttc cga ggc att gac aac gag gcg	288
Asn His Met Gly Pro Thr Ile Ala Phe Arg Gly Ile Asp Asn Glu Ala	
85 90 95	
tac tac cga ctg gtt gag ggc gat cgc cgt cat tac atg gac tac acc	336
Tyr Tyr Arg Leu Val Glu Gly Asp Arg Arg His Tyr Met Asp Tyr Thr	
100 105 110	
ggt act ggt aac tcc ctc aat gtc cgc gac ccg cac tca ctg cag ctg	384
Gly Thr Gly Asn Ser Leu Asn Val Arg Asp Pro His Ser Leu Gln Leu	
115 120 125	
att atg gat tcg ctg cgc tac tgg gtc acc gag atg cat gtc gac ggc	432
Ile Met Asp Ser Leu Arg Tyr Trp Val Thr Glu Met His Val Asp Gly	
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Phe Arg Phe Asp Leu Ala Ser Thr Leu Ala Arg Glu Phe Asp Asp Val	
145 150 155 160	
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Asp Arg Leu Ala Thr Phe Phe Asp Leu Val Gln Gln Asp Pro Val Val	
165 170 175	
tcc cag gtc aag ctc att gct gag ccg tgg gat gtt ggc gaa ggc gga	576
Ser Gln Val Lys Leu Ile Ala Glu Pro Trp Asp Val Gly Glu Gly Gly	
180 185 190	
tac caa gtg ggt aac ttc cca cca ctg tgg act gag tgg aac ggt aaa	624
Tyr Gln Val Gly Asn Phe Pro Pro Leu Trp Thr Glu Trp Asn Gly Lys	
195 200 205	

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Tyr	Arg	Asp	Thr	Val	Arg	Asp	Phe	Trp	Arg	Gly	Glu	Pro	Ala	Thr	Leu	
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ggt	gaa	ttc	gct	tcc	cga	cta	act	ggt	tcc	tct	gat	ttg	tat	gca	aac	720
Gly	Glu	Phe	Ala	Ser	Arg	Leu	Thr	Gly	Ser	Ser	Asp	Leu	Tyr	Ala	Asn	
225					230				235						240	
aac	ggc	cgt	cgc	ccc	act	gca	tcg	atc	aac	ttt	gtg	act	gct	cac	gac	768
Asn	Gly	Arg	Arg	Pro	Thr	Ala	Ser	Ile	Asn	Phe	Val	Thr	Ala	His	Asp	
				245					250					255		
ggc	ttc	acc	ctc	aat	gac	ttg	gtc	agt	tac	aac	gag	aag	cac	aac	atg	816
Gly	Phe	Thr	Leu	Asn	Asp	Leu	Val	Ser	Tyr	Asn	Glu	Lys	His	Asn	Met	
			260					265					270			
gcc	aac	ggt	gaa	gac	ggt	cgg	gac	ggt	gaa	tca	cac	aac	cgt	tcc	tgg	864
Ala	Asn	Gly	Glu	Asp	Gly	Arg	Asp	Gly	Glu	Ser	His	Asn	Arg	Ser	Trp	
		275				280						285				
aac	tgt	ggc	gtc	gaa	gga	cca	act	gac	gat	cct	gag	att	atg	cag	ctg	912
Asn	Cys	Gly	Val	Glu	Gly	Pro	Thr	Asp	Asp	Pro	Glu	Ile	Met	Gln	Leu	
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cgt	gct	cag	caa	cga	cgc	aac	ttc	ctc	acc	acc	ttg	ttg	ctg	tcc	cag	960
Arg	Ala	Gln	Gln	Arg	Arg	Asn	Phe	Leu	Thr	Thr	Leu	Leu	Leu	Ser	Gln	
305					310				315					320		
ggc	acc	cct	atg	ttg	tcc	cac	ggt	gat	gaa	atg	gcc	cgt	acc	caa	aac	1008
Gly	Thr	Pro	Met	Leu	Ser	His	Gly	Asp	Glu	Met	Ala	Arg	Thr	Gln	Asn	
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ggc	aac	aac	aac	gtc	tac	tgc	caa	gac	aat	gaa	ctg	gcg	tgg	gtg	aat	1056
Gly	Asn	Asn	Asn	Val	Tyr	Cys	Gln	Asp	Asn	Glu	Leu	Ala	Trp	Val	Asn	
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tgg	gat	cag	gct	gaa	gaa	aac	gct	gac	ttg	gtg	agc	ttc	acc	agg	cgt	1104
Trp	Asp	Gln	Ala	Glu	Glu	Asn	Ala	Asp	Leu	Val	Ser	Phe	Thr	Arg	Arg	
		355					360					365				
ttg	ctg	cgt	atc	cga	gca	aac	cac	cca	gta	ttt	agg	cgc	agg	cag	ttc	1152
Leu	Leu	Arg	Ile	Arg	Ala	Asn	His	Pro	Val	Phe	Arg	Arg	Arg	Gln	Phe	
	370					375				380						
ctt	gcc	ggt	ggc	cct	ttg	ggc	gcc	gat	gtt	cgt	gac	cgc	gat	atc	gca	1200
Leu	Ala	Gly	Gly	Pro	Leu	Gly	Ala	Asp	Val	Arg	Asp	Arg	Asp	Ile	Ala	
385					390					395				400		
tgg	ctg	gta	cca	aat	gga	acc	ttg	atg	act	caa	gat	gac	tgg	gac	ttc	1248
Trp	Leu	Val	Pro	Asn	Gly	Thr	Leu	Met	Thr	Gln	Asp	Asp	Trp	Asp	Phe	
				405					410					415		
gct	ttc	ggt	aaa	tca	ctg	cag	gtg	ttc	ttc	aac	ggc	gat	gcc	atc	gaa	1296
Ala	Phe	Gly	Lys	Ser	Leu	Gln	Val	Phe	Phe	Asn	Gly	Asp	Ala	Ile	Glu	
			420					425					430			
gag	cct	gat	tat	cga	gga	cag	aaa	atc	cac	gat	gac	tcc	ttc	atc	ttg	1344
Glu	Pro	Asp	Tyr	Arg	Gly	Gln	Lys	Ile	His	Asp	Asp	Ser	Phe	Ile	Leu	
		435					440					445				

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 Met Phe Asn Ala His Phe Glu Pro Ile Asp Phe Asn Leu Pro Pro Glu
 450 455 460

cat ttc ggt atg aag tgg aag ctt ttg gtc gat acc acc gaa gcg gtg 1440
 His Phe Gly Met Lys Trp Lys Leu Leu Val Asp Thr Thr Glu Ala Val
 465 470 475 480

ggc cac ccg ctg gag gat ctc acc atc gaa gct ggc gga acc atc act 1488
 Gly His Pro Leu Glu Asp Leu Thr Ile Glu Ala Gly Gly Thr Ile Thr
 485 490 495

gtt cct gcc cgt tcc acg atg ctg ctg cgc cag gtg gag gct ccg gac 1536
 Val Pro Ala Arg Ser Thr Met Leu Leu Arg Gln Val Glu Ala Pro Asp
 500 505 510

tac acc aag ctt gag gaa aag atc gct gct gaa aag cgt gag caa gaa 1584
 Tyr Thr Lys Leu Glu Glu Lys Ile Ala Ala Glu Lys Arg Glu Gln Glu
 515 520 525

ctt gcg gca gag aag gaa gct gct gag aag cgc gaa ttg gaa ctg gcg 1632
 Leu Ala Ala Glu Lys Glu Ala Ala Glu Lys Arg Glu Leu Glu Leu Ala
 530 535 540

gca gca aag gaa gct gaa gat gct gct gag gct ctc cac ctt gcg gca 1680
 Ala Ala Lys Glu Ala Glu Asp Ala Ala Glu Ala Leu His Leu Ala Ala
 545 550 555 560

gaa cgt gct tcg act cag gaa gct gaa ttg gcc cat caa cac ggt gct 1728
 Glu Arg Ala Ser Thr Gln Glu Ala Glu Leu Ala His Gln His Gly Ala
 565 570 575

gat gcg att gcc gat gag gta gcg gaa gaa cca caa gag ctg cca caa 1776
 Asp Ala Ile Ala Asp Glu Val Ala Glu Glu Pro Gln Glu Leu Pro Gln
 580 585 590

gat gaa gta gcg gca gag gtc gag act gag ccc gac acc gag cct gac 1824
 Asp Glu Val Ala Ala Glu Val Glu Thr Glu Pro Asp Thr Glu Pro Asp
 595 600 605

act gaa tct gac tcc gag cag gct gag gta gct tca gag gag cct gaa 1872
 Thr Glu Ser Asp Ser Glu Gln Ala Glu Val Ala Ser Glu Glu Pro Glu
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<210> 364

<211> 630

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 364

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517

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370						375					380				
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385					390					395					400
Trp	Leu	Val	Pro	Asn	Gly	Thr	Leu	Met	Thr	Gln	Asp	Asp	Trp	Asp	Phe
				405					410					415	
Ala	Phe	Gly	Lys	Ser	Leu	Gln	Val	Phe	Phe	Asn	Gly	Asp	Ala	Ile	Glu
			420					425					430		
Glu	Pro	Asp	Tyr	Arg	Gly	Gln	Lys	Ile	His	Asp	Asp	Ser	Phe	Ile	Leu
		435					440					445			
Met	Phe	Asn	Ala	His	Phe	Glu	Pro	Ile	Asp	Phe	Asn	Leu	Pro	Pro	Glu
	450					455					460				
His	Phe	Gly	Met	Lys	Trp	Lys	Leu	Leu	Val	Asp	Thr	Thr	Glu	Ala	Val
465					470					475					480
Gly	His	Pro	Leu	Glu	Asp	Leu	Thr	Ile	Glu	Ala	Gly	Gly	Thr	Ile	Thr
				485					490					495	
Val	Pro	Ala	Arg	Ser	Thr	Met	Leu	Leu	Arg	Gln	Val	Glu	Ala	Pro	Asp
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Tyr	Thr	Lys	Leu	Glu	Glu	Lys	Ile	Ala	Ala	Glu	Lys	Arg	Glu	Gln	Glu
		515					520					525			
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	530					535					540				
Ala	Ala	Lys	Glu	Ala	Glu	Asp	Ala	Ala	Glu	Ala	Leu	His	Leu	Ala	Ala
545						550					555				560
Glu	Arg	Ala	Ser	Thr	Gln	Glu	Ala	Glu	Leu	Ala	His	Gln	His	Gly	Ala
				565					570					575	
Asp	Ala	Ile	Ala	Asp	Glu	Val	Ala	Glu	Glu	Pro	Gln	Glu	Leu	Pro	Gln
			580						585				590		
Asp	Glu	Val	Ala	Ala	Glu	Val	Glu	Thr	Glu	Pro	Asp	Thr	Glu	Pro	Asp
		595					600					605			
Thr	Glu	Ser	Asp	Ser	Glu	Gln	Ala	Glu	Val	Ala	Ser	Glu	Glu	Pro	Glu
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<211> 1496

<212> DNA

<213> Corynebacterium glutamicum

<220>

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<222> (1)..(1473)

<223> FRXA01884

<400> 365

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caa gac ccg gtg gtc tcc cag gtc aag ctc att gct gag ccg tgg gat	144
Gln Asp Pro Val Val Ser Gln Val Lys Leu Ile Ala Glu Pro Trp Asp	
35 40 45	
gtt ggc gaa ggc gga tac caa gtg ggt aac ttc cca cca ctg tgg act	192
Val Gly Glu Gly Gly Tyr Gln Val Gly Asn Phe Pro Pro Leu Trp Thr	
50 55 60	
gag tgg aac ggt aaa tac cgc gac act gtc cgt gat ttc tgg cgt ggt	240
Glu Trp Asn Gly Lys Tyr Arg Asp Thr Val Arg Asp Phe Trp Arg Gly	
65 70 75 80	
gag cca gca acc ttg ggt gaa ttc gct tcc cga cta act ggt tcc tct	288
Glu Pro Ala Thr Leu Gly Glu Phe Ala Ser Arg Leu Thr Gly Ser Ser	
85 90 95	
gat ttg tat gca aac aac ggc cgt cgc ccc act gca tcg atc aac ttt	336
Asp Leu Tyr Ala Asn Asn Gly Arg Arg Pro Thr Ala Ser Ile Asn Phe	
100 105 110	
gtg act gct cac gac ggc ttc acc ctc aat gac ttg gtc agt tac aac	384
Val Thr Ala His Asp Gly Phe Thr Leu Asn Asp Leu Val Ser Tyr Asn	
115 120 125	
gag aag cac aac atg gcc aac ggt gaa gac ggt cgg gac ggt gaa tca	432
Glu Lys His Asn Met Ala Asn Gly Glu Asp Gly Arg Asp Gly Glu Ser	
130 135 140	
cac aac cgt tcc tgg aac tgt ggc gtc gaa gga cca act gac gat cct	480
His Asn Arg Ser Trp Asn Cys Gly Val Glu Gly Pro Thr Asp Asp Pro	
145 150 155 160	
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Glu Ile Met Gln Leu Arg Ala Gln Gln Arg Arg Asn Phe Leu Thr Thr	
165 170 175	
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Leu Leu Leu Ser Gln Gly Thr Pro Met Leu Ser His Gly Asp Glu Met	
180 185 190	
gcc cgt acc caa aac ggc aac aac aac gtc tac tgc caa gac aat gaa	624
Ala Arg Thr Gln Asn Gly Asn Asn Asn Val Tyr Cys Gln Asp Asn Glu	
195 200 205	
ctg gcg tgg gtg aat tgg gat cag gct gaa gaa aac gct gac ttg gtg	672
Leu Ala Trp Val Asn Trp Asp Gln Ala Glu Glu Asn Ala Asp Leu Val	
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Arg	Arg	Arg	Gln	Phe 245	Leu	Ala	Gly	Gly	Pro 250	Leu	Gly	Ala	Asp	Val 255	Arg	
gac	cgc	gat	atc	gca	tgg	ctg	gta	cca	aat	gga	acc	ttg	atg	act	caa	816
Asp	Arg	Asp	Ile 260	Ala	Trp	Leu	Val	Pro 265	Asn	Gly	Thr	Leu	Met 270	Thr	Gln	
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Asp	Asp	Trp 275	Asp	Phe	Ala	Phe	Gly 280	Lys	Ser	Leu	Gln	Val 285	Phe	Phe	Asn	
ggc	gat	gcc	atc	gaa	gag	cct	gat	tat	cga	gga	cag	aaa	atc	cac	gat	912
Gly	Asp	Ala	Ile	Glu	Glu	Pro 295	Asp	Tyr	Arg	Gly	Gln 300	Lys	Ile	His	Asp	
gac	tcc	ttc	atc	ttg	atg	ttc	aac	gct	cac	ttc	gaa	cct	atc	gat	ttc	960
Asp	Ser	Phe	Ile	Leu	Met 310	Phe	Asn	Ala	His	Phe 315	Glu	Pro	Ile	Asp	Phe 320	
aat	ctc	cct	cct	gag	cat	ttc	ggt	atg	aag	tgg	aag	ctt	ttg	gtc	gat	1008
Asn	Leu	Pro	Pro	Glu 325	His	Phe	Gly	Met	Lys 330	Trp	Lys	Leu	Leu	Val 335	Asp	
acc	acc	gaa	gcg	gtg	ggc	cac	ccg	ctg	gag	gat	ctc	acc	atc	gaa	gct	1056
Thr	Thr	Glu	Ala	Val	Gly	His	Pro	Leu 345	Glu	Asp	Leu	Thr	Ile 350	Glu	Ala	
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Gly	Gly	Thr 355	Ile	Thr	Val	Pro	Ala 360	Arg	Ser	Thr	Met	Leu 365	Leu	Arg	Gln	
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Lys	Arg	Glu	Gln	Glu	Leu 390	Ala	Ala	Glu	Lys	Glu 395	Ala	Ala	Glu	Lys	Arg 400	
gaa	ttg	gaa	ctg	gcg	gca	gca	aag	gaa	gct	gaa	gat	gct	gct	gag	gct	1248
Glu	Leu	Glu	Leu	Ala 405	Ala	Ala	Lys	Glu	Ala 410	Glu	Asp	Ala	Ala	Glu 415	Ala	
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Leu	His	Leu	Ala 420	Ala	Glu	Arg	Ala	Ser 425	Thr	Gln	Glu	Ala	Glu 430	Leu	Ala	
cat	caa	cac	ggt	gct	gat	gcg	att	gcc	gat	gag	gta	gcg	gaa	gaa	cca	1344
His	Gln	His	Gly 435	Ala	Asp	Ala	Ile 440	Ala	Asp	Glu	Val	Ala 445	Glu	Glu	Pro	
caa	gag	ctg	cca	caa	gat	gaa	gta	gcg	gca	gag	gtc	gag	act	gag	ccc	1392
Gln	Glu	Leu	Pro	Gln	Asp	Glu 455	Val	Ala	Ala	Glu 460	Val	Glu	Thr	Glu	Pro	
gac	acc	gag	cct	gac	act	gaa	tct	gac	tcc	gag	cag	gct	gag	gta	gct	1440
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<212> PRT
<213> Corynebacterium glutamicum
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521

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												Val	Gln	Leu	Asn	Asp	
												1				5	
act	cac	cca	gtg	ttg	gct	atc	cct	gag	ctt	atg	cgt	ctg	ctc	atg	gac	163	
Thr	His	Pro	Val	Leu	Ala	Ile	Pro	Glu	Leu	Met	Arg	Leu	Leu	Met	Asp		
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gag	cat	gac	atg	ggc	tgg	gaa	gaa	tcc	tgg	gca	atc	gtg	ttc	aag	acc	211	
Glu	His	Asp	Met	Gly	Trp	Glu	Glu	Ser	Trp	Ala	Ile	Val	Phe	Lys	Thr		
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ttc	gca	tac	acc	aac	cac	acc	gtg	ctc	acc	gaa	gct	ctt	gag	cag	tgg	259	
Phe	Ala	Tyr	Thr	Asn	His	Thr	Val	Leu	Thr	Glu	Ala	Leu	Glu	Gln	Trp		
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gat	cag	cag	atc	ttc	caa	cag	ctg	ttc	tgg	cgc	gtg	tgg	gaa	atc	atc	307	
Asp	Gln	Gln	Ile	Phe	Gln	Gln	Leu	Phe	Trp	Arg	Val	Trp	Glu	Ile	Ile		
				55					60					65			
aca	gag	atc	gat	cgc	cgc	ttc	cgt	ttg	gag	cgc	gca	gcc	gat	gga	ctg	355	
Thr	Glu	Ile	Asp	Arg	Arg	Phe	Arg	Leu	Glu	Arg	Ala	Ala	Asp	Gly	Leu		
70					75					80					85		
gat	gaa	gag	acc	atc	gac	cgc	atg	gct	cca	atc	cag	cac	ggc	act	gtt	403	
Asp	Glu	Glu	Thr	Ile	Asp	Arg	Met	Ala	Pro	Ile	Gln	His	Gly	Thr	Val		
				90					95					100			
cat	atg	gca	tgg	att	gcc	tgt	tac	gcg	gca	tat	tcc	atc	aat	ggc	gtg	451	
His	Met	Ala	Trp	Ile	Ala	Cys	Tyr	Ala	Ala	Tyr	Ser	Ile	Asn	Gly	Val		
				105					110					115			

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Ala Ala Leu His Thr Glu Ile Ile Lys Ala Glu Thr Leu Ala Asp Trp	
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tac gca ctg tgg cca gag aag ttc aac aac aag act aac ggt gtt acc	547
Tyr Ala Leu Trp Pro Glu Lys Phe Asn Asn Lys Thr Asn Gly Val Thr	
135 140 145	
cca cgc cgt tgg ctg cgc atg atc aac cca ggt ctg tct gac ctg ctc	595
Pro Arg Arg Trp Leu Arg Met Ile Asn Pro Gly Leu Ser Asp Leu Leu	
150 155 160 165	
act cga ctt tcc ggt tcc gat gat tgg gta acc gat ctg gat gag ctg	643
Thr Arg Leu Ser Gly Ser Asp Asp Trp Val Thr Asp Leu Asp Glu Leu	
170 175 180	
aag aag ctg cgc tcc tat gcc gac gat aag tcc gtg ctt gaa gaa ctc	691
Lys Lys Leu Arg Ser Tyr Ala Asp Asp Lys Ser Val Leu Glu Glu Leu	
185 190 195	
cgc gct atc aag gct gct aat aag caa gac ttc gcc gag tgg atc ctc	739
Arg Ala Ile Lys Ala Ala Asn Lys Gln Asp Phe Ala Glu Trp Ile Leu	
200 205 210	
gag cgc cag ggc att gag att gat cca gaa tcc atc ttt gac gtg cag	787
Glu Arg Gln Gly Ile Glu Ile Asp Pro Glu Ser Ile Phe Asp Val Gln	
215 220 225	
att aag cgc ctc cac gag tac aag cgc cag ctc atg aac gcg ctc tac	835
Ile Lys Arg Leu His Glu Tyr Lys Arg Gln Leu Met Asn Ala Leu Tyr	
230 235 240 245	
gta cta gac ctt tac ttc cgt att aag gaa gat ggc ctc acc gac atc	883
Val Leu Asp Leu Tyr Phe Arg Ile Lys Glu Asp Gly Leu Thr Asp Ile	
250 255 260	
cca gca cgc act gtc atc ttt ggc gcc aag gcc gcg ccg ggt tat gtc	931
Pro Ala Arg Thr Val Ile Phe Gly Ala Lys Ala Ala Pro Gly Tyr Val	
265 270 275	
cgc gcc aag gcg att atc aag ctc atc aac tct att gct gac ttg gta	979
Arg Ala Lys Ala Ile Ile Lys Leu Ile Asn Ser Ile Ala Asp Leu Val	
280 285 290	
aac aac gat cct gag gtc tcc ccg ctg ctc aag gtg gtc ttt gta gag	1027
Asn Asn Asp Pro Glu Val Ser Pro Leu Leu Lys Val Val Phe Val Glu	
295 300 305	
aac tac aac gtc tcc cct gct gag cac atc ttg cct gcg tct gat gtc	1075
Asn Tyr Asn Val Ser Pro Ala Glu His Ile Leu Pro Ala Ser Asp Val	
310 315 320 325	
tcc gaa cag att tcc acc gcc ggc aag gaa gcc agc ggt acc tcc aac	1123
Ser Glu Gln Ile Ser Thr Ala Gly Lys Glu Ala Ser Gly Thr Ser Asn	
330 335 340	
atg aag ttc atg atg aac ggc gcc ctc acc ctg ggc acc atg gac ggc	1171
Met Lys Phe Met Met Asn Gly Ala Leu Thr Leu Gly Thr Met Asp Gly	
345 350 355	

gcc aac gta gag atc gtg gat tct gtg ggc gag gaa aac gcc tat atc 1219
 Ala Asn Val Glu Ile Val Asp Ser Val Gly Glu Glu Asn Ala Tyr Ile
 360 365 370

ttc ggt gct cgc gtg gaa gaa ttg cca gcc ctg cgc gaa agc tac gag 1267
 Phe Gly Ala Arg Val Glu Glu Leu Pro Ala Leu Arg Glu Ser Tyr Glu
 375 380 385

cca tat gag ctc tat gag acc gtc cct ggc ctc aag cgc gca ttg gac 1315
 Pro Tyr Glu Leu Tyr Glu Thr Val Pro Gly Leu Lys Arg Ala Leu Asp
 390 395 400 405

gcc ctg gat aac ggc acc ctc aac gac aac aac agt ggt ttg ttc tac 1363
 Ala Leu Asp Asn Gly Thr Leu Asn Asp Asn Asn Ser Gly Leu Phe Tyr
 410 415 420

gac ctc aag cat tcc ttg atc cac ggt tat gga aaa gac gcc agc gac 1411
 Asp Leu Lys His Ser Leu Ile His Gly Tyr Gly Lys Asp Ala Ser Asp
 425 430 435

acc tac tac gtg ctt ggc gat ttc gca gat tac cgc gag acc cgc gac 1459
 Thr Tyr Tyr Val Leu Gly Asp Phe Ala Asp Tyr Arg Glu Thr Arg Asp
 440 445 450

cgt atg gcc gcc gac tac gcc tcc gat ccc ctg ggt tgg gca cgc atg 1507
 Arg Met Ala Ala Asp Tyr Ala Ser Asp Pro Leu Gly Trp Ala Arg Met
 455 460 465

gcc tgg atc aac att tgc gag tcc ggc cgt ttc tcc tcc gac cgc acc 1555
 Ala Trp Ile Asn Ile Cys Glu Ser Gly Arg Phe Ser Ser Asp Arg Thr
 470 475 480 485

atc cgc gat tat gcc acc gag atc tgg aag ctc gag cca act cct gct 1603
 Ile Arg Asp Tyr Ala Thr Glu Ile Trp Lys Leu Glu Pro Thr Pro Ala
 490 495 500

gtt aag aag taggttttaa cctccgcttc taa 1635
 Val Lys Lys

<210> 370

<211> 504

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 370

Val Gln Leu Asn Asp Thr His Pro Val Leu Ala Ile Pro Glu Leu Met
 1 5 10 15

Arg Leu Leu Met Asp Glu His Asp Met Gly Trp Glu Glu Ser Trp Ala
 20 25 30

Ile Val Phe Lys Thr Phe Ala Tyr Thr Asn His Thr Val Leu Thr Glu
 35 40 45

Ala Leu Glu Gln Trp Asp Gln Gln Ile Phe Gln Gln Leu Phe Trp Arg
 50 55 60

Val Trp Glu Ile Ile Thr Glu Ile Asp Arg Arg Phe Arg Leu Glu Arg
 65 70 75 80

527

Lys Arg Ala Leu Asp Ala Leu Asp Asn Gly Thr Leu Asn Asp Asn Asn
 405 410 415
 Ser Gly Leu Phe Tyr Asp Leu Lys His Ser Leu Ile His Gly Tyr Gly
 420 425 430
 Lys Asp Ala Ser Asp Thr Tyr Tyr Val Leu Gly Asp Phe Ala Asp Tyr
 435 440 445
 Arg Glu Thr Arg Asp Arg Met Ala Ala Asp Tyr Ala Ser Asp Pro Leu
 450 455 460
 Gly Trp Ala Arg Met Ala Trp Ile Asn Ile Cys Glu Ser Gly Arg Phe
 465 470 475 480
 Ser Ser Asp Arg Thr Ile Arg Asp Tyr Ala Thr Glu Ile Trp Lys Leu
 485 490 495
 Glu Pro Thr Pro Ala Val Lys Lys
 500

<210> 371
 <211> 1367
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (1)..(1344)
 <223> FRXA01550

<400> 371
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 Ile Phe Gln Gln Leu Phe Trp Arg Val Trp Glu Ile Ile Thr Glu Ile
 1 5 10 15
 gat cgc cgc ttc cgt ttg gag cgc gca gcc gat gga ctg gat gaa gag 96
 Asp Arg Arg Phe Arg Leu Glu Arg Ala Ala Asp Gly Leu Asp Glu Glu
 20 25 30
 acc atc gac cgc atg gct cca atc cag cgc ggc act gtt cat atg gca 144
 Thr Ile Asp Arg Met Ala Pro Ile Gln Arg Gly Thr Val His Met Ala
 35 40 45
 tgg att gcc tgt tac gcg gca tat tcc atc aat ggc gtg gca gcg ctg 192
 Trp Ile Ala Cys Tyr Ala Ala Tyr Ser Ile Asn Gly Val Ala Ala Leu
 50 55 60
 cac acc gag atc atc aag gcc gag acc ttg gct gac tgg tac gca ctg 240
 His Thr Glu Ile Ile Lys Ala Glu Thr Leu Ala Asp Trp Tyr Ala Leu
 65 70 75 80
 tgg cca gag aag ttc aac aac aag act aac ggt gtt acc cca cgc cgt 288
 Trp Pro Glu Lys Phe Asn Asn Lys Thr Asn Gly Val Thr Pro Arg Arg
 85 90 95
 tgg ctg cgc atg atc aac cca ggt ctg tct gac ctg ctc act cga ctt 336
 Trp Leu Arg Met Ile Asn Pro Gly Leu Ser Asp Leu Leu Thr Arg Leu
 100 105 110

tcc ggt tcc gat gat tgg gta acc gat ctg gat gag ctg aag aag ctg	384
Ser Gly Ser Asp Asp Trp Val Thr Asp Leu Asp Glu Leu Lys Lys Leu	
115 120 125	
cgc tcc tat gcc gac gat aag tcc gtg ctt gaa gaa ctc cgc gct atc	432
Arg Ser Tyr Ala Asp Asp Lys Ser Val Leu Glu Glu Leu Arg Ala Ile	
130 135 140	
aag gct gct aat aag caa gac ttc gcc gag tgg atc ctc gag cgc cag	480
Lys Ala Ala Asn Lys Gln Asp Phe Ala Glu Trp Ile Leu Glu Arg Gln	
145 150 155 160	
ggc att gag att gat cca gaa tcc atc ttt gac gtg cag att aag cgc	528
Gly Ile Glu Ile Asp Pro Glu Ser Ile Phe Asp Val Gln Ile Lys Arg	
165 170 175	
ctc cac gag tac aag cgc cag ctc atg aac gcg ctc tac gta cta gac	576
Leu His Glu Tyr Lys Arg Gln Leu Met Asn Ala Leu Tyr Val Leu Asp	
180 185 190	
ctt tac ttc cgt att aag gaa gat ggc ctc acc gac atc cca gca cgc	624
Leu Tyr Phe Arg Ile Lys Glu Asp Gly Leu Thr Asp Ile Pro Ala Arg	
195 200 205	
act gtc atc ttt ggc gcc aag gcc gcg ccg ggt tat gtc cgc gcc aag	672
Thr Val Ile Phe Gly Ala Lys Ala Ala Pro Gly Tyr Val Arg Ala Lys	
210 215 220	
gcg att atc aag ctc atc aac tct att gct gac ttg gta aac aac gat	720
Ala Ile Ile Lys Leu Ile Asn Ser Ile Ala Asp Leu Val Asn Asn Asp	
225 230 235 240	
cct gag gtc tcc ccg ctg ctc aag gtg gtc ttt gta gag aac tac aac	768
Pro Glu Val Ser Pro Leu Leu Lys Val Val Phe Val Glu Asn Tyr Asn	
245 250 255	
gtc tcc cct gct gag cac atc ttg cct gcg tct gat gtc tcc gaa cag	816
Val Ser Pro Ala Glu His Ile Leu Pro Ala Ser Asp Val Ser Glu Gln	
260 265 270	
att tcc acc gcc ggc aag gaa gcc agc ggt acc tcc aac atg aag ttc	864
Ile Ser Thr Ala Gly Lys Glu Ala Ser Gly Thr Ser Asn Met Lys Phe	
275 280 285	
atg atg aac ggc gcc ctc acc ctg ggc acc atg gac ggc gcc aac gta	912
Met Met Asn Gly Ala Leu Thr Leu Gly Thr Met Asp Gly Ala Asn Val	
290 295 300	
gag atc gtg gat tct gtg ggc gag gaa aac gcc tat atc ttc ggt gct	960
Glu Ile Val Asp Ser Val Gly Glu Glu Asn Ala Tyr Ile Phe Gly Ala	
305 310 315 320	
cgc gtg gaa gaa ttg cca gcc ctg cgc gaa agc tac gag cca tat gag	1008
Arg Val Glu Glu Leu Pro Ala Leu Arg Glu Ser Tyr Glu Pro Tyr Glu	
325 330 335	
ctc tat gag acc gtc cct ggc ctc aag cgc gca ttg gac gcc ctg gat	1056
Leu Tyr Glu Thr Val Pro Gly Leu Lys Arg Ala Leu Asp Ala Leu Asp	
340 345 350	
aac ggc acc ctc aac gac aac aac agt ggt ttg ttc tac gac ctc aag	1104

Asn Gly Thr Leu Asn Asp Asn Asn Ser Gly Leu Phe Tyr Asp Leu Lys
 355 360 365
 cat tcc ttg atc cac ggt tat gga aaa gac gcc agc gac acc tac tac 1152
 His Ser Leu Ile His Gly Tyr Gly Lys Asp Ala Ser Asp Thr Tyr Tyr
 370 375 380
 gtg ctt ggc gat ttc gca gat tac cgc gag acc cgc gac cgt atg gcc 1200
 Val Leu Gly Asp Phe Ala Asp Tyr Arg Glu Thr Arg Asp Arg Met Ala
 385 390 395 400
 gcc gac tac gcc tcc gat ccc ctg ggt tgg gca cgc atg gcc tgg atc 1248
 Ala Asp Tyr Ala Ser Asp Pro Leu Gly Trp Ala Arg Met Ala Trp Ile
 405 410 415
 aac att tgc gag tcc ggc cgt ttc tcc tcc gac cgc acc atc cgc gat 1296
 Asn Ile Cys Glu Ser Gly Arg Phe Ser Ser Asp Arg Thr Ile Arg Asp
 420 425 430
 tat gcc acc gag atc tgg aag ctg gag cca act cct gct gtt aag aag 1344
 Tyr Ala Thr Glu Ile Trp Lys Leu Glu Pro Thr Pro Ala Val Lys Lys
 435 440 445
 taggttttaa cctccgcttc taa 1367

<210> 372
 <211> 448
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 372
 Ile Phe Gln Gln Leu Phe Trp Arg Val Trp Glu Ile Ile Thr Glu Ile
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 Asp Arg Arg Phe Arg Leu Glu Arg Ala Ala Asp Gly Leu Asp Glu Glu
 20 25 30
 Thr Ile Asp Arg Met Ala Pro Ile Gln Arg Gly Thr Val His Met Ala
 35 40 45
 Trp Ile Ala Cys Tyr Ala Ala Tyr Ser Ile Asn Gly Val Ala Ala Leu
 50 55 60
 His Thr Glu Ile Ile Lys Ala Glu Thr Leu Ala Asp Trp Tyr Ala Leu
 65 70 75 80
 Trp Pro Glu Lys Phe Asn Asn Lys Thr Asn Gly Val Thr Pro Arg Arg
 85 90 95
 Trp Leu Arg Met Ile Asn Pro Gly Leu Ser Asp Leu Leu Thr Arg Leu
 100 105 110
 Ser Gly Ser Asp Asp Trp Val Thr Asp Leu Asp Glu Leu Lys Lys Leu
 115 120 125
 Arg Ser Tyr Ala Asp Asp Lys Ser Val Leu Glu Glu Leu Arg Ala Ile
 130 135 140
 Lys Ala Ala Asn Lys Gln Asp Phe Ala Glu Trp Ile Leu Glu Arg Gln
 145 150 155 160

Gly Ile Glu Ile Asp Pro Glu Ser Ile Phe Asp Val Gln Ile Lys Arg
 165 170 175
 Leu His Glu Tyr Lys Arg Gln Leu Met Asn Ala Leu Tyr Val Leu Asp
 180 185 190
 Leu Tyr Phe Arg Ile Lys Glu Asp Gly Leu Thr Asp Ile Pro Ala Arg
 195 200 205
 Thr Val Ile Phe Gly Ala Lys Ala Ala Pro Gly Tyr Val Arg Ala Lys
 210 215 220
 Ala Ile Ile Lys Leu Ile Asn Ser Ile Ala Asp Leu Val Asn Asn Asp
 225 230 235 240
 Pro Glu Val Ser Pro Leu Leu Lys Val Val Phe Val Glu Asn Tyr Asn
 245 250 255
 Val Ser Pro Ala Glu His Ile Leu Pro Ala Ser Asp Val Ser Glu Gln
 260 265 270
 Ile Ser Thr Ala Gly Lys Glu Ala Ser Gly Thr Ser Asn Met Lys Phe
 275 280 285
 Met Met Asn Gly Ala Leu Thr Leu Gly Thr Met Asp Gly Ala Asn Val
 290 295 300
 Glu Ile Val Asp Ser Val Gly Glu Glu Asn Ala Tyr Ile Phe Gly Ala
 305 310 315 320
 Arg Val Glu Glu Leu Pro Ala Leu Arg Glu Ser Tyr Glu Pro Tyr Glu
 325 330 335
 Leu Tyr Glu Thr Val Pro Gly Leu Lys Arg Ala Leu Asp Ala Leu Asp
 340 345 350
 Asn Gly Thr Leu Asn Asp Asn Asn Ser Gly Leu Phe Tyr Asp Leu Lys
 355 360 365
 His Ser Leu Ile His Gly Tyr Gly Lys Asp Ala Ser Asp Thr Tyr Tyr
 370 375 380
 Val Leu Gly Asp Phe Ala Asp Tyr Arg Glu Thr Arg Asp Arg Met Ala
 385 390 395 400
 Ala Asp Tyr Ala Ser Asp Pro Leu Gly Trp Ala Arg Met Ala Trp Ile
 405 410 415
 Asn Ile Cys Glu Ser Gly Arg Phe Ser Ser Asp Arg Thr Ile Arg Asp
 420 425 430
 Tyr Ala Thr Glu Ile Trp Lys Leu Glu Pro Thr Pro Ala Val Lys Lys
 435 440 445

<210> 373

<211> 2348

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(2325)

<223> RXN02100

<400> 373

cta ggt cga atc aac gcc gag gag caa aac ctc agc gaa tac ctc agc	48
Leu Gly Arg Ile Asn Ala Glu Glu Gln Asn Leu Ser Glu Tyr Leu Ser	
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gac aag ctg tgg tac cag gac acc gca gat gca acc gat gct gtc gga	96
Asp Lys Leu Trp Tyr Gln Asp Thr Ala Asp Ala Thr Asp Ala Val Gly	
20 25 30	
gat cca ctc gtt gcg tac ttc tcc atg gag ttt ggc att cac cca agc	144
Asp Pro Leu Val Ala Tyr Phe Ser Met Glu Phe Gly Ile His Pro Ser	
35 40 45	
ctg cca atc tac tct ggc gga ctt ggt gtg ctt gcg ggc gag aac atg	192
Leu Pro Ile Tyr Ser Gly Gly Leu Gly Val Leu Ala Gly Glu Asn Met	
50 55 60	
aag tct gca tct gac ttg ggt gtg cca ctg atc ggt gtt ggt ttg ctc	240
Lys Ser Ala Ser Asp Leu Gly Val Pro Leu Ile Gly Val Gly Leu Leu	
65 70 75 80	
tac acc cac ggc tac ttc acc cag tca ctg tcc ggt gac ggt tgg cag	288
Tyr Thr His Gly Tyr Phe Thr Gln Ser Leu Ser Gly Asp Gly Trp Gln	
85 90 95	
cag gaa gag tac aag tac cac gat cca gca gaa ctg ccg att gag gca	336
Gln Glu Glu Tyr Lys Tyr His Asp Pro Ala Glu Leu Pro Ile Glu Ala	
100 105 110	
gtt aaa gat aag aac ggc gag cag gtc act gtt tct gtc acc tac cca	384
Val Lys Asp Lys Asn Gly Glu Gln Val Thr Val Ser Val Thr Tyr Pro	
115 120 125	
ggt gcg cag gaa gta aag att gca ctg tgg gta gca aac gtt ggc cgc	432
Gly Ala Gln Glu Val Lys Ile Ala Leu Trp Val Ala Asn Val Gly Arg	
130 135 140	
atc cca ttg ctg ctg ctt gat acc aac atc gag gca aac cca gaa gag	480
Ile Pro Leu Leu Leu Leu Asp Thr Asn Ile Glu Ala Asn Pro Glu Glu	
145 150 155 160	
ctc cgc aac gtt act gac cgc ctg tac ggt ggc gac aat gag cac cgc	528
Leu Arg Asn Val Thr Asp Arg Leu Tyr Gly Gly Asp Asn Glu His Arg	
165 170 175	
atc aag cag gaa ctc gtt ctc ggt gtt ggt ggc gtc cgc gct gtc aac	576
Ile Lys Gln Glu Leu Val Leu Gly Val Gly Gly Val Arg Ala Val Asn	
180 185 190	
gca ttc tgc gaa gct cgt ggt ctg aag cgc tca tct gtt gca cac ctc	624
Ala Phe Cys Glu Ala Arg Gly Leu Lys Arg Ser Ser Val Ala His Leu	
195 200 205	

aac gaa ggc cac gca ggt ttc ctg acc ctg gag cgt atc cgc gag cgc Asn Glu Gly His Ala Gly Phe Leu Thr Leu Glu Arg Ile Arg Glu Arg 210 215 220	672
atc gca gag ggc atg gag tac cca gca gca ttc gag cag gtt cgt gcg Ile Ala Glu Gly Met Glu Tyr Pro Ala Ala Phe Glu Gln Val Arg Ala 225 230 235 240	720
tcc aac atc ttc acc acc cac acc cca gtc cca gca ggc atc gac cgc Ser Asn Ile Phe Thr Thr His Thr Pro Val Pro Ala Gly Ile Asp Arg 245 250 255	768
ttc gac atg gag atg gtg cgt cgt tat ctc ggt ggc ggt cag cca gaa Phe Asp Met Glu Met Val Arg Arg Tyr Leu Gly Gly Gly Gln Pro Glu 260 265 270	816
gat cag cag ctg tgc gtt ggt gtt cca att gag aag gca ctt gag ctt Asp Gln Gln Leu Cys Val Gly Val Pro Ile Glu Lys Ala Leu Glu Leu 275 280 285	864
ggt caa gag tcc gat cca cac cgc ttc aac atg gct cat atg ggc ctt Gly Gln Glu Ser Asp Pro His Arg Phe Asn Met Ala His Met Gly Leu 290 295 300	912
cgc gcg agc caa cat gct aat ggc gtc gca aag ctt cat ggt gaa gta Arg Ala Ser Gln His Ala Asn Gly Val Ala Lys Leu His Gly Glu Val 305 310 315 320	960
agc cgt gac atg ttc gcc ggc ctg tac ccc gga tat gag cct cgt gaa Ser Arg Asp Met Phe Ala Gly Leu Tyr Pro Gly Tyr Glu Pro Arg Glu 325 330 335	1008
gtg ccc atc ggg cac gtc acc aac ggt gtt cac ctg ccg acg tgg gtc Val Pro Ile Gly His Val Thr Asn Gly Val His Leu Pro Thr Trp Val 340 345 350	1056
aag cca gag atg aag gaa ctc atc gat cgc gtc act ggc ggc gct gat Lys Pro Glu Met Lys Glu Leu Ile Asp Arg Val Thr Gly Gly Ala Asp 355 360 365	1104
ctt gcg gtt gct gat tct tgg tca aac cca cag gct gtc gag tct gag Leu Ala Val Ala Asp Ser Trp Ser Asn Pro Gln Ala Val Glu Ser Glu 370 375 380	1152
aag atc tgg aag gtg cgc aac aag ttc cgt gct gac cta gtg gag gtt Lys Ile Trp Lys Val Arg Asn Lys Phe Arg Ala Asp Leu Val Glu Val 385 390 395 400	1200
gct cgc gct gca act gca aag tcc tgg tct cac cgt gga cac acc gaa Ala Arg Ala Ala Thr Ala Lys Ser Trp Ser His Arg Gly His Thr Glu 405 410 415	1248
gca gaa ctt gcg tgg acc tcc cgc gtt ctg gat cca aac gtg ctg acc Ala Glu Leu Ala Trp Thr Ser Arg Val Leu Asp Pro Asn Val Leu Thr 420 425 430	1296
att ggt ttc gca cgt cgc gta tcc acc tac aag cgc ttg acc ttg atg Ile Gly Phe Ala Arg Arg Val Ser Thr Tyr Lys Arg Leu Thr Leu Met 435 440 445	1344
ctg cgc aac cct gaa cgc ctg cgt tcc atc ttg ctt aat gag gaa cgc	1392

Leu	Arg	Asn	Pro	Glu	Arg	Leu	Arg	Ser	Ile	Leu	Leu	Asn	Glu	Glu	Arg	
450						455				460						
cca	gtt	cag	ttc	gtt	att	gct	ggg	aag	gca	cac	cca	cat	gac	atg	ggg	1440
Pro	Val	Gln	Phe	Val	Ile	Ala	Gly	Lys	Ala	His	Pro	His	Asp	Met	Gly	
465					470				475						480	
ggc	aag	aag	ctc	atg	cag	gaa	atc	gtc	cac	ttc	gct	gat	caa	gct	ggg	1488
Gly	Lys	Lys	Leu	Met	Gln	Glu	Ile	Val	His	Phe	Ala	Asp	Gln	Ala	Gly	
				485				490						495		
gtc	cgt	gac	cgt	ttc	ctc	ttc	ctg	cct	gat	tac	gac	atc	aac	ctg	gcc	1536
Val	Arg	Asp	Arg	Phe	Leu	Phe	Leu	Pro	Asp	Tyr	Asp	Ile	Asn	Leu	Ala	
			500					505					510			
agc	tac	ctg	atc	tct	ggg	gct	gac	gtg	tgg	ctg	aac	aac	cca	gtg	cgc	1584
Ser	Tyr	Leu	Ile	Ser	Gly	Ala	Asp	Val	Trp	Leu	Asn	Asn	Pro	Val	Arg	
		515					520					525				
cct	cag	gaa	gca	tcg	gga	acc	tcc	ggg	atg	aag	gcc	gtc	atg	aat	ggg	1632
Pro	Gln	Glu	Ala	Ser	Gly	Thr	Ser	Gly	Met	Lys	Ala	Val	Met	Asn	Gly	
		530				535					540					
ggc	ctg	acc	ctg	tcc	atc	tct	gat	ggg	tgg	tgg	gat	gaa	atg	cct	aag	1680
Gly	Leu	Thr	Leu	Ser	Ile	Ser	Asp	Gly	Trp	Trp	Asp	Glu	Met	Pro	Lys	
545					550				555						560	
gag	acc	acc	ggc	tgg	acc	atc	cca	acc	gtt	gag	tcc	cag	gac	ttg	gaa	1728
Glu	Thr	Thr	Gly	Trp	Thr	Ile	Pro	Thr	Val	Glu	Ser	Gln	Asp	Leu	Glu	
				565					570					575		
tgc	cgc	gac	cac	ctg	gaa	tcc	cag	gcg	ctg	tac	gac	ctg	ctg	gaa	aac	1776
Cys	Arg	Asp	His	Leu	Glu	Ser	Gln	Ala	Leu	Tyr	Asp	Leu	Leu	Glu	Asn	
			580					585					590			
gaa	gtt	gca	ccg	ctg	ttt	tac	aag	cgc	gac	aag	aac	ggc	atc	cca	cag	1824
Glu	Val	Ala	Pro	Leu	Phe	Tyr	Lys	Arg	Asp	Lys	Asn	Gly	Ile	Pro	Gln	
		595					600					605				
gac	tgg	ctg	gac	ctg	gtt	cgc	gaa	tcc	tgg	acc	acc	ctg	tca	cca	atg	1872
Asp	Trp	Leu	Asp	Leu	Val	Arg	Glu	Ser	Trp	Thr	Thr	Leu	Ser	Pro	Met	
	610					615						620				
gtc	acc	tcc	acc	cgc	atg	gtg	cgc	gac	tac	acc	acc	cag	tac	tac	cgc	1920
Val	Thr	Ser	Thr	Arg	Met	Val	Arg	Asp	Tyr	Thr	Thr	Gln	Tyr	Tyr	Arg	
625					630				635						640	
cca	acc	aaa	cac	cag	gca	gag	ctc	att	gcg	cag	cct	gca	gaa	gca	gcg	1968
Pro	Thr	Lys	His	Gln	Ala	Glu	Leu	Ile	Ala	Gln	Pro	Ala	Glu	Ala	Ala	
				645					650					655		
gat	tac	gcg	gca	tgg	ctt	gag	cac	atc	aaa	gca	gag	tgg	gct	ggc	gtc	2016
Asp	Tyr	Ala	Ala	Trp	Leu	Glu	His	Ile	Lys	Ala	Glu	Trp	Ala	Gly	Val	
			660					665					670			
aag	gtc	tca	gac	ctg	aag	atc	agc	gag	agc	gcc	atc	acg	gcg	cag	gag	2064
Lys	Val	Ser	Asp	Leu	Lys	Ile	Ser	Glu	Ser	Ala	Ile	Thr	Ala	Gln	Glu	
		675					680					685				
ctt	gaa	gtc	agc	gtt	cgc	gtt	gat	tcc	ggg	tcg	ctt	aac	gac	gac	gag	2112
Leu	Glu	Val	Ser	Val	Arg	Val	Asp	Ser	Gly	Ser	Leu	Asn	Asp	Asp	Glu	

690	695	700	
ttc caa gct cag gca ctc ttt ggt gcg ctc gga cac aac ggt gac atc			2160
Phe Gln Ala Gln Ala Leu Phe Gly Ala Leu Gly His Asn Gly Asp Ile			
705	710	715	720
gaa gat cca gaa atc acc gtt ttg acc cca cgc ggc gat ggc gcc tac			2208
Glu Asp Pro Glu Ile Thr Val Leu Thr Pro Arg Gly Asp Gly Ala Tyr			
	725	730	735
gcg gca aag gtc agc act gac ctg cca ggc aac tac ggc atc act gcc			2256
Ala Ala Lys Val Ser Thr Asp Leu Pro Gly Asn Tyr Gly Ile Thr Ala			
	740	745	750
cgc gtt gtt cca aac aac agg atg ctg gtc agc cca gcg gaa acc cgc			2304
Arg Val Val Pro Asn Asn Arg Met Leu Val Ser Pro Ala Glu Thr Arg			
	755	760	765
ctg atc acc tac ttg gag aac tagggcgaaa ctagctttac caa			2348
Leu Ile Thr Tyr Leu Glu Asn			
770	775		

<210> 374

<211> 775

<212> PRT

<213> Corynebacterium glutamicum

<400> 374

Leu Gly Arg Ile Asn Ala Glu Glu Gln Asn Leu Ser Glu Tyr Leu Ser			
1	5	10	15
Asp Lys Leu Trp Tyr Gln Asp Thr Ala Asp Ala Thr Asp Ala Val Gly			
	20	25	30
Asp Pro Leu Val Ala Tyr Phe Ser Met Glu Phe Gly Ile His Pro Ser			
	35	40	45
Leu Pro Ile Tyr Ser Gly Gly Leu Gly Val Leu Ala Gly Glu Asn Met			
	50	55	60
Lys Ser Ala Ser Asp Leu Gly Val Pro Leu Ile Gly Val Gly Leu Leu			
	65	70	75
Tyr Thr His Gly Tyr Phe Thr Gln Ser Leu Ser Gly Asp Gly Trp Gln			
	85	90	95
Gln Glu Glu Tyr Lys Tyr His Asp Pro Ala Glu Leu Pro Ile Glu Ala			
	100	105	110
Val Lys Asp Lys Asn Gly Glu Gln Val Thr Val Ser Val Thr Tyr Pro			
	115	120	125
Gly Ala Gln Glu Val Lys Ile Ala Leu Trp Val Ala Asn Val Gly Arg			
	130	135	140
Ile Pro Leu Leu Leu Leu Asp Thr Asn Ile Glu Ala Asn Pro Glu Glu			
	145	150	155
Leu Arg Asn Val Thr Asp Arg Leu Tyr Gly Gly Asp Asn Glu His Arg			
	165	170	175

Ile Lys Gln Glu Leu Val Leu Gly Val Gly Gly Val Arg Ala Val Asn
 180 185 190
 Ala Phe Cys Glu Ala Arg Gly Leu Lys Arg Ser Ser Val Ala His Leu
 195 200 205
 Asn Glu Gly His Ala Gly Phe Leu Thr Leu Glu Arg Ile Arg Glu Arg
 210 215 220
 Ile Ala Glu Gly Met Glu Tyr Pro Ala Ala Phe Glu Gln Val Arg Ala
 225 230 235 240
 Ser Asn Ile Phe Thr Thr His Thr Pro Val Pro Ala Gly Ile Asp Arg
 245 250 255
 Phe Asp Met Glu Met Val Arg Arg Tyr Leu Gly Gly Gly Gln Pro Glu
 260 265 270
 Asp Gln Gln Leu Cys Val Gly Val Pro Ile Glu Lys Ala Leu Glu Leu
 275 280 285
 Gly Gln Glu Ser Asp Pro His Arg Phe Asn Met Ala His Met Gly Leu
 290 295 300
 Arg Ala Ser Gln His Ala Asn Gly Val Ala Lys Leu His Gly Glu Val
 305 310 315 320
 Ser Arg Asp Met Phe Ala Gly Leu Tyr Pro Gly Tyr Glu Pro Arg Glu
 325 330 335
 Val Pro Ile Gly His Val Thr Asn Gly Val His Leu Pro Thr Trp Val
 340 345 350
 Lys Pro Glu Met Lys Glu Leu Ile Asp Arg Val Thr Gly Gly Ala Asp
 355 360 365
 Leu Ala Val Ala Asp Ser Trp Ser Asn Pro Gln Ala Val Glu Ser Glu
 370 375 380
 Lys Ile Trp Lys Val Arg Asn Lys Phe Arg Ala Asp Leu Val Glu Val
 385 390 395 400
 Ala Arg Ala Ala Thr Ala Lys Ser Trp Ser His Arg Gly His Thr Glu
 405 410 415
 Ala Glu Leu Ala Trp Thr Ser Arg Val Leu Asp Pro Asn Val Leu Thr
 420 425 430
 Ile Gly Phe Ala Arg Arg Val Ser Thr Tyr Lys Arg Leu Thr Leu Met
 435 440 445
 Leu Arg Asn Pro Glu Arg Leu Arg Ser Ile Leu Leu Asn Glu Glu Arg
 450 455 460
 Pro Val Gln Phe Val Ile Ala Gly Lys Ala His Pro His Asp Met Gly
 465 470 475 480
 Gly Lys Lys Leu Met Gln Glu Ile Val His Phe Ala Asp Gln Ala Gly
 485 490 495

Val Arg Asp Arg Phe Leu Phe Leu Pro Asp Tyr Asp Ile Asn Leu Ala
 500 505 510
 Ser Tyr Leu Ile Ser Gly Ala Asp Val Trp Leu Asn Asn Pro Val Arg
 515 520 525
 Pro Gln Glu Ala Ser Gly Thr Ser Gly Met Lys Ala Val Met Asn Gly
 530 535 540
 Gly Leu Thr Leu Ser Ile Ser Asp Gly Trp Trp Asp Glu Met Pro Lys
 545 550 555 560
 Glu Thr Thr Gly Trp Thr Ile Pro Thr Val Glu Ser Gln Asp Leu Glu
 565 570 575
 Cys Arg Asp His Leu Glu Ser Gln Ala Leu Tyr Asp Leu Leu Glu Asn
 580 585 590
 Glu Val Ala Pro Leu Phe Tyr Lys Arg Asp Lys Asn Gly Ile Pro Gln
 595 600 605
 Asp Trp Leu Asp Leu Val Arg Glu Ser Trp Thr Thr Leu Ser Pro Met
 610 615 620
 Val Thr Ser Thr Arg Met Val Arg Asp Tyr Thr Thr Gln Tyr Tyr Arg
 625 630 635 640
 Pro Thr Lys His Gln Ala Glu Leu Ile Ala Gln Pro Ala Glu Ala Ala
 645 650 655
 Asp Tyr Ala Ala Trp Leu Glu His Ile Lys Ala Glu Trp Ala Gly Val
 660 665 670
 Lys Val Ser Asp Leu Lys Ile Ser Glu Ser Ala Ile Thr Ala Gln Glu
 675 680 685
 Leu Glu Val Ser Val Arg Val Asp Ser Gly Ser Leu Asn Asp Asp Glu
 690 695 700
 Phe Gln Ala Gln Ala Leu Phe Gly Ala Leu Gly His Asn Gly Asp Ile
 705 710 715 720
 Glu Asp Pro Glu Ile Thr Val Leu Thr Pro Arg Gly Asp Gly Ala Tyr
 725 730 735
 Ala Ala Lys Val Ser Thr Asp Leu Pro Gly Asn Tyr Gly Ile Thr Ala
 740 745 750
 Arg Val Val Pro Asn Asn Arg Met Leu Val Ser Pro Ala Glu Thr Arg
 755 760 765
 Leu Ile Thr Tyr Leu Glu Asn
 770 775

<210> 375

<211> 941

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS
 <222> (1)..(918)
 <223> FRXA02100

<400> 375

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Ile Ala Gly Lys Ala His Pro His Asp Met Gly Gly Lys Lys Leu Met	
1 5 10 15	
cag gaa atc gtc cac ttc gct gat caa gct ggt gtc cgt gac cgt ttc	96
Gln Glu Ile Val His Phe Ala Asp Gln Ala Gly Val Arg Asp Arg Phe	
20 25 30	
ctc ttc ctg cct gat tac gac atc aac ctg gcc agc tac ctg atc tct	144
Leu Phe Leu Pro Asp Tyr Asp Ile Asn Leu Ala Ser Tyr Leu Ile Ser	
35 40 45	
ggt gct gac gtg tgg ctg aac aac cca gtg cgc cct cag gaa gca tcg	192
Gly Ala Asp Val Trp Leu Asn Asn Pro Val Arg Pro Gln Glu Ala Ser	
50 55 60	
gga acc tcc ggt atg aag gcc gtc atg aat ggt ggc ctg acc ctg tcc	240
Gly Thr Ser Gly Met Lys Ala Val Met Asn Gly Gly Leu Thr Leu Ser	
65 70 75 80	
atc tct gat ggt tgg tgg gat gaa atg cct aag gag acc acc ggc tgg	288
Ile Ser Asp Gly Trp Trp Asp Glu Met Pro Lys Glu Thr Thr Gly Trp	
85 90 95	
acc atc cca acc gtt gag tcc cag gac ttg gaa tgc cgc gac cac ctg	336
Thr Ile Pro Thr Val Glu Ser Gln Asp Leu Glu Cys Arg Asp His Leu	
100 105 110	
gaa tcc cag gcg ctg tac gac ctg ctg gaa aac gaa gtt gca ccg ctg	384
Glu Ser Gln Ala Leu Tyr Asp Leu Leu Glu Asn Glu Val Ala Pro Leu	
115 120 125	
ttt tac aag cgc gac aag aac ggc atc cca cag gac tgg ctg gac ctg	432
Phe Tyr Lys Arg Asp Lys Asn Gly Ile Pro Gln Asp Trp Leu Asp Leu	
130 135 140	
gtt cgc gaa tcc tgg acc acc ctg tca cca atg gtc acc tcc acc cgc	480
Val Arg Glu Ser Trp Thr Thr Leu Ser Pro Met Val Thr Ser Thr Arg	
145 150 155 160	
atg gtg cgc gac tac acc acc cag tac tac cgc cca acc aaa cac cag	528
Met Val Arg Asp Tyr Thr Thr Gln Tyr Tyr Arg Pro Thr Lys His Gln	
165 170 175	
gca gag ctc att gcg cag cct gca gaa gca gcg gat tac gcg gca tgg	576
Ala Glu Leu Ile Ala Gln Pro Ala Glu Ala Ala Asp Tyr Ala Ala Trp	
180 185 190	
ctt gag cac atc aaa gca gag tgg gct ggc gtc aag gtc tca gac ctg	624
Leu Glu His Ile Lys Ala Glu Trp Ala Gly Val Lys Val Ser Asp Leu	
195 200 205	
aag atc agc gag agc gcc atc acg gcg cag gag ctt gaa gtc agc gtt	672
Lys Ile Ser Glu Ser Ala Ile Thr Ala Gln Glu Leu Glu Val Ser Val	
210 215 220	

cgc gtt gat tcc ggt tcg ctt aac gac gac gag ttc caa gct cag gca 720
 Arg Val Asp Ser Gly Ser Leu Asn Asp Asp Glu Phe Gln Ala Gln Ala
 225 230 235 240
 ctc ttt ggt gcg ctc gga cac aac ggt gac atc gaa gat cca gaa atc 768
 Leu Phe Gly Ala Leu Gly His Asn Gly Asp Ile Glu Asp Pro Glu Ile
 245 250 255
 acc gtt ttg acc cca cgc gcc gat gcc tac gcg gca aag gtc agc 816
 Thr Val Leu Thr Pro Arg Gly Asp Gly Ala Tyr Ala Ala Lys Val Ser
 260 265 270
 act gac ctg cca gcc aac tac gcc atc act gcc cgc gtt gtt cca aac 864
 Thr Asp Leu Pro Gly Asn Tyr Gly Ile Thr Ala Arg Val Val Pro Asn
 275 280 285
 aac agg atg ctg gtc agc cca gcg gaa acc cgc ctg atc acc tac ttg 912
 Asn Arg Met Leu Val Ser Pro Ala Glu Thr Arg Leu Ile Thr Tyr Leu
 290 295 300
 gag aac tagggcgaaa ctagctttac caa 941
 Glu Asn
 305

<210> 376

<211> 306

<212> PRT

<213> Corynebacterium glutamicum

<400> 376

Ile Ala Gly Lys Ala His Pro His Asp Met Gly Gly Lys Lys Leu Met
 1 5 10 15
 Gln Glu Ile Val His Phe Ala Asp Gln Ala Gly Val Arg Asp Arg Phe
 20 25 30
 Leu Phe Leu Pro Asp Tyr Asp Ile Asn Leu Ala Ser Tyr Leu Ile Ser
 35 40 45
 Gly Ala Asp Val Trp Leu Asn Asn Pro Val Arg Pro Gln Glu Ala Ser
 50 55 60
 Gly Thr Ser Gly Met Lys Ala Val Met Asn Gly Gly Leu Thr Leu Ser
 65 70 75 80
 Ile Ser Asp Gly Trp Trp Asp Glu Met Pro Lys Glu Thr Thr Gly Trp
 85 90 95
 Thr Ile Pro Thr Val Glu Ser Gln Asp Leu Glu Cys Arg Asp His Leu
 100 105 110
 Glu Ser Gln Ala Leu Tyr Asp Leu Leu Glu Asn Glu Val Ala Pro Leu
 115 120 125
 Phe Tyr Lys Arg Asp Lys Asn Gly Ile Pro Gln Asp Trp Leu Asp Leu
 130 135 140
 Val Arg Glu Ser Trp Thr Thr Leu Ser Pro Met Val Thr Ser Thr Arg
 145 150 155 160

Met Val Arg Asp Tyr Thr Thr Gln Tyr Tyr Arg Pro Thr Lys His Gln
 165 170 175

Ala Glu Leu Ile Ala Gln Pro Ala Glu Ala Ala Asp Tyr Ala Ala Trp
 180 185 190

Leu Glu His Ile Lys Ala Glu Trp Ala Gly Val Lys Val Ser Asp Leu
 195 200 205

Lys Ile Ser Glu Ser Ala Ile Thr Ala Gln Glu Leu Glu Val Ser Val
 210 215 220

Arg Val Asp Ser Gly Ser Leu Asn Asp Asp Glu Phe Gln Ala Gln Ala
 225 230 235 240

Leu Phe Gly Ala Leu Gly His Asn Gly Asp Ile Glu Asp Pro Glu Ile
 245 250 255

Thr Val Leu Thr Pro Arg Gly Asp Gly Ala Tyr Ala Ala Lys Val Ser
 260 265 270

Thr Asp Leu Pro Gly Asn Tyr Gly Ile Thr Ala Arg Val Val Pro Asn
 275 280 285

Asn Arg Met Leu Val Ser Pro Ala Glu Thr Arg Leu Ile Thr Tyr Leu
 290 295 300

Glu Asn
 305

<210> 377
 <211> 1206
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (1)..(1206)
 <223> FRXA02113

<400> 377

cta ggt cga atc aac gcc gag gag caa aac ctc agc gaa tac ctc agc	48
Leu Gly Arg Ile Asn Ala Glu Glu Gln Asn Leu Ser Glu Tyr Leu Ser	
1 5 10 15	
gac aag ctg tgg tac cag gac acc gca gat gca acc gat gct gtc gga	96
Asp Lys Leu Trp Tyr Gln Asp Thr Ala Asp Ala Thr Asp Ala Val Gly	
20 25 30	
gat cca ctc gtt gcg tac ttc tcc atg gag ttt ggc att cac cca agc	144
Asp Pro Leu Val Ala Tyr Phe Ser Met Glu Phe Gly Ile His Pro Ser	
35 40 45	
ctg cca atc tac tct ggc gga ctt ggt gtg ctt gcg ggc gag aac atg	192
Leu Pro Ile Tyr Ser Gly Gly Leu Gly Val Leu Ala Gly Glu Asn Met	
50 55 60	
aag tct gca tct gac ttg ggt gtg cca ctg atc ggt gtt ggt ttg ctc	240
Lys Ser Ala Ser Asp Leu Gly Val Pro Leu Ile Gly Val Gly Leu Leu	
65 70 75 80	

tac acc cac ggc tac ttc acc cag tca ctg tcc ggt gac ggt tgg cag	288
Tyr Thr His Gly Tyr Phe Thr Gln Ser Leu Ser Gly Asp Gly Trp Gln	
85 90 95	
cag gaa gag tac aag tac cac gat cca gca gaa ctg ccg att gag gca	336
Gln Glu Glu Tyr Lys Tyr His Asp Pro Ala Glu Leu Pro Ile Glu Ala	
100 105 110	
ggt aaa gat aag aac ggc gag cag gtc act ggt tct gtc acc tac cca	384
Val Lys Asp Lys Asn Gly Glu Gln Val Thr Val Ser Val Thr Tyr Pro	
115 120 125	
ggt gcg cag gaa gta aag att gca ctg tgg gta gca aac gtt ggc cgc	432
Gly Ala Gln Glu Val Lys Ile Ala Leu Trp Val Ala Asn Val Gly Arg	
130 135 140	
atc cca ttg ctg ctg ctt gat acc aac atc gag gca aac cca gaa gag	480
Ile Pro Leu Leu Leu Leu Asp Thr Asn Ile Glu Ala Asn Pro Glu Glu	
145 150 155 160	
ctc cgc aac gtt act gac cgc ctg tac ggt ggc gac aat gag cac cgc	528
Leu Arg Asn Val Thr Asp Arg Leu Tyr Gly Gly Asp Asn Glu His Arg	
165 170 175	
atc aag cag gaa ctc gtt ctc ggt gtt ggt ggc gtc cgc gct gtc aac	576
Ile Lys Gln Glu Leu Val Leu Gly Val Gly Gly Val Arg Ala Val Asn	
180 185 190	
gca ttc tgc gaa gct cgt ggt ctg aag cgc tca tct gtt gca cac ctc	624
Ala Phe Cys Glu Ala Arg Gly Leu Lys Arg Ser Ser Val Ala His Leu	
195 200 205	
aac gaa ggc cac gca ggt ttc ctg acc ctg gag cgt atc cgc gag cgc	672
Asn Glu Gly His Ala Gly Phe Leu Thr Leu Glu Arg Ile Arg Glu Arg	
210 215 220	
atc gca gag ggc atg gag tac cca gca gca ttc gag cag gtt cgt gcg	720
Ile Ala Glu Gly Met Glu Tyr Pro Ala Ala Phe Glu Gln Val Arg Ala	
225 230 235 240	
tcc aac atc ttc acc acc cac acc cca gtc cca gca ggc atc gac cgc	768
Ser Asn Ile Phe Thr Thr His Thr Pro Val Pro Ala Gly Ile Asp Arg	
245 250 255	
ttc gac atg gag atg gtg cgt cgt tat ctc ggt ggc ggt cag cca gaa	816
Phe Asp Met Glu Met Val Arg Arg Tyr Leu Gly Gly Gly Gln Pro Glu	
260 265 270	
gat cag cag ctg tgc gtt ggt gtt cca att gag aag gca ctt gag ctt	864
Asp Gln Gln Leu Cys Val Gly Val Pro Ile Glu Lys Ala Leu Glu Leu	
275 280 285	
ggt caa gag tcc gat cca cac cgc ttc aac atg gct cat atg ggc ctt	912
Gly Gln Glu Ser Asp Pro His Arg Phe Asn Met Ala His Met Gly Leu	
290 295 300	
cgc gcg agc caa cat gct aat ggc gtc gca aag ctt cat ggt gaa gta	960
Arg Ala Ser Gln His Ala Asn Gly Val Ala Lys Leu His Gly Glu Val	
305 310 315 320	

agc cgt gac atg ttc gcc ggc ctg tac ccc gga tat gag cct cgt gaa 1008
 Ser Arg Asp Met Phe Ala Gly Leu Tyr Pro Gly Tyr Glu Pro Arg Glu
 325 330 335
 gtg ccc atc ggg cac gtc acc aac ggt gtt cac ctg ccg acg tgg gtc 1056
 Val Pro Ile Gly His Val Thr Asn Gly Val His Leu Pro Thr Trp Val
 340 345 350
 aag cca gag atg aag gaa ctc atc gat cgc gtc act ggc ggc gct gat 1104
 Lys Pro Glu Met Lys Glu Leu Ile Asp Arg Val Thr Gly Gly Ala Asp
 355 360 365
 ctt gcg gtt gct gat tct tgg tca aac cca cag gct gtc gag tct gag 1152
 Leu Ala Val Ala Asp Ser Trp Ser Asn Pro Gln Ala Val Glu Ser Glu
 370 375 380
 aag atc tgg aag gtg cgc aac aag ttc cgt gct gac cta gtg gag gtt 1200
 Lys Ile Trp Lys Val Arg Asn Lys Phe Arg Ala Asp Leu Val Glu Val
 385 390 395 400
 gct cgc 1206
 Ala Arg

<210> 378

<211> 402

<212> PRT

<213> Corynebacterium glutamicum

<400> 378

Leu Gly Arg Ile Asn Ala Glu Glu Gln Asn Leu Ser Glu Tyr Leu Ser
 1 5 10 15
 Asp Lys Leu Trp Tyr Gln Asp Thr Ala Asp Ala Thr Asp Ala Val Gly
 20 25 30
 Asp Pro Leu Val Ala Tyr Phe Ser Met Glu Phe Gly Ile His Pro Ser
 35 40 45
 Leu Pro Ile Tyr Ser Gly Gly Leu Gly Val Leu Ala Gly Glu Asn Met
 50 55 60
 Lys Ser Ala Ser Asp Leu Gly Val Pro Leu Ile Gly Val Gly Leu Leu
 65 70 75 80
 Tyr Thr His Gly Tyr Phe Thr Gln Ser Leu Ser Gly Asp Gly Trp Gln
 85 90 95
 Gln Glu Glu Tyr Lys Tyr His Asp Pro Ala Glu Leu Pro Ile Glu Ala
 100 105 110
 Val Lys Asp Lys Asn Gly Glu Gln Val Thr Val Ser Val Thr Tyr Pro
 115 120 125
 Gly Ala Gln Glu Val Lys Ile Ala Leu Trp Val Ala Asn Val Gly Arg
 130 135 140
 Ile Pro Leu Leu Leu Leu Asp Thr Asn Ile Glu Ala Asn Pro Glu Glu
 145 150 155 160

Leu Arg Asn Val Thr Asp Arg Leu Tyr Gly Gly Asp Asn Glu His Arg
 165 170 175
 Ile Lys Gln Glu Leu Val Leu Gly Val Gly Gly Val Arg Ala Val Asn
 180 185 190
 Ala Phe Cys Glu Ala Arg Gly Leu Lys Arg Ser Ser Val Ala His Leu
 195 200 205
 Asn Glu Gly His Ala Gly Phe Leu Thr Leu Glu Arg Ile Arg Glu Arg
 210 215 220
 Ile Ala Glu Gly Met Glu Tyr Pro Ala Ala Phe Glu Gln Val Arg Ala
 225 230 235 240
 Ser Asn Ile Phe Thr Thr His Thr Pro Val Pro Ala Gly Ile Asp Arg
 245 250 255
 Phe Asp Met Glu Met Val Arg Arg Tyr Leu Gly Gly Gly Gln Pro Glu
 260 265 270
 Asp Gln Gln Leu Cys Val Gly Val Pro Ile Glu Lys Ala Leu Glu Leu
 275 280 285
 Gly Gln Glu Ser Asp Pro His Arg Phe Asn Met Ala His Met Gly Leu
 290 295 300
 Arg Ala Ser Gln His Ala Asn Gly Val Ala Lys Leu His Gly Glu Val
 305 310 315 320
 Ser Arg Asp Met Phe Ala Gly Leu Tyr Pro Gly Tyr Glu Pro Arg Glu
 325 330 335
 Val Pro Ile Gly His Val Thr Asn Gly Val His Leu Pro Thr Trp Val
 340 345 350
 Lys Pro Glu Met Lys Glu Leu Ile Asp Arg Val Thr Gly Gly Ala Asp
 355 360 365
 Leu Ala Val Ala Asp Ser Trp Ser Asn Pro Gln Ala Val Glu Ser Glu
 370 375 380
 Lys Ile Trp Lys Val Arg Asn Lys Phe Arg Ala Asp Leu Val Glu Val
 385 390 395 400

Ala Arg

<210> 379

<211> 1140

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(1117)

<223> RXA02147

<400> 379

aaaagttgag agcggcttgc ttcttttccct tggctaggct tttgtaatcg ggtagagta 60

gtggagttgc ttgaatgagg ttgatagggg atttttgaag	atg ttt ggt cgc cgt	115
	Met Phe Gly Arg Arg	
	1 5	
tgg gtg agc gtt gtg gcg tca tgt gtt atc gca agc acg ctg att ctg	163	
Trp Val Ser Val Val Ala Ser Cys Val Ile Ala Ser Thr Leu Ile Leu		
10 15 20		
gtg cct tcg cat tcc ggt gcg gag gaa gtc gat caa ctg att gct gat	211	
Val Pro Ser His Ser Gly Ala Glu Glu Val Asp Gln Leu Ile Ala Asp		
25 30 35		
atc gag cat gtc tct cag gaa acg tct gcc cag aat gag gaa gtc aaa	259	
Ile Glu His Val Ser Gln Glu Thr Ser Ala Gln Asn Glu Glu Val Lys		
40 45 50		
cag ctt gag att gat att gag gct cgt gag gtc acg atc aag gaa gtt	307	
Gln Leu Glu Ile Asp Ile Glu Ala Arg Glu Val Thr Ile Lys Glu Val		
55 60 65		
cag gag cag tcg gta agc tac cgt gag gcg gct gat caa gca tcg gag	355	
Gln Glu Gln Ser Val Ser Tyr Arg Glu Ala Ala Asp Gln Ala Ser Glu		
70 75 80 85		
aat gtc gaa gct tat cgt tcg gag atc aat cgg atc gct cag gcg aag	403	
Asn Val Glu Ala Tyr Arg Ser Glu Ile Asn Arg Ile Ala Gln Ala Lys		
90 95 100		
tat cgt ggc aca gtc acg gat cct ttg agc att gcg gtg tct gca gaa	451	
Tyr Arg Gly Thr Val Thr Asp Pro Leu Ser Ile Ala Val Ser Ala Glu		
105 110 115		
gat cca caa aac gtg att gat cgg atg agc tac ctt tca acg ttg act	499	
Asp Pro Gln Asn Val Ile Asp Arg Met Ser Tyr Leu Ser Thr Leu Thr		
120 125 130		
aag tcc act agt gat gtg gtt gaa tcc ctc aac gcg gag act gag aag	547	
Lys Ser Thr Ser Asp Val Val Glu Ser Leu Asn Ala Glu Thr Glu Lys		
135 140 145		
tcc gca gaa gct gtg tat caa gca aac cgt act aag gcg gaa gcg gag	595	
Ser Ala Glu Ala Val Tyr Gln Ala Asn Arg Thr Lys Ala Glu Ala Glu		
150 155 160 165		
ttc cag ttg ggg cag ctg aag gta cgc cag gcg gag ctt gaa tct gaa	643	
Phe Gln Leu Gly Gln Leu Lys Val Arg Gln Ala Glu Leu Glu Ser Glu		
170 175 180		
aag gaa gca ttg gat ggt cga aaa tcg gag atc cga gac cgg gtg gat	691	
Lys Glu Ala Leu Asp Gly Arg Lys Ser Glu Ile Arg Asp Arg Val Asp		
185 190 195		
gcc ctg acg cca cag gag cgg gaa atg tgg gtt gct aag aat ggt cca	739	
Ala Leu Thr Pro Gln Glu Arg Glu Met Trp Val Ala Lys Asn Gly Pro		
200 205 210		
ttg gac att gat ctg act gat ttg ctt ggt ctt tcc gct gcg act tcg	787	
Leu Asp Ile Asp Leu Thr Asp Leu Leu Gly Leu Ser Ala Ala Thr Ser		
215 220 225		

ggt gcg gtg gat gct gcc ttg tct aag ttg gga agc cct tat ggt tgg 835
 Gly Ala Val Asp Ala Ala Leu Ser Lys Leu Gly Ser Pro Tyr Gly Trp
 230 235 240 245
 ggt ggc att ggc cca aat gag ttt gat tgc tca ggt ttg atc tat tgg 883
 Gly Gly Ile Gly Pro Asn Glu Phe Asp Cys Ser Gly Leu Ile Tyr Trp
 250 255 260
 gcg tat cag cag atg ggt aag act ttg cca cgt acg tct caa gct cag 931
 Ala Tyr Gln Gln Met Gly Lys Thr Leu Pro Arg Thr Ser Gln Ala Gln
 265 270 275
 atg gct ggc gga acg ccg gtg agc aga gat gag ctg cag cct ggc gat 979
 Met Ala Gly Gly Thr Pro Val Ser Arg Asp Glu Leu Gln Pro Gly Asp
 280 285 290
 gtc att gga tat tac cca ggt gct act cac gtg gga ctg tat att ggg 1027
 Val Ile Gly Tyr Tyr Pro Gly Ala Thr His Val Gly Leu Tyr Ile Gly
 295 300 305
 gac gga aag att gtg cac gcc tca gac tac gga atc cct gtg cag gtg 1075
 Asp Gly Lys Ile Val His Ala Ser Asp Tyr Gly Ile Pro Val Gln Val
 310 315 320 325
 gta tct gtt gat tca gca ccg ttt tat ggt gcg cgt cgc tac 1117
 Val Ser Val Asp Ser Ala Pro Phe Tyr Gly Ala Arg Arg Tyr
 330 335
 taagaaatag ttcgtcagga gaa 1140

<210> 380

<211> 339

<212> PRT

<213> Corynebacterium glutamicum

<400> 380

Met Phe Gly Arg Arg Trp Val Ser Val Val Ala Ser Cys Val Ile Ala
 1 5 10 15
 Ser Thr Leu Ile Leu Val Pro Ser His Ser Gly Ala Glu Glu Val Asp
 20 25 30
 Gln Leu Ile Ala Asp Ile Glu His Val Ser Gln Glu Thr Ser Ala Gln
 35 40 45
 Asn Glu Glu Val Lys Gln Leu Glu Ile Asp Ile Glu Ala Arg Glu Val
 50 55 60
 Thr Ile Lys Glu Val Gln Glu Gln Ser Val Ser Tyr Arg Glu Ala Ala
 65 70 75 80
 Asp Gln Ala Ser Glu Asn Val Glu Ala Tyr Arg Ser Glu Ile Asn Arg
 85 90 95
 Ile Ala Gln Ala Lys Tyr Arg Gly Thr Val Thr Asp Pro Leu Ser Ile
 100 105 110
 Ala Val Ser Ala Glu Asp Pro Gln Asn Val Ile Asp Arg Met Ser Tyr
 115 120 125

Leu Ser Thr Leu Thr Lys Ser Thr Ser Asp Val Val Glu Ser Leu Asn
 130 135 140
 Ala Glu Thr Glu Lys Ser Ala Glu Ala Val Tyr Gln Ala Asn Arg Thr
 145 150 155 160
 Lys Ala Glu Ala Glu Phe Gln Leu Gly Gln Leu Lys Val Arg Gln Ala
 165 170 175
 Glu Leu Glu Ser Glu Lys Glu Ala Leu Asp Gly Arg Lys Ser Glu Ile
 180 185 190
 Arg Asp Arg Val Asp Ala Leu Thr Pro Gln Glu Arg Glu Met Trp Val
 195 200 205
 Ala Lys Asn Gly Pro Leu Asp Ile Asp Leu Thr Asp Leu Leu Gly Leu
 210 215 220
 Ser Ala Ala Thr Ser Gly Ala Val Asp Ala Ala Leu Ser Lys Leu Gly
 225 230 235 240
 Ser Pro Tyr Gly Trp Gly Gly Ile Gly Pro Asn Glu Phe Asp Cys Ser
 245 250 255
 Gly Leu Ile Tyr Trp Ala Tyr Gln Gln Met Gly Lys Thr Leu Pro Arg
 260 265 270
 Thr Ser Gln Ala Gln Met Ala Gly Gly Thr Pro Val Ser Arg Asp Glu
 275 280 285
 Leu Gln Pro Gly Asp Val Ile Gly Tyr Tyr Pro Gly Ala Thr His Val
 290 295 300
 Gly Leu Tyr Ile Gly Asp Gly Lys Ile Val His Ala Ser Asp Tyr Gly
 305 310 315 320
 Ile Pro Val Gln Val Val Ser Val Asp Ser Ala Pro Phe Tyr Gly Ala
 325 330 335

Arg Arg Tyr

<210> 381
 <211> 1959
 <212> DNA
 <213> *Corynebacterium glutamicum*

<220>
 <221> CDS
 <222> (101)..(1936)
 <223> RXA01478

<400> 381
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 tattggagtc acctggcctg aaatcctcta ctctgggcgc atg acc att cca gga 115
 Met Thr Ile Pro Gly
 1 5
 gct tcc aca cag act gat atc cct ctg gac aca ctt ctt gag gat tac 163

Ala	Ser	Thr	Gln	Thr	Asp	Ile	Pro	Leu	Asp	Thr	Leu	Leu	Glu	Asp	Tyr	
				10					15					20		
gcg	cta	ctg	tca	gac	act	cac	acc	ggc	gct	ctg	ctg	tcc	aac	atg	ggc	211
Ala	Leu	Leu	Ser	Asp	Thr	His	Thr	Gly	Ala	Leu	Leu	Ser	Asn	Met	Gly	
			25					30					35			
agt	ttg	gac	tgg	ttg	tgc	ctg	cct	cgt	ttt	gat	tcc	caa	gcc	atg	ttc	259
Ser	Leu	Asp	Trp	Leu	Cys	Leu	Pro	Arg	Phe	Asp	Ser	Gln	Ala	Met	Phe	
		40					45					50				
acc	agg	ctg	ctt	ggt	gat	cgc	gag	cac	gga	cac	tgg	agt	ttg	cgt	gtc	307
Thr	Arg	Leu	Leu	Gly	Asp	Arg	Glu	His	Gly	His	Trp	Ser	Leu	Arg	Val	
	55					60					65					
cca	ggt	ggt	gag	gtg	atc	agc	caa	aac	tac	ctc	ggc	gat	tcc	ttc	gtg	355
Pro	Gly	Gly	Glu	Val	Ile	Ser	Gln	Asn	Tyr	Leu	Gly	Asp	Ser	Phe	Val	
	70				75					80					85	
gtg	cag	acc	gtg	tgg	cgt	tca	gag	acc	ggt	act	gcc	cgg	gtt	gtt	gat	403
Val	Gln	Thr	Val	Trp	Arg	Ser	Glu	Thr	Gly	Thr	Ala	Arg	Val	Val	Asp	
				90					95					100		
ttc	atg	cca	att	cac	ggt	caa	gaa	caa	ccc	gat	atc	acc	gac	ctg	gtg	451
Phe	Met	Pro	Ile	His	Gly	Gln	Glu	Gln	Pro	Asp	Ile	Thr	Asp	Leu	Val	
			105					110					115			
cgc	tct	gtg	cac	tgc	gtg	gaa	ggc	gaa	gtg	gat	gtg	gaa	tcg	atc	ctg	499
Arg	Ser	Val	His	Cys	Val	Glu	Gly	Glu	Val	Asp	Val	Glu	Ser	Ile	Leu	
		120					125					130				
cgc	ctg	cgt	ttt	gat	tat	ggc	gag	tcc	act	ccg	tat	ttc	cgc	acc	agc	547
Arg	Leu	Arg	Phe	Asp	Tyr	Gly	Glu	Ser	Thr	Pro	Tyr	Phe	Arg	Thr	Ser	
	135					140					145					
act	gtc	gac	ggc	atc	agc	atc	gtg	cag	gct	gtc	gcc	ggc	ccc	aat	gcg	595
Thr	Val	Asp	Gly	Ile	Ser	Ile	Val	Gln	Ala	Val	Ala	Gly	Pro	Asn	Ala	
	150				155					160					165	
gta	tat	gtt	cgt	gga	cct	gag	atg	cca	cac	cgc	cct	gca	aag	gat	tgt	643
Val	Tyr	Val	Arg	Gly	Pro	Glu	Met	Pro	His	Arg	Pro	Ala	Lys	Asp	Cys	
				170					175					180		
cac	agt	ggc	acc	ttc	cac	ctg	acg	gcc	ggc	gaa	tcc	gtg	gaa	tgg	gtt	691
His	Ser	Gly	Thr	Phe	His	Leu	Thr	Ala	Gly	Glu	Ser	Val	Glu	Trp	Val	
			185					190					195			
ctc	acc	tgg	gca	ccg	tcg	ttc	gaa	ccg	cat	ccc	ccc	atg	ccg	gat	tac	739
Leu	Thr	Trp	Ala	Pro	Ser	Phe	Glu	Pro	His	Pro	Pro	Met	Pro	Asp	Tyr	
		200					205					210				
acc	cgc	tct	ttg	gag	agc	acc	ttg	agc	ttc	tgg	gca	tca	tgg	gtt	gaa	787
Thr	Arg	Ser	Leu	Glu	Ser	Thr	Leu	Ser	Phe	Trp	Ala	Ser	Trp	Val	Glu	
	215					220					225					
gag	ctc	ccc	cac	cag	cgc	ctc	tac	gac	gct	gaa	gtc	cgc	cgc	tcc	atg	835
Glu	Leu	Pro	His	Gln	Arg	Leu	Tyr	Asp	Ala	Glu	Val	Arg	Arg	Ser	Met	
	230				235					240					245	
ctc	gta	ctg	cgc	gcc	ttg	acc	gat	cta	caa	acc	ggt	ggc	atc	gtg	gcc	883
Leu	Val	L u	Arg	Ala	Leu	Thr	Asp	Leu	Gln	Thr	Gly	Gly	Ile	Val	Ala	

250							255							260							
gca	ccg	acc	acc	tca	cta	cca	gag	gat	ttc	gga	ggc	atc	cgt	aac	tgg	931					
Ala	Pro	Thr	Thr	Ser	Leu	Pro	Glu	Asp	Phe	Gly	Gly	Ile	Arg	Asn	Trp						
			265				270						275								
gac	tac	cgc	tac	gtg	tgg	ctg	cgc	gac	tcc	gca	ctc	acc	att	gaa	gcc	979					
Asp	Tyr	Arg	Tyr	Val	Trp	Leu	Arg	Asp	Ser	Ala	Leu	Thr	Ile	Glu	Ala						
			280				285						290								
ctc	gtg	gaa	tac	gga	ttc	tcc	caa	gca	gcc	ctc	caa	tgg	cgc	acc	tgg	1027					
Leu	Val	Glu	Tyr	Gly	Phe	Ser	Gln	Ala	Ala	Leu	Gln	Trp	Arg	Thr	Trp						
			295				300						305								
ctg	ctg	cgc	gcc	atc	gca	ggc	gac	ccg	gaa	aac	ctc	cgc	atc	atg	tat	1075					
Leu	Leu	Arg	Ala	Ile	Ala	Gly	Asp	Pro	Glu	Asn	Leu	Arg	Ile	Met	Tyr						
			310				315						320			325					
ggc	ctc	ggc	ggc	gaa	cga	cac	ctc	cct	gaa	cgc	gaa	ctc	caa	cac	ctg	1123					
Gly	Leu	Gly	Gly	Glu	Arg	His	Leu	Pro	Glu	Arg	Glu	Leu	Gln	His	Leu						
			330							335			340								
cgc	gga	tac	gaa	aac	tcc	gtg	cct	gtt	cgc	gtt	ggc	aac	gga	gcc	gcc	1171					
Arg	Gly	Tyr	Glu	Asn	Ser	Val	Pro	Val	Arg	Val	Gly	Asn	Gly	Ala	Ala						
			345							350			355								
gaa	caa	tac	caa	gca	gat	gtc	gtc	ggc	gaa	gta	atg	gtc	gcg	ctt	gaa	1219					
Glu	Gln	Tyr	Gln	Ala	Asp	Val	Val	Gly	Glu	Val	Met	Val	Ala	Leu	Glu						
			360				365						370								
acc	atc	cgc	cgc	gcc	ggg	tgc	ctc	gag	gac	gaa	ttc	tcc	tgg	ggc	atg	1267					
Thr	Ile	Arg	Arg	Ala	Gly	Cys	Leu	Glu	Asp	Glu	Phe	Ser	Trp	Gly	Met						
			375				380						385								
caa	aaa	gcc	atc	ctc	gat	ttc	caa	gaa	gcc	aac	ttc	gac	cgc	aag	gat	1315					
Gln	Lys	Ala	Ile	Leu	Asp	Phe	Gln	Glu	Ala	Asn	Phe	Asp	Arg	Lys	Asp						
			390				395						400			405					
caa	ggc	atc	tgg	gaa	atg	cgc	tcc	gaa	ccg	caa	tat	ttc	acc	cac	ggc	1363					
Gln	Gly	Ile	Trp	Glu	Met	Arg	Ser	Glu	Pro	Gln	Tyr	Phe	Thr	His	Gly						
			410							415			420								
cgc	gcc	atg	atg	tgg	gcc	ggc	ttc	gac	cgc	ggc	atc	aaa	gcc	atc	gaa	1411					
Arg	Ala	Met	Met	Trp	Ala	Gly	Phe	Asp	Arg	Gly	Ile	Lys	Ala	Ile	Glu						
			425							430			435								
gaa	ttc	aac	ctc	gac	ggc	ccc	atc	gag	cgc	tgg	cgt	gaa	ctc	cgc	gcc	1459					
Glu	Phe	Asn	Leu	Asp	Gly	Pro	Ile	Glu	Arg	Trp	Arg	Glu	Leu	Arg	Ala						
			440				445						450								
aaa	ctc	cgc	gaa	gaa	atc	atg	acc	aac	ggc	ttc	aac	gaa	gag	atc	caa	1507					
Lys	Leu	Arg	Glu	Glu	Ile	Met	Thr	Asn	Gly	Phe	Asn	Glu	Glu	Ile	Gln						
			455				460						465								
tcc	ttc	acc	cag	tgc	tac	gac	aac	acc	caa	gtc	gac	gcc	tcg	ctg	ctt	1555					
Ser	Phe	Thr	Gln	Cys	Tyr	Asp	Asn	Thr	Gln	Val	Asp	Ala	Ser	Leu	Leu						
			470				475						480			485					
cag	ctc	gcc	caa	ata	ggc	ttc	atc	ggc	ttc	gac	gat	cca	aaa	atg	ctc	1603					
Gln	Leu	Ala	Gln	Ile	Gly	Phe	Ile	Gly	Phe	Asp	Asp	Pro	Lys	Met	Leu						
			490							495			500								

agc acc gta gcg cgc att gag caa gag ctt ctc gac gcc cac ggc ttt 1651
 Ser Thr Val Ala Arg Ile Glu Gln Glu Leu Leu Asp Ala His Gly Phe
 505 510 515
 ctt cac agg tac cac acc gac ggg tct gac ggc ctt gcc ggc gac gaa 1699
 Leu His Arg Tyr His Thr Asp Gly Ser Asp Gly Leu Ala Gly Asp Glu
 520 525 530
 tac ccc ttc ctc atc tgt tca ttc tgg ctg gta gaa caa tac gca agc 1747
 Tyr Pro Phe Leu Ile Cys Ser Phe Trp Leu Val Glu Gln Tyr Ala Ser
 535 540 545
 tcc aac cgc ctc gac gag gcc aaa gaa aag atg aac cgc atc ctt gcc 1795
 Ser Asn Arg Leu Asp Glu Ala Lys Glu Lys Met Asn Arg Ile Leu Ala
 550 555 560 565
 gtc caa agc cca ctt ggc cta ctg gct gag gaa tac tcc acc cac cat 1843
 Val Gln Ser Pro Leu Gly Leu Leu Ala Glu Glu Tyr Ser Thr His His
 570 575 580
 ggc agg ctc gct gga aac tac cct cag gcc ttt tcc cac att ggt ctg 1891
 Gly Arg Leu Ala Gly Asn Tyr Pro Gln Ala Phe Ser His Ile Gly Leu
 585 590 595
 atc agc gct gcc cgt gcc ata aat ttc gaa gaa gcg cga aac agg 1936
 Ile Ser Ala Ala Arg Ala Ile Asn Phe Glu Glu Ala Arg Asn Arg
 600 605 610
 tagagtctaa ggtgtcattc ttg 1959

<210> 382

<211> 612

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 382

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 20 25 30
 Leu Ser Asn Met Gly Ser Leu Asp Trp Leu Cys Leu Pro Arg Phe Asp
 35 40 45
 Ser Gln Ala Met Phe Thr Arg Leu Leu Gly Asp Arg Glu His Gly His
 50 55 60
 Trp Ser Leu Arg Val Pro Gly Gly Glu Val Ile Ser Gln Asn Tyr Leu
 65 70 75 80
 Gly Asp Ser Phe Val Val Gln Thr Val Trp Arg Ser Glu Thr Gly Thr
 85 90 95
 Ala Arg Val Val Asp Phe Met Pro Ile His Gly Gln Glu Gln Pro Asp
 100 105 110
 Ile Thr Asp Leu Val Arg Ser Val His Cys Val Glu Gly Glu Val Asp
 115 120 125

Val Glu Ser Ile Leu Arg Leu Arg Phe Asp Tyr Gly Glu Ser Thr Pro
 130 135 140
 Tyr Phe Arg Thr Ser Thr Val Asp Gly Ile Ser Ile Val Gln Ala Val
 145 150 155 160
 Ala Gly Pro Asn Ala Val Tyr Val Arg Gly Pro Glu Met Pro His Arg
 165 170 175
 Pro Ala Lys Asp Cys His Ser Gly Thr Phe His Leu Thr Ala Gly Glu
 180 185 190
 Ser Val Glu Trp Val Leu Thr Trp Ala Pro Ser Phe Glu Pro His Pro
 195 200 205
 Pro Met Pro Asp Tyr Thr Arg Ser Leu Glu Ser Thr Leu Ser Phe Trp
 210 215 220
 Ala Ser Trp Val Glu Glu Leu Pro His Gln Arg Leu Tyr Asp Ala Glu
 225 230 235 240
 Val Arg Arg Ser Met Leu Val Leu Arg Ala Leu Thr Asp Leu Gln Thr
 245 250 255
 Gly Gly Ile Val Ala Ala Pro Thr Thr Ser Leu Pro Glu Asp Phe Gly
 260 265 270
 Gly Ile Arg Asn Trp Asp Tyr Arg Tyr Val Trp Leu Arg Asp Ser Ala
 275 280 285
 Leu Thr Ile Glu Ala Leu Val Glu Tyr Gly Phe Ser Gln Ala Ala Leu
 290 295 300
 Gln Trp Arg Thr Trp Leu Leu Arg Ala Ile Ala Gly Asp Pro Glu Asn
 305 310 315 320
 Leu Arg Ile Met Tyr Gly Leu Gly Gly Glu Arg His Leu Pro Glu Arg
 325 330 335
 Glu Leu Gln His Leu Arg Gly Tyr Glu Asn Ser Val Pro Val Arg Val
 340 345 350
 Gly Asn Gly Ala Ala Glu Gln Tyr Gln Ala Asp Val Val Gly Glu Val
 355 360 365
 Met Val Ala Leu Glu Thr Ile Arg Arg Ala Gly Cys Leu Glu Asp Glu
 370 375 380
 Phe Ser Trp Gly Met Gln Lys Ala Ile Leu Asp Phe Gln Glu Ala Asn
 385 390 395 400
 Phe Asp Arg Lys Asp Gln Gly Ile Trp Glu Met Arg Ser Glu Pro Gln
 405 410 415
 Tyr Phe Thr His Gly Arg Ala Met Met Trp Ala Gly Phe Asp Arg Gly
 420 425 430
 Ile Lys Ala Ile Glu Glu Phe Asn Leu Asp Gly Pro Ile Glu Arg Trp
 435 440 445

Arg Glu Leu Arg Ala Lys Leu Arg Glu Glu Ile Met Thr Asn Gly Phe
 450 455 460
 Asn Glu Glu Ile Gln Ser Phe Thr Gln Cys Tyr Asp Asn Thr Gln Val
 465 470 475 480
 Asp Ala Ser Leu Leu Gln Leu Ala Gln Ile Gly Phe Ile Gly Phe Asp
 485 490 495
 Asp Pro Lys Met Leu Ser Thr Val Ala Arg Ile Glu Gln Glu Leu Leu
 500 505 510
 Asp Ala His Gly Phe Leu His Arg Tyr His Thr Asp Gly Ser Asp Gly
 515 520 525
 Leu Ala Gly Asp Glu Tyr Pro Phe Leu Ile Cys Ser Phe Trp Leu Val
 530 535 540
 Glu Gln Tyr Ala Ser Ser Asn Arg Leu Asp Glu Ala Lys Glu Lys Met
 545 550 555 560
 Asn Arg Ile Leu Ala Val Gln Ser Pro Leu Gly Leu Leu Ala Glu Glu
 565 570 575
 Tyr Ser Thr His His Gly Arg Leu Ala Gly Asn Tyr Pro Gln Ala Phe
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 595 600 605
 Ala Arg Asn Arg
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 <222> (101)..(658)
 <223> RXA01888

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 Met Ala Asp Val Ala
 1 5
 aaa gct gct gga gta tcc act gcg ctg gtc tcc atc gtg ttt cgc gat 163
 Lys Ala Ala Gly Val Ser Thr Ala Leu Val Ser Ile Val Phe Arg Asp
 10 15 20
 gcc ccc gga gca agt gaa tcc acc gcg aac cat gtg aaa gaa aaa gcc 211
 Ala Pro Gly Ala Ser Glu Ser Thr Arg Asn His Val Lys Glu Lys Ala
 25 30 35
 gcc gaa ctc gga tac att cct gat cga cga gcc caa aaa ctt cgc caa 259
 Ala Glu Leu Gly Tyr Ile Pro Asp Arg Arg Ala Gln Lys Leu Arg Gln

40	45	50	
aac cgc tcc gga ctc atc ggt gtg gca ttc gaa atg cac caa gca ttc			307
Asn Arg Ser Gly Leu Ile Gly Val Ala Phe Glu Met His Gln Ala Phe			
55	60	65	
cac ggc gat atc gtc gaa cac ctc tat ccc acc gcc cga aaa cat ggc			355
His Gly Asp Ile Val Glu His Leu Tyr Pro Thr Ala Arg Lys His Gly			
70	75	80	85
ttc gac ctg tac ctt agc gcg atc aca ccg act cgc act gaa aaa gat			403
Phe Asp Leu Tyr Leu Ser Ala Ile Thr Pro Thr Arg Thr Glu Lys Asp			
90	95	100	
gcc gtc aac gcc ctg atc agg gaa cga tgc gaa gca gta att ctt cta			451
Ala Val Asn Ala Leu Ile Arg Glu Arg Cys Glu Ala Val Ile Leu Leu			
105	110	115	
gga tct cgc atg tca cct agt gat ttg gaa aca atc gca cag caa ctt			499
Gly Ser Arg Met Ser Pro Ser Asp Leu Glu Thr Ile Ala Gln Gln Leu			
120	125	130	
ccc gtc caa gta att gcc cgc ggt tcc gga acc ccc aaa gtc agt tcc			547
Pro Val Gln Val Ile Ala Arg Gly Ser Gly Thr Pro Lys Val Ser Ser			
135	140	145	
gtc cat gtc gac gac gca gtt ggc gcc caa tta gcc ctc aac cac ctc			595
Val His Val Asp Asp Ala Val Gly Ala Gln Leu Ala Leu Asn His Leu			
150	155	160	165
atc gaa tta ggc cac gaa cac atc atc tac atc gat ggt ggc gac gcc			643
Ile Glu Leu Gly His Glu His Ile Ile Tyr Ile Asp Gly Gly Asp Ala			
170	175	180	
cct ggc acc cag gaa			658
Pro Gly Thr Gln Glu			
185			

<210> 384

<211> 186

<212> PRT

<213> Corynebacterium glutamicum

<400> 384

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Ile	Val	Phe	Arg	Asp	Ala	Pro	Gly	Ala	Ser	Glu	Ser	Thr	Arg	Asn	His
			20					25					30		

Val	Lys	Glu	Lys	Ala	Ala	Glu	Leu	Gly	Tyr	Ile	Pro	Asp	Arg	Arg	Ala
	35						40					45			

Gln	Lys	Leu	Arg	Gln	Asn	Arg	Ser	Gly	Leu	Ile	Gly	Val	Ala	Phe	Glu
50						55					60				

Met	His	Gln	Ala	Phe	His	Gly	Asp	Ile	Val	Glu	His	Leu	Tyr	Pro	Thr
65					70					75				80	

Ala	Arg	Lys	His	Gly	Phe	Asp	Leu	Tyr	Leu	Ser	Ala	Ile	Thr	Pro	Thr
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

	85		90		95
Arg Thr Glu Lys Asp Ala Val Asn Ala Leu Ile Arg Glu Arg Cys Glu	100		105		110
Ala Val Ile Leu Leu Gly Ser Arg Met Ser Pro Ser Asp Leu Glu Thr	115		120		125
Ile Ala Gln Gln Leu Pro Val Gln Val Ile Ala Arg Gly Ser Gly Thr	130		135		140
Pro Lys Val Ser Ser Val His Val Asp Asp Ala Val Gly Ala Gln Leu	145		150		155
Ala Leu Asn His Leu Ile Glu Leu Gly His Glu His Ile Ile Tyr Ile	165		170		175
Asp Gly Gly Asp Ala Pro Gly Thr Gln Glu	180		185		

<210> 385
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<220>
 <221> CDS
 <222> (101)..(1480)
 <223> RXN01927

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 Met Ala Leu Val Leu 5
 gga atc gat agt tcc acc caa tcc tgc aag gct ttg ctt gtc gac gcc 163
 Gly Ile Asp Ser Ser Thr Gln Ser Cys Lys Ala Leu Leu Val Asp Ala 20
 gcc acc ggc cag gtt atc gac gaa ggc cgc gcg agt cac ccg agc ggg 211
 Ala Thr Gly Gln Val Ile Asp Glu Gly Arg Ala Ser His Pro Ser Gly 35
 tcg gag gta gat cca cgt gcg tgg atc gct gcg ctg gat caa gct acc 259
 Ser Glu Val Asp Pro Arg Ala Trp Ile Ala Ala Leu Asp Gln Ala Thr 50
 gag ggg ttg tta gaa cgc gcg gac gct gta tct att gca ggc cag cag 307
 Glu Gly Leu Leu Glu Arg Ala Asp Ala Val Ser Ile Ala Gly Gln Gln 65
 cac ggc atg gtg gcg ttg gat gaa aac gat gaa atc gtt cgc ccg gcg 355
 His Gly Met Val Ala Leu Asp Glu Asn Asp Glu Ile Val Arg Pro Ala 85
 ttg tta tgg aat gac act cgt tct gcc cag gct gcg ttg gat ctc aat 403
 Leu Leu Trp Asn Asp Thr Arg Ser Ala Gln Ala Ala Leu Asp Leu Asn 100
 90 95 100

gag gag atc ggc ggc gat cag gct gcg gta gat gcc acg gga agt gtg	451
Glu Glu Ile Gly Gly Asp Gln Ala Ala Val Asp Ala Thr Gly Ser Val	
105 110 115	
tat gtt gct tct tta act gcc acc aaa atg cgg tgg atg cgt gat cat	499
Tyr Val Ala Ser Leu Thr Ala Thr Lys Met Arg Trp Met Arg Asp His	
120 125 130	
gaa cca gaa aat gca gcg cgc acg gcg tcg gtg atg ttg cct cat gat	547
Glu Pro Glu Asn Ala Ala Arg Thr Ala Ser Val Met Leu Pro His Asp	
135 140 145	
ttc ctc acc tgg cat ttg atg gga cgc gga cgc aaa gtc acc gac cat	595
Phe Leu Thr Trp His Leu Met Gly Arg Gly Arg Lys Val Thr Asp His	
150 155 160 165	
ggt gat gct tct gga acg ggc tac tac agc acg cgt gat cgt gcg tgg	643
Gly Asp Ala Ser Gly Thr Gly Tyr Tyr Ser Thr Arg Asp Arg Ala Trp	
170 175 180	
cgc acc gat cta gct gcc ttg gcg ctg ggc cat gag gtg gaa ctt cct	691
Arg Thr Asp Leu Ala Ala Leu Ala Leu Gly His Glu Val Glu Leu Pro	
185 190 195	
gaa ctc ctg gcc cca aat gcg att gcg gga aca act cca ggt gga gtg	739
Glu Leu Leu Ala Pro Asn Ala Ile Ala Gly Thr Thr Pro Gly Gly Val	
200 205 210	
aaa gtt gct gca ggc acg gga gat aat gct gcg gct gcg ctt ggc ctt	787
Lys Val Ala Ala Gly Thr Gly Asp Asn Ala Ala Ala Leu Gly Leu	
215 220 225	
gat ttg cag cct ggt gat gtc agc gtg tcg atc gcc acc tct ggc gtt	835
Asp Leu Gln Pro Gly Asp Val Ser Val Ser Ile Gly Thr Ser Gly Val	
230 235 240 245	
gcc ggc atg acc gtt caa cat agc gtc cac gat cca tct ggt ttg gtc	883
Ala Gly Met Thr Val Gln His Ser Val His Asp Pro Ser Gly Leu Val	
250 255 260	
act ggt ttc gcc gat gcc acg ggt gcg tat ttc ccg ctg gcc tgc acg	931
Thr Gly Phe Ala Asp Ala Thr Gly Ala Tyr Phe Pro Leu Ala Cys Thr	
265 270 275	
ctt aat ggc gca ccg gtg ttg gaa ttc ggc cgc cgc att ctg ggc gtg	979
Leu Asn Gly Ala Pro Val Leu Glu Phe Gly Arg Arg Ile Leu Gly Val	
280 285 290	
gaa tgg gaa gag ttc gat gcg ctt gca ctg gct gct caa ccc ggt tca	1027
Glu Trp Glu Glu Phe Asp Ala Leu Ala Leu Ala Ala Gln Pro Gly Ser	
295 300 305	
ggt ggc gtg acg ctc cag cct tat ttg gag ggc gag cgt acg ccg aat	1075
Gly Gly Val Thr Leu Gln Pro Tyr Leu Glu Gly Glu Arg Thr Pro Asn	
310 315 320 325	
cgt ccc gca gca cgt ggc gtt ttg gct gga cta aac tgt gca acg acc	1123
Arg Pro Ala Ala Arg Gly Val Leu Ala Gly Leu Asn Cys Ala Thr Thr	
330 335 340	

cgc gag gac ttt gcc cga gca act gtt gaa ggc ttg ttg ttg gca ttg 1171
 Arg Glu Asp Phe Ala Arg Ala Thr Val Glu Gly Leu Leu Leu Ala Leu
 345 350 355
 gat gat gct gta acg gcg ctg gtt gag gcc acg gga gtg ccc gtt cag 1219
 Asp Asp Ala Val Thr Ala Leu Val Glu Ala Thr Gly Val Pro Val Gln
 360 365 370
 cgc atc cag ctc atc ggt ggc ggc gcg cgt tca cag gcg gtt cgt gag 1267
 Arg Ile Gln Leu Ile Gly Gly Gly Ala Arg Ser Gln Ala Val Arg Glu
 375 380 385
 att gcc cct gag att ttc ggc cat gag att gtg gtt cca gaa ccc gct 1315
 Ile Ala Pro Glu Ile Phe Gly His Glu Ile Val Val Pro Glu Pro Ala
 390 395 400 405
 gaa tat gtg gcg ttg ggt gca gct cgt cag gcg gca tgg gcg ctg tcg 1363
 Glu Tyr Val Ala Leu Gly Ala Ala Arg Gln Ala Ala Trp Ala Leu Ser
 410 415 420
 ggt gag gcc acg cca ccg cag tgg cca act ccc ggt tcc gat ccg cac 1411
 Gly Glu Ala Thr Pro Pro Gln Trp Pro Thr Pro Gly Ser Asp Pro His
 425 430 435
 cgc gca cct aaa aac act gag ctg agc acg cgt tat gcg aag ctg cgt 1459
 Arg Ala Pro Lys Asn Thr Glu Leu Ser Thr Arg Tyr Ala Lys Leu Arg
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 Ala Ala Thr Gln Gly Trp Tyr
 455 460

<210> 386

<211> 460

<212> PRT

<213> Corynebacterium glutamicum

<400> 386

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 20 25 30
 Ser His Pro Ser Gly Ser Glu Val Asp Pro Arg Ala Trp Ile Ala Ala
 35 40 45
 Leu Asp Gln Ala Thr Glu Gly Leu Leu Glu Arg Ala Asp Ala Val Ser
 50 55 60
 Ile Ala Gly Gln Gln His Gly Met Val Ala Leu Asp Glu Asn Asp Glu
 65 70 75 80
 Ile Val Arg Pro Ala Leu Leu Trp Asn Asp Thr Arg Ser Ala Gln Ala
 85 90 95
 Ala Leu Asp Leu Asn Glu Glu Ile Gly Gly Asp Gln Ala Ala Val Asp
 100 105 110
 Ala Thr Gly Ser Val Tyr Val Ala Ser Leu Thr Ala Thr Lys Met Arg

115					120					125					
Trp	Met	Arg	Asp	His	Glu	Pro	Glu	Asn	Ala	Ala	Arg	Thr	Ala	Ser	Val
130						135					140				
Met	Leu	Pro	His	Asp	Phe	Leu	Thr	Trp	His	Leu	Met	Gly	Arg	Gly	Arg
145					150					155					160
Lys	Val	Thr	Asp	His	Gly	Asp	Ala	Ser	Gly	Thr	Gly	Tyr	Tyr	Ser	Thr
				165					170					175	
Arg	Asp	Arg	Ala	Trp	Arg	Thr	Asp	Leu	Ala	Ala	Leu	Ala	Leu	Gly	His
			180					185					190		
Glu	Val	Glu	Leu	Pro	Glu	Leu	Leu	Ala	Pro	Asn	Ala	Ile	Ala	Gly	Thr
		195					200					205			
Thr	Pro	Gly	Gly	Val	Lys	Val	Ala	Ala	Gly	Thr	Gly	Asp	Asn	Ala	Ala
	210					215					220				
Ala	Ala	Leu	Gly	Leu	Asp	Leu	Gln	Pro	Gly	Asp	Val	Ser	Val	Ser	Ile
225					230					235					240
Gly	Thr	Ser	Gly	Val	Ala	Gly	Met	Thr	Val	Gln	His	Ser	Val	His	Asp
				245					250					255	
Pro	Ser	Gly	Leu	Val	Thr	Gly	Phe	Ala	Asp	Ala	Thr	Gly	Ala	Tyr	Phe
			260					265					270		
Pro	Leu	Ala	Cys	Thr	Leu	Asn	Gly	Ala	Pro	Val	Leu	Glu	Phe	Gly	Arg
		275					280					285			
Arg	Ile	Leu	Gly	Val	Glu	Trp	Glu	Glu	Phe	Asp	Ala	Leu	Ala	Leu	Ala
	290					295					300				
Ala	Gln	Pro	Gly	Ser	Gly	Gly	Val	Thr	Leu	Gln	Pro	Tyr	Leu	Glu	Gly
305					310					315					320
Glu	Arg	Thr	Pro	Asn	Arg	Pro	Ala	Ala	Arg	Gly	Val	Leu	Ala	Gly	Leu
				325					330					335	
Asn	Cys	Ala	Thr	Thr	Arg	Glu	Asp	Phe	Ala	Arg	Ala	Thr	Val	Glu	Gly
			340					345					350		
Leu	Leu	Leu	Ala	Leu	Asp	Asp	Ala	Val	Thr	Ala	Leu	Val	Glu	Ala	Thr
		355					360					365			
Gly	Val	Pro	Val	Gln	Arg	Ile	Gln	Leu	Ile	Gly	Gly	Gly	Ala	Arg	Ser
	370					375					380				
Gln	Ala	Val	Arg	Glu	Ile	Ala	Pro	Glu	Ile	Phe	Gly	His	Glu	Ile	Val
385					390					395					400
Val	Pro	Glu	Pro	Ala	Glu	Tyr	Val	Ala	Leu	Gly	Ala	Ala	Arg	Gln	Ala
				405					410					415	
Ala	Trp	Ala	Leu	Ser	Gly	Glu	Ala	Thr	Pro	Pro	Gln	Trp	Pro	Thr	Pro
			420					425					430		
Gly	Ser	Asp	Pro	His	Arg	Ala	Pro	Lys	Asn	Thr	Glu	Leu	Ser	Thr	Arg
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Tyr Ala Lys Leu Arg Ala Ala Thr Gln Gly Trp Tyr
 450 455 460

<210> 387

<211> 1139

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(1116)

<223> FRXA01927

<400> 387

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Asn Asp Thr Arg Ser Ala Gln Ala Ala Leu Asp Leu Asn Glu Glu Ile	
1 5 10 15	
ggc ggc gat cag gct gcg gta gat gcc acg gga agt gtg tat gtt gct	96
Gly Gly Asp Gln Ala Ala Val Asp Ala Thr Gly Ser Val Tyr Val Ala	
20 25 30	
tct tta act gcc acc aaa atg cgg tgg atg cgt gat cat gaa cca gaa	144
Ser Leu Thr Ala Thr Lys Met Arg Trp Met Arg Asp His Glu Pro Glu	
35 40 45	
aat gca gcg cgc acg gcg tcg gtg atg ttg cct cat gat ttc ctc acc	192
Asn Ala Ala Arg Thr Ala Ser Val Met Leu Pro His Asp Phe Leu Thr	
50 55 60	
tgg cat ttg atg gga cgc gga cgc aaa gtc acc gac cat ggt gat gct	240
Trp His Leu Met Gly Arg Gly Arg Lys Val Thr Asp His Gly Asp Ala	
65 70 75 80	
tct gga acg ggc tac tac agc acg cgt gat cgt gcg tgg cgc acc gat	288
Ser Gly Thr Gly Tyr Tyr Ser Thr Arg Asp Arg Ala Trp Arg Thr Asp	
85 90 95	
cta gct gcc ttg gcg ctg ggc cat gag gtg gaa ctt cct gaa ctc ctg	336
Leu Ala Ala Leu Ala Leu Gly His Glu Val Glu Leu Pro Glu Leu Leu	
100 105 110	
gcc cca aat gcg att gcg gga aca act cca ggt gga gtg aaa gtt gct	384
Ala Pro Asn Ala Ile Ala Gly Thr Thr Pro Gly Gly Val Lys Val Ala	
115 120 125	
gca ggc acg gga gat aat gct gcg gct gcg ctt ggc ctt gat ttg cag	432
Ala Gly Thr Gly Asp Asn Ala Ala Ala Leu Gly Leu Asp Leu Gln	
130 135 140	
cct ggt gat gtc agc gtg tcg atc ggc acc tct ggc gtt gcc ggc atg	480
Pro Gly Asp Val Ser Val Ser Ile Gly Thr Ser Gly Val Ala Gly Met	
145 150 155 160	
acc gtt caa cat agc gtc cac gat cca tct ggt ttg gtc act ggt ttc	528
Thr Val Gln His Ser Val His Asp Pro Ser Gly Leu Val Thr Gly Phe	
165 170 175	
gcc gat gcc acg ggt gcg tat ttc ccg ctg gcc tgc acg ctt aat ggc	576

Ala	Asp	Ala	Thr	Gly	Ala	Tyr	Phe	Pro	Leu	Ala	Cys	Thr	Leu	Asn	Gly		
			180					185					190				
gca	ccg	gtg	ttg	gaa	ttc	ggc	cgc	cgc	att	ctg	ggc	gtg	gaa	tgg	gaa	624	
Ala	Pro	Val	Leu	Glu	Phe	Gly	Arg	Arg	Ile	Leu	Gly	Val	Glu	Trp	Glu		
			195				200					205					
gag	ttc	gat	gcg	ctt	gca	ctg	gct	gct	caa	ccc	ggg	tca	ggg	ggc	gtg	672	
Glu	Phe	Asp	Ala	Leu	Ala	Leu	Ala	Ala	Gln	Pro	Gly	Ser	Gly	Gly	Val		
			210				215				220						
acg	ctc	cag	cct	tat	ttg	gag	ggc	gag	cgt	acg	ccg	aat	cgt	ccc	gca	720	
Thr	Leu	Gln	Pro	Tyr	Leu	Glu	Gly	Glu	Arg	Thr	Pro	Asn	Arg	Pro	Ala		
					230					235					240		
gca	cgt	ggc	gtt	ttg	gct	gga	cta	aac	tgt	gca	acg	acc	cgc	gag	gac	768	
Ala	Arg	Gly	Val	Leu	Ala	Gly	Leu	Asn	Cys	Ala	Thr	Thr	Arg	Glu	Asp		
				245					250					255			
ttt	gcc	cga	gca	act	gtt	gaa	ggc	ttg	ttg	ttg	gca	ttg	gat	gat	gct	816	
Phe	Ala	Arg	Ala	Thr	Val	Glu	Gly	Leu	Leu	Leu	Ala	Leu	Asp	Asp	Ala		
			260					265					270				
gta	acg	gcg	ctg	gtt	gag	gcc	acg	gga	gtg	ccc	gtt	cag	cgc	atc	cag	864	
Val	Thr	Ala	Leu	Val	Glu	Ala	Thr	Gly	Val	Pro	Val	Gln	Arg	Ile	Gln		
			275					280					285				
ctc	atc	ggg	ggc	ggc	gcg	cgt	tca	cag	gcg	gtt	cgt	gag	att	gcc	cct	912	
Leu	Ile	Gly	Gly	Gly	Ala	Arg	Ser	Gln	Ala	Val	Arg	Glu	Ile	Ala	Pro		
			290				295				300						
gag	att	ttc	ggc	cat	gag	att	gtg	gtt	cca	gaa	ccc	gct	gaa	tat	gtg	960	
Glu	Ile	Phe	Gly	His	Glu	Ile	Val	Val	Pro	Glu	Pro	Ala	Glu	Tyr	Val		
					310					315					320		
gcg	ttg	ggg	gca	gct	cgt	cag	gcg	gca	tgg	gcg	ctg	tcg	ggg	gag	gcc	1008	
Ala	Leu	Gly	Ala	Ala	Arg	Gln	Ala	Ala	Trp	Ala	Leu	Ser	Gly	Glu	Ala		
				325					330					335			
acg	cca	ccg	cag	tgg	cca	act	ccc	ggg	tcc	gat	ccg	cac	cgc	gca	cct	1056	
Thr	Pro	Pro	Gln	Trp	Pro	Thr	Pro	Gly	Ser	Asp	Pro	His	Arg	Ala	Pro		
			340					345					350				
aaa	aac	act	gag	ctg	agc	acg	cgt	tat	gcg	aag	ctg	cgt	gct	gca	acg	1104	
Lys	Asn	Thr	Glu	Leu	Ser	Thr	Arg	Tyr	Ala	Lys	Leu	Arg	Ala	Ala	Thr		
			355				360					365					
cag	ggg	tgg	tac	tagagctcga	tattgtcga	caa										1139	
Gln	Gly	Trp	Tyr														
			370														

<210> 388

<211> 372

<212> PRT

<213> Corynebacterium glutamicum

<400> 388

Asn Asp Thr Arg Ser Ala Gln Ala Ala Leu Asp Leu Asn Glu Glu Ile

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5

10

15

Gly Gly Asp Gln Ala Ala Val Asp Ala Thr Gly Ser Val Tyr Val Ala
 20 25 30
 Ser Leu Thr Ala Thr Lys Met Arg Trp Met Arg Asp His Glu Pro Glu
 35 40 45
 Asn Ala Ala Arg Thr Ala Ser Val Met Leu Pro His Asp Phe Leu Thr
 50 55 60
 Trp His Leu Met Gly Arg Gly Arg Lys Val Thr Asp His Gly Asp Ala
 65 70 75 80
 Ser Gly Thr Gly Tyr Tyr Ser Thr Arg Asp Arg Ala Trp Arg Thr Asp
 85 90 95
 Leu Ala Ala Leu Ala Leu Gly His Glu Val Glu Leu Pro Glu Leu Leu
 100 105 110
 Ala Pro Asn Ala Ile Ala Gly Thr Thr Pro Gly Gly Val Lys Val Ala
 115 120 125
 Ala Gly Thr Gly Asp Asn Ala Ala Ala Ala Leu Gly Leu Asp Leu Gln
 130 135 140
 Pro Gly Asp Val Ser Val Ser Ile Gly Thr Ser Gly Val Ala Gly Met
 145 150 155 160
 Thr Val Gln His Ser Val His Asp Pro Ser Gly Leu Val Thr Gly Phe
 165 170 175
 Ala Asp Ala Thr Gly Ala Tyr Phe Pro Leu Ala Cys Thr Leu Asn Gly
 180 185 190
 Ala Pro Val Leu Glu Phe Gly Arg Arg Ile Leu Gly Val Glu Trp Glu
 195 200 205
 Glu Phe Asp Ala Leu Ala Leu Ala Ala Gln Pro Gly Ser Gly Gly Val
 210 215 220
 Thr Leu Gln Pro Tyr Leu Glu Gly Glu Arg Thr Pro Asn Arg Pro Ala
 225 230 235 240
 Ala Arg Gly Val Leu Ala Gly Leu Asn Cys Ala Thr Thr Arg Glu Asp
 245 250 255
 Phe Ala Arg Ala Thr Val Glu Gly Leu Leu Leu Ala Leu Asp Asp Ala
 260 265 270
 Val Thr Ala Leu Val Glu Ala Thr Gly Val Pro Val Gln Arg Ile Gln
 275 280 285
 Leu Ile Gly Gly Gly Ala Arg Ser Gln Ala Val Arg Glu Ile Ala Pro
 290 295 300
 Glu Ile Phe Gly His Glu Ile Val Val Pro Glu Pro Ala Glu Tyr Val
 305 310 315 320
 Ala Leu Gly Ala Ala Arg Gln Ala Ala Trp Ala Leu Ser Gly Glu Ala
 325 330 335
 Thr Pro Pro Gln Trp Pro Thr Pro Gly Ser Asp Pro His Arg Ala Pro

340 345 350
 Lys Asn Thr Glu Leu Ser Thr Arg Tyr Ala Lys Leu Arg Ala Ala Thr
 355 360 365
 Gln Gly Trp Tyr
 370

 <210> 389
 <211> 844
 <212> DNA
 <213> Corynebacterium glutamicum

 <220>
 <221> CDS
 <222> (101)..(844)
 <223> RXA02729

 <400> 389
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 catcgtgaat caatcatcaa ctccacttta aggaagaagg atg gac tcc cca atg 115
 Met Asp Ser Pro Met
 1 5

 agt aac tca acc ggt acc gac att gtc gtt gtc gga tcc atc aat gcc 163
 Ser Asn Ser Thr Gly Thr Asp Ile Val Val Val Gly Ser Ile Asn Ala
 10 15 20

 gat ctc acc gca aaa gtt caa cgc cac cct gaa cct gga gaa acc ctc 211
 Asp Leu Thr Ala Lys Val Gln Arg His Pro Glu Pro Gly Glu Thr Leu
 25 30 35

 ctg ggt agc ggc ggc aca gtg agt gct ggt ggc aaa ggc gcc aac caa 259
 Leu Gly Ser Gly Gly Thr Val Ser Ala Gly Gly Lys Gly Ala Asn Gln
 40 45 50

 gct gtg gcg gca gcg caa tta ggt gcc aaa gtc acc atg atc ggt gcg 307
 Ala Val Ala Ala Ala Gln Leu Gly Ala Lys Val Thr Met Ile Gly Ala
 55 60 65

 gtc gga acc gat caa atg gct ggc gag gcg ctg aca cat ttg cgt caa 355
 Val Gly Thr Asp Gln Met Ala Gly Glu Ala Leu Thr His Leu Arg Gln
 70 75 80 85

 tca gga gca gat atg tcc gcg att gcc act gtg gac ggt ccc act ggt 403
 Ser Gly Ala Asp Met Ser Ala Ile Ala Thr Val Asp Gly Pro Thr Gly
 90 95 100

 ctt gcc atc atc act gtg tct gac gat ggg gaa aac acc atc atc gtt 451
 Leu Ala Ile Ile Thr Val Ser Asp Asp Gly Glu Asn Thr Ile Ile Val
 105 110 115

 atc cct ggc gct aac gct tct gtc acc gcg gaa ttt gtt gat aaa cac 499
 Ile Pro Gly Ala Asn Ala Ser Val Thr Ala Glu Phe Val Asp Lys His
 120 125 130

 tcc caa ctc att gag aac gcc ggc att gtg ttg ctt cag ggt gag atc 547
 Ser Gln Leu Ile Glu Asn Ala Gly Ile Val Leu Leu Gln Gly Glu Ile
 135 140 145

cct gcc gat ggt ttc gag cgt gcc gtt gat ctt tca caa gga cgt gtg 595
 Pro Ala Asp Gly Phe Glu Arg Ala Val Asp Leu Ser Gln Gly Arg Val
 150 155 160 165
 gtg atc aat ctg gct cca gtt gtg ccc gtg gga cat gat cag ctg cgt 643
 Val Ile Asn Leu Ala Pro Val Val Pro Val Gly His Asp Gln Leu Arg
 170 175 180
 cgt gcc gat cca ttg ctg gtc aac gaa cac gaa ggc gct ctg gtg ctg 691
 Arg Ala Asp Pro Leu Leu Val Asn Glu His Glu Gly Ala Leu Val Leu
 185 190 195
 gac atg ctt gga act cca gcg acc. acg tct gat ccc caa agt ttg gtc 739
 Asp Met Leu Gly Thr Pro Ala Thr Ser Asp Pro Gln Ser Leu Val
 200 205 210
 act gaa ttg ctg gag cag ggt ttt act tcc gtg gtg atg aca ctt ggt 787
 Thr Glu Leu Leu Glu Gln Gly Phe Thr Ser Val Val Met Thr Leu Gly
 215 220 225
 gcc gaa ggt gct ctg gtt ggc acg ccg ggc caa ctc acg gca att cct 835
 Ala Glu Gly Ala Leu Val Gly Thr Pro Gly Gln Leu Thr Ala Ile Pro
 230 235 240 245
 acc cca aag 844
 Thr Pro Lys

<210> 390

<211> 248

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 390

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 Gly Ser Ile Asn Ala Asp Leu Thr Ala Lys Val Gln Arg His Pro Glu
 20 25 30
 Pro Gly Glu Thr Leu Leu Gly Ser Gly Gly Thr Val Ser Ala Gly Gly
 35 40 45
 Lys Gly Ala Asn Gln Ala Val Ala Ala Ala Gln Leu Gly Ala Lys Val
 50 55 60
 Thr Met Ile Gly Ala Val Gly Thr Asp Gln Met Ala Gly Glu Ala Leu
 65 70 75 80
 Thr His Leu Arg Gln Ser Gly Ala Asp Met Ser Ala Ile Ala Thr Val
 85 90 95
 Asp Gly Pro Thr Gly Leu Ala Ile Ile Thr Val Ser Asp Asp Gly Glu
 100 105 110
 Asn Thr Ile Ile Val Ile Pro Gly Ala Asn Ala Ser Val Thr Ala Glu
 115 120 125
 Phe Val Asp Lys His Ser Gln Leu Ile Glu Asn Ala Gly Ile Val Leu

130	135	140
Leu Gln Gly Glu Ile Pro Ala Asp Gly Phe Glu Arg Ala Val Asp Leu		
145	150	155
Ser Gln Gly Arg Val Val Ile Asn Leu Ala Pro Val Val Pro Val Gly		
	165	170
His Asp Gln Leu Arg Arg Ala Asp Pro Leu Leu Val Asn Glu His Glu		
	180	185
Gly Ala Leu Val Leu Asp Met Leu Gly Thr Pro Ala Thr Thr Ser Asp		
	195	200
Pro Gln Ser Leu Val Thr Glu Leu Leu Glu Gln Gly Phe Thr Ser Val		
	210	215
Val Met Thr Leu Gly Ala Glu Gly Ala Leu Val Gly Thr Pro Gly Gln		
225	230	235
Leu Thr Ala Ile Pro Thr Pro Lys		
	245	

<210> 391
 <211> 1026
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1003)
 <223> RXA02797

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 ccttatgaaa acgtttgcat aactccgcta aggatgttcc atg aat aat cga att 115
 Met Asn Asn Arg Ile
 1 5
 gtc gta gtc ggc tcc atc aac gct gat ctt aat gtt ctc gtt gac cgc 163
 Val Val Val Gly Ser Ile Asn Ala Asp Leu Asn Val Leu Val Asp Arg
 10 15 20
 cac cca gca cct ggc gaa aca ctg ttg ggc agt ggt gga cac atc act 211
 His Pro Ala Pro Gly Glu Thr Leu Leu Gly Ser Gly Gly His Ile Thr
 25 30 35
 gca gga ggc aaa ggc gcc aac cag gca gta gct gcc gct ctt caa ggt 259
 Ala Gly Gly Lys Gly Ala Asn Gln Ala Val Ala Ala Leu Gln Gly
 40 45 50
 gca gac gtc gcc ttt gtc ggc gct gtg ggc aag gat cct tac gct gcc 307
 Ala Asp Val Ala Phe Val Gly Ala Val Gly Lys Asp Pro Tyr Ala Ala
 55 60 65
 cca gcc tta gaa ttc ctt cgt tcg tca ggc gtc gac ctt acg gca gta 355
 Pro Ala Leu Glu Phe Leu Arg Ser Ser Gly Val Asp Leu Thr Ala Val
 70 75 80 85

tcc gaa gta gat gac acc acc ggg ctt gca gtt atc acc gtt gcc aaa	403
Ser Glu Val Asp Asp Thr Thr Gly Leu Ala Val Ile Thr Val Ala Lys	
90 95 100	
gac ggc gag aac aat atc gtt gtc atc ccc ggc gcg aat tcc ctg gtc	451
Asp Gly Glu Asn Asn Ile Val Val Ile Pro Gly Ala Asn Ser Leu Val	
105 110 115	
aat tgt gat tat gta agc agc caa tcc gct ctt tta gct gaa gct gga	499
Asn Cys Asp Tyr Val Ser Ser Gln Ser Ala Leu Leu Ala Glu Ala Gly	
120 125 130	
atc ctg ttg ctg caa ggt gag atc cct gcg gat ggc ttc aaa gag gcc	547
Ile Leu Leu Leu Gln Gly Glu Ile Pro Ala Asp Gly Phe Lys Glu Ala	
135 140 145	
att cac cac acc atg ggt cgc gtc gtg gtg aat cta gcg ccc gtc atc	595
Ile His His Thr Met Gly Arg Val Val Val Asn Leu Ala Pro Val Ile	
150 155 160 165	
gag gta gag aag tcc gcg tta ctt gag gct gat ccg atc atc gcc aat	643
Glu Val Glu Lys Ser Ala Leu Leu Glu Ala Asp Pro Ile Ile Ala Asn	
170 175 180	
gag cac gag gcc ggc ctg att ctg gat caa ttc ggg gca ggc atc gat	691
Glu His Glu Ala Gly Leu Ile Leu Asp Gln Phe Gly Ala Gly Ile Asp	
185 190 195	
tcc atg gat ccc cac gag ctc gcg caa gct ctc ctc gac gcc ggt ttc	739
Ser Met Asp Pro His Glu Leu Ala Gln Ala Leu Leu Asp Ala Gly Phe	
200 205 210	
gcc tct gtt gtt tta acg ctt gga tcc gca ggc gcg ttg gtc gcc gat	787
Ala Ser Val Val Leu Thr Leu Gly Ser Ala Gly Ala Leu Val Ala Asp	
215 220 225	
gcc acc ggt atc acg gac atc gcc aca cca acg gtg cag gca gtt gac	835
Ala Thr Gly Ile Thr Asp Ile Ala Thr Pro Thr Val Gln Ala Val Asp	
230 235 240 245	
acc acg gga gcc ggt gac gct ttt gcc gga gcc ttc tgc gca cga cta	883
Thr Thr Gly Ala Gly Asp Ala Phe Ala Gly Ala Phe Cys Ala Arg Leu	
250 255 260	
att aaa ggc gat tcg ctt atc gac gcc gcc acc cac gca gca cgc gtc	931
Ile Lys Gly Asp Ser Leu Ile Asp Ala Ala Thr His Ala Ala Arg Val	
265 270 275	
ggc gct tac tcg gtg caa acc gcc gga gcg caa gcg tcc tat ccg gac	979
Gly Ala Tyr Ser Val Gln Thr Ala Gly Ala Gln Ala Ser Tyr Pro Asp	
280 285 290	
gcg agc gtt tca ctt ccc tct gtt taaaaaaaaact atttaagaag agg	1026
Ala Ser Val Ser Leu Pro Ser Val	
295 300	

<210> 392

<211> 301

<212> PRT

<213> Corynebacterium glutamicum

<400> 392

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 Val Leu Val Asp Arg His Pro Ala Pro Gly Glu Thr Leu Leu Gly Ser
 20 25 30
 Gly Gly His Ile Thr Ala Gly Gly Lys Gly Ala Asn Gln Ala Val Ala
 35 40 45
 Ala Ala Leu Gln Gly Ala Asp Val Ala Phe Val Gly Ala Val Gly Lys
 50 55 60
 Asp Pro Tyr Ala Ala Pro Ala Leu Glu Phe Leu Arg Ser Ser Gly Val
 65 70 75 80
 Asp Leu Thr Ala Val Ser Glu Val Asp Asp Thr Thr Gly Leu Ala Val
 85 90 95
 Ile Thr Val Ala Lys Asp Gly Glu Asn Asn Ile Val Val Ile Pro Gly
 100 105 110
 Ala Asn Ser Leu Val Asn Cys Asp Tyr Val Ser Ser Gln Ser Ala Leu
 115 120 125
 Leu Ala Glu Ala Gly Ile Leu Leu Leu Gln Gly Glu Ile Pro Ala Asp
 130 135 140
 Gly Phe Lys Glu Ala Ile His His Thr Met Gly Arg Val Val Val Asn
 145 150 155 160
 Leu Ala Pro Val Ile Glu Val Glu Lys Ser Ala Leu Leu Glu Ala Asp
 165 170 175
 Pro Ile Ile Ala Asn Glu His Glu Ala Gly Leu Ile Leu Asp Gln Phe
 180 185 190
 Gly Ala Gly Ile Asp Ser Met Asp Pro His Glu Leu Ala Gln Ala Leu
 195 200 205
 Leu Asp Ala Gly Phe Ala Ser Val Val Leu Thr Leu Gly Ser Ala Gly
 210 215 220
 Ala Leu Val Ala Asp Ala Thr Gly Ile Thr Asp Ile Ala Thr Pro Thr
 225 230 235 240
 Val Gln Ala Val Asp Thr Thr Gly Ala Gly Asp Ala Phe Ala Gly Ala
 245 250 255
 Phe Cys Ala Arg Leu Ile Lys Gly Asp Ser Leu Ile Asp Ala Ala Thr
 260 265 270
 His Ala Ala Arg Val Gly Ala Tyr Ser Val Gln Thr Ala Gly Ala Gln
 275 280 285
 Ala Ser Tyr Pro Asp Ala Ser Val Ser Leu Pro Ser Val
 290 295 300

<210> 393

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<211> 1161
<212> DNA
<213> Corynebacterium glutamicum
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<220>
<221> CDS
<222> (101)..(1138)
<223> RXA02730
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<400> 393

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Met Ala Thr Glu Lys															15
ttc cga ccg act ctt aaa gat gtc gct cgt caa gca ggt gtc tcc atc															163
Phe Arg Pro Thr Leu Lys Asp Val Ala Arg Gln Ala Gly Val Ser Ile															20
gcc aca gca tca cga gca cta gcg gat aat ccg gcg gtt gct gca tcg															211
Ala Thr Ala Ser Arg Ala Leu Ala Asp Asn Pro Ala Val Ala Ala Ser															25
act cgt gaa aga atc caa caa tta gcc tct gat ctg ggt tac cgg gcc															259
Thr Arg Glu Arg Ile Gln Gln Leu Ala Ser Asp Leu Gly Tyr Arg Ala															40
aat gct caa gct cgt gcg ctt cgc agt tct cgc agc aac acc att ggt															307
Asn Ala Gln Ala Arg Ala Leu Arg Ser Ser Arg Ser Asn Thr Ile Gly															55
gtg att gtt ccc agt ttg att aac cat tac ttc gcc gca atg gtt act															355
Val Ile Val Pro Ser Leu Ile Asn His Tyr Phe Ala Ala Met Val Thr															70
gaa att caa agc acc gcc agc aaa gct gga ctt gcc acg att atc acc															403
Glu Ile Gln Ser Thr Ala Ser Lys Ala Gly Leu Ala Thr Ile Ile Thr															90
aac agc aat gaa gat gcg acc act atg tct ggg tct ttg gag ttt ctc															451
Asn Ser Asn Glu Asp Ala Thr Thr Met Ser Gly Ser Leu Glu Phe Leu															105
acc tcg cat ggt gtc gat gga atc atc tgc gta cct aat gag gaa tgc															499
Thr Ser His Gly Val Asp Gly Ile Ile Cys Val Pro Asn Glu Glu Cys															120
gcg aat caa cta gag gac ttg cag aag caa gga atg cca gtg gtg ttg															547
Ala Asn Gln Leu Glu Asp Leu Gln Lys Gln Gly Met Pro Val Val Leu															135
gtt gac cga gag ctt cca gga gac tcc acc atc cca acg gcg acc tct															595
Val Asp Arg Glu Leu Pro Gly Asp Ser Thr Ile Pro Thr Ala Thr Ser															150
aac ccc caa cca gga atc gcc gca gca gta gaa ctc ctg gct cac aac															643
Asn Pro Gln Pro Gly Ile Ala Ala Ala Val Glu Leu Leu Ala His Asn															170
aac qcq ttg ccq att qqt tac ctc tca qqt ccc atq gac acc tca aca															691

Asn	Ala	Leu	Pro	Ile	Gly	Tyr	Leu	Ser	Gly	Pro	Met	Asp	Thr	Ser	Thr		
			185					190					195				
ggt	aga	gag	cga	tta	gag	gat	ttc	aaa	gca	gcc	tgc	gcc	aac	tcc	aaa	739	
Gly	Arg	Glu	Arg	Leu	Glu	Asp	Phe	Lys	Ala	Ala	Cys	Ala	Asn	Ser	Lys		
		200					205					210					
att	ggc	gaa	cag	ctc	gtt	ttt	ctg	ggt	ggg	tac	gaa	caa	agc	gtt	gga	787	
Ile	Gly	Glu	Gln	Leu	Val	Phe	Leu	Gly	Gly	Tyr	Glu	Gln	Ser	Val	Gly		
	215					220					225						
ttt	gaa	ggc	gct	acg	aaa	ttg	ctc	gat	caa	gga	gct	aaa	act	ctt	ttt	835	
Phe	Glu	Gly	Ala	Thr	Lys	Leu	Leu	Asp	Gln	Gly	Ala	Lys	Thr	Leu	Phe		
230					235					240					245		
gcc	ggc	gat	tct	atg	atg	acg	atc	ggt	gtc	att	gaa	gcc	tgc	cat	aag	883	
Ala	Gly	Asp	Ser	Met	Met	Thr	Ile	Gly	Val	Ile	Glu	Ala	Cys	His	Lys		
				250					255					260			
gct	ggt	ttg	gtt	atc	ggc	aag	gat	gtc	agc	gtg	att	ggt	ttt	gat	aca	931	
Ala	Gly	Leu	Val	Ile	Gly	Lys	Asp	Val	Ser	Val	Ile	Gly	Phe	Asp	Thr		
		265					270						275				
cat	ccg	ctt	ttt	gcc	ctg	caa	cct	cat	ccg	ttg	aca	gtg	att	gat	caa	979	
His	Pro	Leu	Phe	Ala	Leu	Gln	Pro	His	Pro	Leu	Thr	Val	Ile	Asp	Gln		
		280					285					290					
aat	gta	gaa	caa	cta	gcc	caa	cga	gca	gtg	tct	atc	ctc	acc	gaa	tta	1027	
Asn	Val	Glu	Gln	Leu	Ala	Gln	Arg	Ala	Val	Ser	Ile	Leu	Thr	Glu	Leu		
	295					300					305						
att	gca	ggc	acg	gta	cct	agc	gtg	acg	aaa	act	acg	atc	ccc	act	gcc	1075	
Ile	Ala	Gly	Thr	Val	Pro	Ser	Val	Thr	Lys	Thr	Thr	Ile	Pro	Thr	Ala		
310					315					320					325		
ctt	att	cat	cgt	gaa	tca	atc	atc	aac	tcc	act	tta	agg	aag	aag	gat	1123	
Leu	Ile	His	Arg	Glu	Ser	Ile	Ile	Asn	Ser	Thr	Leu	Arg	Lys	Lys	Asp		
				330					335					340			
gga	ctc	ccc	aat	gag	taactcaacc	ggtaccgaca	ttg									1161	
Gly	Leu	Pro	Asn	Glu													
			345														

<210> 394

<211> 346

<212> PRT

<213> Corynebacterium glutamicum

<400> 394

Met	Ala	Thr	Glu	Lys	Phe	Arg	Pro	Thr	Leu	Lys	Asp	Val	Ala	Arg	Gln		
1				5					10					15			
Ala	Gly	Val	Ser	Ile	Ala	Thr	Ala	Ser	Arg	Ala	Leu	Ala	Asp	Asn	Pro		
		20						25					30				
Ala	Val	Ala	Ala	Ser	Thr	Arg	Glu	Arg	Ile	Gln	Gln	Leu	Ala	Ser	Asp		
		35					40					45					
Leu	Gly	Tyr	Arg	Ala	Asn	Ala	Gln	Ala	Arg	Ala	Leu	Arg	Ser	Ser	Arg		
	50					55					60						

Ser Asn Thr Ile Gly Val Ile Val Pro Ser Leu Ile Asn His Tyr Phe
 65 70 75 80
 Ala Ala Met Val Thr Glu Il Gln Ser Thr Ala Ser Lys Ala Gly Leu
 85 90 95
 Ala Thr Ile Ile Thr Asn Ser Asn Glu Asp Ala Thr Thr Met Ser Gly
 100 105 110
 Ser Leu Glu Phe Leu Thr Ser His Gly Val Asp Gly Ile Ile Cys Val
 115 120 125
 Pro Asn Glu Glu Cys Ala Asn Gln Leu Glu Asp Leu Gln Lys Gln Gly
 130 135 140
 Met Pro Val Val Leu Val Asp Arg Glu Leu Pro Gly Asp Ser Thr Ile
 145 150 155 160
 Pro Thr Ala Thr Ser Asn Pro Gln Pro Gly Ile Ala Ala Ala Val Glu
 165 170 175
 Leu Leu Ala His Asn Asn Ala Leu Pro Ile Gly Tyr Leu Ser Gly Pro
 180 185 190
 Met Asp Thr Ser Thr Gly Arg Glu Arg Leu Glu Asp Phe Lys Ala Ala
 195 200 205
 Cys Ala Asn Ser Lys Ile Gly Glu Gln Leu Val Phe Leu Gly Gly Tyr
 210 215 220
 Glu Gln Ser Val Gly Phe Glu Gly Ala Thr Lys Leu Leu Asp Gln Gly
 225 230 235 240
 Ala Lys Thr Leu Phe Ala Gly Asp Ser Met Met Thr Ile Gly Val Ile
 245 250 255
 Glu Ala Cys His Lys Ala Gly Leu Val Ile Gly Lys Asp Val Ser Val
 260 265 270
 Ile Gly Phe Asp Thr His Pro Leu Phe Ala Leu Gln Pro His Pro Leu
 275 280 285
 Thr Val Ile Asp Gln Asn Val Glu Gln Leu Ala Gln Arg Ala Val Ser
 290 295 300
 Ile Leu Thr Glu Leu Ile Ala Gly Thr Val Pro Ser Val Thr Lys Thr
 305 310 315 320
 Thr Ile Pro Thr Ala Leu Ile His Arg Glu Ser Ile Ile Asn Ser Thr
 325 330 335
 Leu Arg Lys Lys Asp Gly Leu Pro Asn Glu
 340 345

<210> 395

<211> 483

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(460)

<223> RXA02551

<400> 395

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ttaaaaaaac accgtcgatt tcatttcctt ctcctattac atg tcc gta tgt gaa 115
                                   Met Ser Val Cys Glu
                                   1 5

gcc cac aac ccc gaa aac tac tca acc ggt ggc ggt aac atc atc ggc 163
Ala His Asn Pro Glu Asn Tyr Ser Thr Gly Gly Gly Asn Ile Ile Gly
                                   10 15 20

gga gtg gtc agc ccc act ctc gcg gct tcc gaa tgg ggt tgg caa gtt 211
Gly Val Val Ser Pro Thr Leu Ala Ala Ser Glu Trp Gly Trp Gln Val
                                   25 30 35

gat ccc ctc ggt ttg cgc atc gtc ctg aac aac tac tgg gag cgc tgg 259
Asp Pro Leu Gly Leu Arg Ile Val Leu Asn Asn Tyr Trp Glu Arg Trp
                                   40 45 50

cag aag cca ctg ttc atc gtc gaa aac gga cta gga gca aag gac gtg 307
Gln Lys Pro Leu Phe Ile Val Glu Asn Gly Leu Gly Ala Lys Asp Val
                                   55 60 65

ctt atc gac gga ccc tcc ggc cca aca gta aac gat gac tac cgc atc 355
Leu Ile Asp Gly Pro Ser Gly Pro Thr Val Asn Asp Asp Tyr Arg Ile
                                   70 75 80 85

aaa tac ctc gac gac ggc ggc tca gga atc ttg aag cgc tac aag aag 403
Lys Tyr Leu Asp Asp Gly Gly Ser Gly Ile Leu Lys Arg Tyr Lys Lys
                                   90 95 100

aag tcc ttt gat tgg tgc cgc gac atc atc gcc acc aat ggc gaa agc 451
Lys Ser Phe Asp Trp Cys Arg Asp Ile Ile Ala Thr Asn Gly Glu Ser
                                   105 110 115

ctg gaa tcc taagaaataa aggtagggtgt cac 483
Leu Glu Ser
                                   120

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<210> 396

<211> 120

<212> PRT

<213> Corynebacterium glutamicum

<400> 396

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Met Ser Val Cys Glu Ala His Asn Pro Glu Asn Tyr Ser Thr Gly Gly
 1 5 10 15

Gly Asn Ile Ile Gly Gly Val Val Ser Pro Thr Leu Ala Ala Ser Glu
 20 25 30

Trp Gly Trp Gln Val Asp Pro Leu Gly Leu Arg Ile Val Leu Asn Asn
 35 40 45

Tyr Trp Glu Arg Trp Gln Lys Pro Leu Phe Ile Val Glu Asn Gly Leu

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50					55					60					
Gly	Ala	Lys	Asp	Val	Leu	Ile	Asp	Gly	Pro	Ser	Gly	Pro	Thr	Val	Asn
65					70					75					80
Asp	Asp	Tyr	Arg	Ile	Lys	Tyr	Leu	Asp	Asp	Gly	Gly	Ser	Gly	Ile	Leu
				85					90					95	
Lys	Arg	Tyr	Lys	Lys	Lys	Ser	Phe	Asp	Trp	Cys	Arg	Asp	Ile	Ile	Ala
			100					105					110		
Thr	Asn	Gly	Glu	Ser	Leu	Glu	Ser								
		115					120								

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<210> 397
<211> 795
<212> DNA
<213> Corynebacterium glutamicum
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<221> CDS
<222> (101)..(772)
<223> RXA01325
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cctggaaatt ttccacact aagtcagggtc taagtaggggt atg gat atg acg att 115
Met Asp Met Thr Ile
1 5

tcc cgc tcc acc atg gcc caa atc ctt gac tac acc ctc ctc gga cca 163
Ser Arg Ser Thr Met Ala Gln Ile Leu Asp Tyr Thr Leu Leu Gly Pro
10 15 20

gaa gta acc aac tcc gaa ctg gcc gca ttt ata gat tcc gca att gag 211
Glu Val Thr Asn Ser Glu Leu Ala Ala Phe Ile Asp Ser Ala Ile Glu
25 30 35

ctg gga gtc ggc acg atc tgt gtc ccc aac agc atg gtc aac cta act 259
Leu Gly Val Gly Thr Ile Cys Val Pro Asn Ser Met Val Asn Leu Thr
40 45 50

gca aaa gcc caa gaa gct gga att cga gtg gcc acc gtc gca gga ttc 307
Ala Lys Ala Gln Glu Ala Gly Ile Arg Val Ala Thr Val Ala Gly Phe
55 60 65

ccg cac ggc aaa acc ccc gcg ttg gtg aaa gcc gcc gaa gcg cgc ctt 355
Pro His Gly Lys Thr Pro Ala Leu Val Lys Ala Ala Glu Ala Arg Leu
70 75 80 85

gcc gta cag tcc gga gct tcc gaa gta gat gtt gtt ttg gat att gcg 403
Ala Val Gln Ser Gly Ala Ser Glu Val Asp Val Val Leu Asp Ile Ala
90 95 100

gta gtg aaa gag gga gat gcc aat agg ttg ctg cag gaa att gtg gca 451
Val Val Lys Glu Gly Asp Ala Asn Arg Leu Leu Gln Glu Ile Val Ala
105 110 115

atc agg gag gct gtt cca tct cct gtg gtg ctg aaa ttc atc ctc qaa 499

Ile Arg Glu Ala Val Pro Ser Pro Val Val Leu Lys Phe Ile Leu Glu
 120 125 130

aca gct gtt gtg agt gat gaa gca att gtg act gca gtg aat gcg ttg 547
 Thr Ala Val Val Ser Asp Glu Ala Ile Val Thr Ala Val Asn Ala Leu
 135 140 145

att gct gct ggt gct gac ttc gct aaa act tcc acg gga ttc cac cca 595
 Ile Ala Ala Gly Ala Asp Phe Ala Lys Thr Ser Thr Gly Phe His Pro
 150 155 160 165

gcg gga ggg gca act gtt gag gct gtt cgg gtg atg gct tcg gct tct 643
 Ala Gly Gly Ala Thr Val Glu Ala Val Arg Val Met Ala Ser Ala Ser
 170 175 180

cgg gga agg gtt gga att aag gct gcc ggt ggg gtg aaa act tgg gaa 691
 Arg Gly Arg Val Gly Ile Lys Ala Ala Gly Gly Val Lys Thr Trp Glu
 185 190 195

gat gcg gtg gcg ttt gtt gaa gca ggg gct act cgc att gga act tct 739
 Asp Ala Val Ala Phe Val Glu Ala Gly Ala Thr Arg Ile Gly Thr Ser
 200 205 210

aat gcg gga gcc att ttg gag ggt gcg ccg gag tagtttggcg ttctaatacgg 792
 Asn Ala Gly Ala Ile Leu Glu Gly Ala Pro Glu
 215 220

gac 795

<210> 398

<211> 224

<212> PRT

<213> Corynebacterium glutamicum

<400> 398

Met Asp Met Thr Ile Ser Arg Ser Thr Met Ala Gln Ile Leu Asp Tyr
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Thr Leu Leu Gly Pro Glu Val Thr Asn Ser Glu Leu Ala Ala Phe Ile
 20 25 30

Asp Ser Ala Ile Glu Leu Gly Val Gly Thr Ile Cys Val Pro Asn Ser
 35 40 45

Met Val Asn Leu Thr Ala Lys Ala Gln Glu Ala Gly Ile Arg Val Ala
 50 55 60

Thr Val Ala Gly Phe Pro His Gly Lys Thr Pro Ala Leu Val Lys Ala
 65 70 75 80

Ala Glu Ala Arg Leu Ala Val Gln Ser Gly Ala Ser Glu Val Asp Val
 85 90 95

Val Leu Asp Ile Ala Val Val Lys Glu Gly Asp Ala Asn Arg Leu Leu
 100 105 110

Gln Glu Ile Val Ala Ile Arg Glu Ala Val Pro Ser Pro Val Val Leu
 115 120 125

Lys Phe Ile Leu Glu Thr Ala Val Val Ser Asp Glu Ala Ile Val Thr

130	135	140
Ala Val Asn Ala Leu Ile Ala Ala Gly Ala Asp Phe Ala Lys Thr Ser		
145	150	155
Thr Gly Phe His Pro Ala Gly Gly Ala Thr Val Glu Ala Val Arg Val		
	165	170
Met Ala Ser Ala Ser Arg Gly Arg Val Gly Ile Lys Ala Ala Gly Gly		
	180	185
Val Lys Thr Trp Glu Asp Ala Val Ala Phe Val Glu Ala Gly Ala Thr		
	195	200
Arg Ile Gly Thr Ser Asn Ala Gly Ala Ile Leu Glu Gly Ala Pro Glu		
	210	215
		220

<210> 399
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 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(661)
 <223> RXA00195

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 tagtgggtgc gtttacccaa caagtgaag aatgggagtc gtg act aaa aag atc 115
 Val Thr Lys Lys Ile
 1 5
 ctt att ttg gga agc act ggt tcg att gga act cag gcg ctg gac gtt 163
 Leu Ile Leu Gly Ser Thr Gly Ser Ile Gly Thr Gln Ala Leu Asp Val
 10 15 20
 att gct gat aat tca gac aag ttt gag gtg gtg ggt atc gct gcg ggc 211
 Ile Ala Asp Asn Ser Asp Lys Phe Glu Val Val Gly Ile Ala Ala Gly
 25 30 35
 ggt tct cag cca gac ctc gtt att tcg cag gcg cag cag ttg ggg ctg 259
 Gly Ser Gln Pro Asp Leu Val Ile Ser Gln Ala Gln Gln Leu Gly Leu
 40 45 50
 gct gca gac aag gtt gcg gtt gct gat gca cag gct gcc gca gta att 307
 Ala Ala Asp Lys Val Ala Val Ala Asp Ala Gln Ala Ala Ala Val Ile
 55 60 65
 tcg aag gct ctc ggc ggc gag atc atc tct gga acc gat gct gcg aag 355
 Ser Lys Ala Leu Gly Gly Glu Ile Ile Ser Gly Thr Asp Ala Ala Lys
 70 75 80 85
 att ctg gtg gaa acc aca aag gcc gac act gtg ctt aat gct ctg gtt 403
 Ile Leu Val Glu Thr Thr Lys Ala Asp Thr Val Leu Asn Ala Leu Val
 90 95 100

ggt tct ttg ggg ctt gcg gca acg ctg gcc act ctg gaa tct ggt gcg 451
 Gly Ser Leu Gly Leu Ala Ala Thr Leu Ala Thr Leu Glu Ser Gly Ala
 105 110 115
 cat ctt gcc ttg gct aac aaa gaa tcg ctg gtt gcc ggt ggt gag ttt 499
 His Leu Ala Leu Ala Asn Lys Glu Ser Leu Val Ala Gly Gly Glu Phe
 120 125 130
 gtt acc tca aag gca aag ctg ggg cag atc att ccg gtc gat tcg gag 547
 Val Thr Ser Lys Ala Lys Leu Gly Gln Ile Ile Pro Val Asp Ser Glu
 135 140 145
 cac tct gcc atg gcg cag tgt ttg cgt tcg ggt act cgt gat gag gtt 595
 His Ser Ala Met Ala Gln Cys Leu Arg Ser Gly Thr Arg Asp Glu Val
 150 155 160 165
 gcg cgg att gtg ctg aca gct tcg ggc gga cct ttc agg gct gga cca 643
 Ala Arg Ile Val Leu Thr Ala Ser Gly Gly Pro Phe Arg Ala Gly Pro
 170 175 180
 ggg aga aga tgt ggg agg tgactcccgca gcaggcagca gcg 684
 Gly Arg Arg Cys Gly Arg
 185

<210> 400

<211> 187

<212> PRT

<213> Corynebacterium glutamicum

<400> 400

Val Thr Lys Lys Ile Leu Ile Leu Gly Ser Thr Gly Ser Ile Gly Thr
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 Gln Ala Leu Asp Val Ile Ala Asp Asn Ser Asp Lys Phe Glu Val Val
 20 25 30
 Gly Ile Ala Ala Gly Gly Ser Gln Pro Asp Leu Val Ile Ser Gln Ala
 35 40 45
 Gln Gln Leu Gly Leu Ala Ala Asp Lys Val Ala Val Ala Asp Ala Gln
 50 55 60
 Ala Ala Ala Val Ile Ser Lys Ala Leu Gly Gly Glu Ile Ile Ser Gly
 65 70 75 80
 Thr Asp Ala Ala Lys Ile Leu Val Glu Thr Thr Lys Ala Asp Thr Val
 85 90 95
 Leu Asn Ala Leu Val Gly Ser Leu Gly Leu Ala Ala Thr Leu Ala Thr
 100 105 110
 Leu Glu Ser Gly Ala His Leu Ala Leu Ala Asn Lys Glu Ser Leu Val
 115 120 125
 Ala Gly Gly Glu Phe Val Thr Ser Lys Ala Lys Leu Gly Gln Ile Ile
 130 135 140
 Pro Val Asp Ser Glu His Ser Ala Met Ala Gln Cys Leu Arg Ser Gly
 145 150 155 160

Thr Arg Asp Glu Val Ala Arg Ile Val Leu Thr Ala Ser Gly Gly Pro
 165 170 175

Phe Arg Ala Gly Pro Gly Arg Arg Cys Gly Arg
 180 185

<210> 401

<211> 738

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(715)

<223> RXA00196

<400> 401

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 cagcttcggg cggacctttc agggctggac cagggagaag atg tgg gag gtg act 115
 Met Trp Glu Val Thr
 1 5
 ccc gag cag gca gca gcg cac cca acg tgg gcg atg ggg cag atg aac 163
 Pro Glu Gln Ala Ala Ala His Pro Thr Trp Ala Met Gly Gln Met Asn
 10 15 20
 acg ttg aac tcc gcc acc ctt att aat aaa ggc ctc gaa ctc atc gag 211
 Thr Leu Asn Ser Ala Thr Leu Ile Asn Lys Gly Leu Glu Leu Ile Glu
 25 30 35
 gcg acc ctg ctg ttt gaa acg gat gcg gat ctc att gat gtg acg gtg 259
 Ala Thr Leu Leu Phe Glu Thr Asp Ala Asp Leu Ile Asp Val Thr Val
 40 45 50
 cat ccg cag tcg atc atc cac tcc atg atc acg ttt acg gat ggt gcg 307
 His Pro Gln Ser Ile Ile His Ser Met Ile Thr Phe Thr Asp Gly Ala
 55 60 65
 acc atc gcg cag gcg tcg cca cca tcg atg aaa ctg ccg atc gcg ttg 355
 Thr Ile Ala Gln Ala Ser Pro Pro Ser Met Lys Leu Pro Ile Ala Leu
 70 75 80 85
 gcg ctt gat tgg cca cat cgg gtg ccg aag gct cag ccg gcg ctg gat 403
 Ala Leu Asp Trp Pro His Arg Val Pro Lys Ala Gln Pro Ala Leu Asp
 90 95 100
 ttc acc gct gct cat acc tgg gct ttt gag ccg gtg gat gat gcc gca 451
 Phe Thr Ala Ala His Thr Trp Ala Phe Glu Pro Val Asp Asp Ala Ala
 105 110 115
 ttc cct gcg gtg cag ctg gct agg cac gtc gca aag caa aaa ggc acg 499
 Phe Pro Ala Val Gln Leu Ala Arg His Val Ala Lys Gln Lys Gly Thr
 120 125 130
 tac ccc gcg gtg tat aac gcc gcc aac gag gag gcg gct gag gcg ttt 547
 Tyr Pro Ala Val Tyr Asn Ala Ala Asn Glu Glu Ala Ala Glu Ala Phe
 135 140 145

ttg cgc ggg cga atc aag ttt ccg cag atc gtg gac gtg gtg gac gag 595
 Leu Arg Gly Arg Ile Lys Phe Pro Gln Ile Val Asp Val Val Asp Glu
 150 155 160 165

 gtc ctc caa gga gct tct cag ttt gct ggt gta gca tca cac gtc gat 643
 Val Leu Gln Gly Ala Ser Gln Phe Ala Gly Val Ala Ser His Val Asp
 170 175 180

 gat att ttg gca acc gaa tct gag gca cgc gcg cgt gcg aat gct ttg 691
 Asp Ile Leu Ala Thr Glu Ser Glu Ala Arg Ala Arg Ala Asn Ala Leu
 185 190 195

 atc aac cgg ttg gca acc aac ttg taagctaagg agcttccgcc tcg 738
 Ile Asn Arg Leu Ala Thr Asn Leu
 200 205

<210> 402

<211> 205

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 402

Met Trp Glu Val Thr Pro Glu Gln Ala Ala Ala His Pro Thr Trp Ala
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 20 25 30

 Leu Glu Leu Ile Glu Ala Thr Leu Leu Phe Glu Thr Asp Ala Asp Leu
 35 40 45

 Ile Asp Val Thr Val His Pro Gln Ser Ile Ile His Ser Met Ile Thr
 50 55 60

 Phe Thr Asp Gly Ala Thr Ile Ala Gln Ala Ser Pro Pro Ser Met Lys
 65 70 75 80

 Leu Pro Ile Ala Leu Ala Leu Asp Trp Pro His Arg Val Pro Lys Ala
 85 90 95

 Gln Pro Ala Leu Asp Phe Thr Ala Ala His Thr Trp Ala Phe Glu Pro
 100 105 110

 Val Asp Asp Ala Ala Phe Pro Ala Val Gln Leu Ala Arg His Val Ala
 115 120 125

 Lys Gln Lys Gly Thr Tyr Pro Ala Val Tyr Asn Ala Ala Asn Glu Glu
 130 135 140

 Ala Ala Glu Ala Phe Leu Arg Gly Arg Ile Lys Phe Pro Gln Ile Val
 145 150 155 160

 Asp Val Val Asp Glu Val Leu Gln Gly Ala Ser Gln Phe Ala Gly Val
 165 170 175

 Ala Ser His Val Asp Asp Ile Leu Ala Thr Glu Ser Glu Ala Arg Ala
 180 185 190

 Arg Ala Asn Ala Leu Il Asn Arg Leu Ala Thr Asn Leu
 195 200 205


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<210> 403
<211> 2031
<212> DNA
<213> Corynebacterium glutamicum
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<221> CDS
<222> (101) .. (2008)
<223> RXN01562
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Met Gly Ile Leu Asn															5
1															
agt att tca aca cct gct gac tta aag gcc ctt aat gat gag gat ttg															163
Ser Ile Ser Thr Pro Ala Asp Leu Lys Ala Leu Asn Asp Glu Asp Leu															20
10 15															
gac gct ctt gcc aaa gaa atc cga act ttc ctg gtc gat aaa gtc gca															211
Asp Ala Leu Ala Lys Glu Ile Arg Thr Phe Leu Val Asp Lys Val Ala															35
25 30															
gca act ggt ggc cac tta ggt cca aat ttg ggc gta gtg gaa tta acc															259
Ala Thr Gly Gly His Leu Gly Pro Asn Leu Gly Val Val Glu Leu Thr															50
40 45															
atc ggt ctt cat cga gtt ttc gat tcg cct caa gac ccg atc atc ttt															307
Ile Gly Leu His Arg Val Phe Asp Ser Pro Gln Asp Pro Ile Ile Phe															65
55 60															
gat act tct cac cag tcc tat gtg cat aag atc ctg acg ggt cgc gct															355
Asp Thr Ser His Gln Ser Tyr Val His Lys Ile Leu Thr Gly Arg Ala															85
70 75 80															
aaa gat ttt gat tct ttg cgt caa aaa gat ggc ctt tct ggt tac acc															403
Lys Asp Phe Asp Ser Leu Arg Gln Lys Asp Gly Leu Ser Gly Tyr Thr															100
90															
tgc cgt gct gaa agt gag cac gat tgg act gag tct tcg cat gct tcg															451
Cys Arg Ala Glu Ser Glu His Asp Trp Thr Glu Ser Ser His Ala Ser															115
105 110															
gcg gcc ttg tct tat gcg gat ggt ttg tct aaa gcc aag cag ttg gat															499
Ala Ala Leu Ser Tyr Ala Asp Gly Leu Ser Lys Ala Lys Gln Leu Asp															130
120 125															
ggc gat acc acg cat agt gtg gtt gct gtc gtt ggt gat ggc gct cta															547
Gly Asp Thr Thr His Ser Val Val Ala Val Val Gly Asp Gly Ala Leu															145
135 140															
act ggc ggc atg tgt tgg gaa gca ctg aac aat att gct gct ggt aaa															595
Thr Gly Gly Met Cys Trp Glu Ala Leu Asn Asn Ile Ala Ala Gly Lys															165
150 155 160															
gac cgc aaa gtt gtt gtc gta gtc aat gac aat ggc cgg agt tat tct															643
Asp Arg Lys Val Val Val Val Val Asn Asp Asn Gly Arg Ser Tyr Ser															

170	175	180	
cca acc att ggc gga ttt gcg gaa aac ctt gcg ggc ctt cgc atg cag Pro Thr Ile Gly Gly Phe Ala Glu Asn Leu Ala Gly Leu Arg Met Gln 185 190 195			691
cct ttc tat gat cgc ttc atg gaa aag ggc aag acg tcc ctg aaa tcc Pro Phe Tyr Asp Arg Phe Met Glu Lys Gly Lys Thr Ser Leu Lys Ser 200 205 210			739
atg ggg tgg gta ggg gag cgt act ttt gaa gcg ctc cat gca ttt aaa Met Gly Trp Val Gly Glu Arg Thr Phe Glu Ala Leu His Ala Phe Lys 215 220 225			787
gaa ggt gtg aag agc acc gtc att ccc acc gaa atg ttc cct gaa ctg Glu Gly Val Lys Ser Thr Val Ile Pro Thr Glu Met Phe Pro Glu Leu 230 235 240 245			835
ggc atg aaa tac gtg ggt ccg gtt gat gga cat aac caa aaa gct gtc Gly Met Lys Tyr Val Gly Pro Val Asp Gly His Asn Gln Lys Ala Val 250 255 260			883
gac aat gcg ctg aaa tac gct cat gat tat gat ggc ccc atc atc gtg Asp Asn Ala Leu Lys Tyr Ala His Asp Tyr Asp Gly Pro Ile Ile Val 265 270 275			931
cac atg gtc acc gaa aag ggt cgt ggt tac gcg cct gct gag cag gat His Met Val Thr Glu Lys Gly Arg Gly Tyr Ala Pro Ala Glu Gln Asp 280 285 290			979
ttg gac gaa ttg atg cac tcc acg ggc gtc atc gat ccg ctc aca gga Leu Asp Glu Leu Met His Ser Thr Gly Val Ile Asp Pro Leu Thr Gly 295 300 305			1027
gct cct aaa tct gca tca aag ccc ggt tgg acc tct gtg ttc agc gat Ala Pro Lys Ser Ala Ser Lys Pro Gly Trp Thr Ser Val Phe Ser Asp 310 315 320 325			1075
gag ctg gtc aag att ggt gcg cag aat gaa aac gtt gtt gcc atc acc Glu Leu Val Lys Ile Gly Ala Gln Asn Glu Asn Val Val Ala Ile Thr 330 335 340			1123
gcc gcg atg gca ggt cct acc ggt ctg tcc aag ttc gaa gcc aat ttc Ala Ala Met Ala Gly Pro Thr Gly Leu Ser Lys Phe Glu Ala Asn Phe 345 350 355			1171
ccc aac cga ttc ttt gat gtc ggc att gct gag cag cac gcg gta act Pro Asn Arg Phe Phe Asp Val Gly Ile Ala Glu Gln His Ala Val Thr 360 365 370			1219
tct gcc gca ggc ctc gca ttg ggt gga aaa cac cct gtg gtg gct att Ser Ala Ala Gly Leu Ala Leu Gly Gly Lys His Pro Val Val Ala Ile 375 380 385			1267
tac tcc acg ttc ttg aac cgc gct ttt gat cag ctg ctc atg gat gtg Tyr Ser Thr Phe Leu Asn Arg Ala Phe Asp Gln Leu Leu Met Asp Val 390 395 400 405			1315
ggc atg ctc aac cag cct gtt act ttg gtg ctt gat cgc tca ggt gtc Gly Met Leu Asn Gln Pro Val Thr Leu Val Leu Asp Arg Ser Gly Val 410 415 420			1363

acg ggt tcg gat gga gcg agc cac aat ggc gtc tgg gat atg gcg ctg 1411
 Thr Gly Ser Asp Gly Ala Ser His Asn Gly Val Trp Asp Met Ala Leu
 425 430 435

acc tcg atc gtt cca ggc gtg cag gtg gcg gca cca cgt gat gag gat 1459
 Thr Ser Ile Val Pro Gly Val Gln Val Ala Ala Pro Arg Asp Glu Asp
 440 445 450

tcc ttg cgt gag ctg ctc aat gag gct att tcc atc gat gat ggc ccc 1507
 Ser Leu Arg Glu Leu Leu Asn Glu Ala Ile Ser Ile Asp Asp Gly Pro
 455 460 465

aca gtt gtg cgt ttc ccc aag ggc gac ttg cca act cca att gtt gct 1555
 Thr Val Val Arg Phe Pro Lys Gly Asp Leu Pro Thr Pro Ile Val Ala
 470 475 480 485

atc gac acc ttg gaa gac ggc gtg gat gtc ctc gca tat gaa gac gcc 1603
 Ile Asp Thr Leu Glu Asp Gly Val Asp Val Leu Ala Tyr Glu Asp Ala
 490 495 500

act gac gtt gaa tca acc gac gat gcg cca tca gtt ctc atc att gcg 1651
 Thr Asp Val Glu Ser Thr Asp Asp Ala Pro Ser Val Leu Ile Ile Ala
 505 510 515

gta ggc gag cgc gca act gtt gca ctt gac gtt gct tcc agg att aaa 1699
 Val Gly Glu Arg Ala Thr Val Ala Leu Asp Val Ala Ser Arg Ile Lys
 520 525 530

cag cac ggc gtg aac gtc acg gtt gtt gac ccc cgc tgg att gtc ccc 1747
 Gln His Gly Val Asn Val Thr Val Val Asp Pro Arg Trp Ile Val Pro
 535 540 545

atc ccg cag tcc ttg gtc gcg ctg tct gat gat cat gac ctc gtg atc 1795
 Ile Pro Gln Ser Leu Val Ala Leu Ser Asp Asp His Asp Leu Val Ile
 550 555 560 565

acc atc gaa gac ggc gtc atc cac ggc ggc gtg gga tcc ttg ctc tct 1843
 Thr Ile Glu Asp Gly Val Ile His Gly Gly Val Gly Ser Leu Leu Ser
 570 575 580

gat gcg ctt aac gcc tct gag gtg gat acc cct cgc cga caa atc gcc 1891
 Asp Ala Leu Asn Ala Ser Glu Val Asp Thr Pro Arg Arg Gln Ile Ala
 585 590 595

gtg ccc cag aag tac ctg gat cac gcg tcc cgc aat gaa gtg ctc gcc 1939
 Val Pro Gln Lys Tyr Leu Asp His Ala Ser Arg Asn Glu Val Leu Ala
 600 605 610

gat tat ggc ctc gac gcc gac ggc att gaa acc act gtt gtt gga tgg 1987
 Asp Tyr Gly Leu Asp Ala Asp Gly Ile Glu Thr Thr Val Val Gly Trp
 615 620 625

ctg gat tcc ctg ttc ggg gaa taaaaccctg cttatcgacg ccg 2031
 Leu Asp Ser Leu Phe Gly Glu
 630 635

<210> 404

<211> 636

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 404

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 Asn Asp Glu Asp Leu Asp Ala Leu Ala Lys Glu Ile Arg Thr Phe Leu
 20 25 30
 Val Asp Lys Val Ala Ala Thr Gly Gly His Leu Gly Pro Asn Leu Gly
 35 40 45
 Val Val Glu Leu Thr Ile Gly Leu His Arg Val Phe Asp Ser Pro Gln
 50 55 60
 Asp Pro Ile Ile Phe Asp Thr Ser His Gln Ser Tyr Val His Lys Ile
 65 70 75 80
 Leu Thr Gly Arg Ala Lys Asp Phe Asp Ser Leu Arg Gln Lys Asp Gly
 85 90 95
 Leu Ser Gly Tyr Thr Cys Arg Ala Glu Ser Glu His Asp Trp Thr Glu
 100 105 110
 Ser Ser His Ala Ser Ala Ala Leu Ser Tyr Ala Asp Gly Leu Ser Lys
 115 120 125
 Ala Lys Gln Leu Asp Gly Asp Thr Thr His Ser Val Val Ala Val Val
 130 135 140
 Gly Asp Gly Ala Leu Thr Gly Gly Met Cys Trp Glu Ala Leu Asn Asn
 145 150 155 160
 Ile Ala Ala Gly Lys Asp Arg Lys Val Val Val Val Val Asn Asp Asn
 165 170 175
 Gly Arg Ser Tyr Ser Pro Thr Ile Gly Gly Phe Ala Glu Asn Leu Ala
 180 185 190
 Gly Leu Arg Met Gln Pro Phe Tyr Asp Arg Phe Met Glu Lys Gly Lys
 195 200 205
 Thr Ser Leu Lys Ser Met Gly Trp Val Gly Glu Arg Thr Phe Glu Ala
 210 215 220
 Leu His Ala Phe Lys Glu Gly Val Lys Ser Thr Val Ile Pro Thr Glu
 225 230 235 240
 Met Phe Pro Glu Leu Gly Met Lys Tyr Val Gly Pro Val Asp Gly His
 245 250 255
 Asn Gln Lys Ala Val Asp Asn Ala Leu Lys Tyr Ala His Asp Tyr Asp
 260 265 270
 Gly Pro Ile Ile Val His Met Val Thr Glu Lys Gly Arg Gly Tyr Ala
 275 280 285
 Pro Ala Glu Gln Asp Leu Asp Glu Leu Met His Ser Thr Gly Val Ile
 290 295 300
 Asp Pro Leu Thr Gly Ala Pro Lys Ser Ala Ser Lys Pro Gly Trp Thr

305	310	315	320
Ser Val Phe Ser Asp Glu Leu Val Lys Ile Gly Ala Gln Asn Glu Asn	325	330	335
Val Val Ala Ile Thr Ala Ala Met Ala Gly Pro Thr Gly Leu Ser Lys	340	345	350
Phe Glu Ala Asn Phe Pro Asn Arg Phe Phe Asp Val Gly Ile Ala Glu	355	360	365
Gln His Ala Val Thr Ser Ala Ala Gly Leu Ala Leu Gly Gly Lys His	370	375	380
Pro Val Val Ala Ile Tyr Ser Thr Phe Leu Asn Arg Ala Phe Asp Gln	385	390	395
Leu Leu Met Asp Val Gly Met Leu Asn Gln Pro Val Thr Leu Val Leu	405	410	415
Asp Arg Ser Gly Val Thr Gly Ser Asp Gly Ala Ser His Asn Gly Val	420	425	430
Trp Asp Met Ala Leu Thr Ser Ile Val Pro Gly Val Gln Val Ala Ala	435	440	445
Pro Arg Asp Glu Asp Ser Leu Arg Glu Leu Leu Asn Glu Ala Ile Ser	450	455	460
Ile Asp Asp Gly Pro Thr Val Val Arg Phe Pro Lys Gly Asp Leu Pro	465	470	475
Thr Pro Ile Val Ala Ile Asp Thr Leu Glu Asp Gly Val Asp Val Leu	485	490	495
Ala Tyr Glu Asp Ala Thr Asp Val Glu Ser Thr Asp Asp Ala Pro Ser	500	505	510
Val Leu Ile Ile Ala Val Gly Glu Arg Ala Thr Val Ala Leu Asp Val	515	520	525
Ala Ser Arg Ile Lys Gln His Gly Val Asn Val Thr Val Val Asp Pro	530	535	540
Arg Trp Ile Val Pro Ile Pro Gln Ser Leu Val Ala Leu Ser Asp Asp	545	550	555
His Asp Leu Val Ile Thr Ile Glu Asp Gly Val Ile His Gly Gly Val	565	570	575
Gly Ser Leu Leu Ser Asp Ala Leu Asn Ala Ser Glu Val Asp Thr Pro	580	585	590
Arg Arg Gln Ile Ala Val Pro Gln Lys Tyr Leu Asp His Ala Ser Arg	595	600	605
Asn Glu Val Leu Ala Asp Tyr Gly Leu Asp Ala Asp Gly Ile Glu Thr	610	615	620
Thr Val Val Gly Trp Leu Asp Ser Leu Phe Gly Glu	625	630	635

<210> 405
 <211> 1061
 <212> DNA
 <213> *Corynebacterium glutamicum*

<220>
 <221> CDS
 <222> (1)..(1038)
 <223> FRXA01562

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 Glu Gln Asp Leu Asp Glu Leu Met His Ser Thr Gly Val Ile Asp Pro
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 ctc aca gga gct cct aaa tct gca tca aag ccc ggt tgg acc tct gtg 96
 Leu Thr Gly Ala Pro Lys Ser Ala Ser Lys Pro Gly Trp Thr Ser Val
 20 25 30
 ttc agc gat gag ctg gtc aag att ggt gcg cag aat gaa aac gtt gtt 144
 Phe Ser Asp Glu Leu Val Lys Ile Gly Ala Gln Asn Glu Asn Val Val
 35 40 45
 gcc atc acc gcc gcg atg gca ggt cct acc ggt ctg tcc aag ttc gaa 192
 Ala Ile Thr Ala Ala Met Ala Gly Pro Thr Gly Leu Ser Lys Phe Glu
 50 55 60
 gcc aat ttc ccc aac cga ttc ttt gat gtc ggc att gct gag cag cac 240
 Ala Asn Phe Pro Asn Arg Phe Phe Asp Val Gly Ile Ala Glu Gln His
 65 70 75 80
 gcg gta act tct gcc gca ggc ctc gca ttg ggt gga aaa cac cct gtg 288
 Ala Val Thr Ser Ala Ala Gly Leu Ala Leu Gly Gly Lys His Pro Val
 85 90 95
 gtg gct att tac tcc acg ttc ttg aac cgc gct ttt gat cag ctg ctc 336
 Val Ala Ile Tyr Ser Thr Phe Leu Asn Arg Ala Phe Asp Gln Leu Leu
 100 105 110
 atg gat gtg ggc atg ctc aac cag cct gtt act ttg gtg ctt gat cgc 384
 Met Asp Val Gly Met Leu Asn Gln Pro Val Thr Leu Val Leu Asp Arg
 115 120 125
 tca ggt gtc acg ggt tcg gat gga gcg agc cac aat ggc gtc tgg gat 432
 Ser Gly Val Thr Gly Ser Asp Gly Ala Ser His Asn Gly Val Trp Asp
 130 135 140
 atg gcg ctg acc tcg atc gtt cca ggc gtg cag gtg gcg gca cca cgt 480
 Met Ala Leu Thr Ser Ile Val Pro Gly Val Gln Val Ala Ala Pro Arg
 145 150 155 160
 gat gag gat tcc ttg cgt gag ctg ctc aat gag gct att tcc atc gat 528
 Asp Glu Asp Ser Leu Arg Glu Leu Leu Asn Glu Ala Ile Ser Ile Asp
 165 170 175
 gat ggc ccc aca gtt gtg cgt ttc ccc aag ggc gac ttg cca act cca 576
 Asp Gly Pro Thr Val Val Arg Phe Pro Lys Gly Asp Leu Pro Thr Pro
 180 185 190

att gtt gct atc gac acc ttg gaa gac ggc gtg gat gtc ctc gca tat 624
 Ile Val Ala Ile Asp Thr Leu Glu Asp Gly Val Asp Val Leu Ala Tyr
 195 200 205

gaa gac gcc act gac gtt gaa tca acc gac gat gcg cca tca gtt ctc 672
 Glu Asp Ala Thr Asp Val Glu Ser Thr Asp Asp Ala Pro Ser Val Leu
 210 215 220

atc att gcg gta ggc gag cgc gca act gtt gca ctt gac gtt gct tcc 720
 Ile Ile Ala Val Gly Glu Arg Ala Thr Val Ala Leu Asp Val Ala Ser
 225 230 235 240

agg att aaa cag cac ggc gtg aac gtc acg gtt gtt gac ccc cgc tgg 768
 Arg Ile Lys Gln His Gly Val Asn Val Thr Val Val Asp Pro Arg Trp
 245 250 255

att gtc ccc atc ccg cag tcc ttg gtc gcg ctg tct gat gat cat gac 816
 Ile Val Pro Ile Pro Gln Ser Leu Val Ala Leu Ser Asp Asp His Asp
 260 265 270

ctc gtg atc acc atc gaa gac ggc gtc atc cac ggc ggc gtg gga tcc 864
 Leu Val Ile Thr Ile Glu Asp Gly Val Ile His Gly Gly Val Gly Ser
 275 280 285

ttg ctc tct gat gcg ctt aac gcc tct gag gtg gat acc cct cgc cga 912
 Leu Leu Ser Asp Ala Leu Asn Ala Ser Glu Val Asp Thr Pro Arg Arg
 290 295 300

caa atc gcc gtg ccc cag aag tac ctg gat cac gcg tcc cgc aat gaa 960
 Gln Ile Ala Val Pro Gln Lys Tyr Leu Asp His Ala Ser Arg Asn Glu
 305 310 315 320

gtg ctc gcc gat tat ggc ctc gac gcc gac ggc att gaa acc act gtt 1008
 Val Leu Ala Asp Tyr Gly Leu Asp Ala Asp Gly Ile Glu Thr Thr Val
 325 330 335

gtt gga tgg ctg gat tcc ctg ttc ggg gaa taaaaccctg cttatcgacg 1058
 Val Gly Trp Leu Asp Ser Leu Phe Gly Glu
 340 345

ccg 1061

<210> 406

<211> 346

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 406

Glu Gln Asp Leu Asp Glu Leu Met His Ser Thr Gly Val Ile Asp Pro
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Leu Thr Gly Ala Pro Lys Ser Ala Ser Lys Pro Gly Trp Thr Ser Val
 20 25 30

Phe Ser Asp Glu Leu Val Lys Ile Gly Ala Gln Asn Glu Asn Val Val
 35 40 45

Ala Ile Thr Ala Ala Met Ala Gly Pro Thr Gly Leu Ser Lys Phe Glu
 50 55 60

Ala Asn Phe Pro Asn Arg Phe Phe Asp Val Gly Ile Ala Glu Gln His
 65 70 75 80
 Ala Val Thr Ser Ala Ala Gly Leu Ala Leu Gly Gly Lys His Pro Val
 85 90 95
 Val Ala Ile Tyr Ser Thr Phe Leu Asn Arg Ala Phe Asp Gln Leu Leu
 100 105 110
 Met Asp Val Gly Met Leu Asn Gln Pro Val Thr Leu Val Leu Asp Arg
 115 120 125
 Ser Gly Val Thr Gly Ser Asp Gly Ala Ser His Asn Gly Val Trp Asp
 130 135 140
 Met Ala Leu Thr Ser Ile Val Pro Gly Val Gln Val Ala Ala Pro Arg
 145 150 155 160
 Asp Glu Asp Ser Leu Arg Glu Leu Leu Asn Glu Ala Ile Ser Ile Asp
 165 170 175
 Asp Gly Pro Thr Val Val Arg Phe Pro Lys Gly Asp Leu Pro Thr Pro
 180 185 190
 Ile Val Ala Ile Asp Thr Leu Glu Asp Gly Val Asp Val Leu Ala Tyr
 195 200 205
 Glu Asp Ala Thr Asp Val Glu Ser Thr Asp Asp Ala Pro Ser Val Leu
 210 215 220
 Ile Ile Ala Val Gly Glu Arg Ala Thr Val Ala Leu Asp Val Ala Ser
 225 230 235 240
 Arg Ile Lys Gln His Gly Val Asn Val Thr Val Val Asp Pro Arg Trp
 245 250 255
 Ile Val Pro Ile Pro Gln Ser Leu Val Ala Leu Ser Asp Asp His Asp
 260 265 270
 Leu Val Ile Thr Ile Glu Asp Gly Val Ile His Gly Gly Val Gly Ser
 275 280 285
 Leu Leu Ser Asp Ala Leu Asn Ala Ser Glu Val Asp Thr Pro Arg Arg
 290 295 300
 Gln Ile Ala Val Pro Gln Lys Tyr Leu Asp His Ala Ser Arg Asn Glu
 305 310 315 320
 Val Leu Ala Asp Tyr Gly Leu Asp Ala Asp Gly Ile Glu Thr Thr Val
 325 330 335
 Val Gly Trp Leu Asp Ser Leu Phe Gly Glu
 340 345

<210> 407

<211> 703

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(703)

<223> FRXA01705

<400> 407

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ccgtccgcat ccgagaagca aaggtgtctg actcgcgcca atg gga att ctg aac 115
                                         Met Gly Ile Leu Asn
                                         1                               5

agt att tca aca cct gct gac tta aag gcc ctt aat gat gag gat ttg 163
Ser Ile Ser Thr Pro Ala Asp Leu Lys Ala Leu Asn Asp Glu Asp Leu
                        10                        15                        20

gac gct ctt gcc aaa gaa atc cga act ttc ctg gtc gat aaa gtc gca 211
Asp Ala Leu Ala Lys Glu Ile Arg Thr Phe Leu Val Asp Lys Val Ala
                        25                        30                        35

gca act ggt ggc cac tta ggt cca aat ttg ggc gta gtg gaa tta acc 259
Ala Thr Gly Gly His Leu Gly Pro Asn Leu Gly Val Val Glu Leu Thr
                        40                        45                        50

atc ggt ctt cat cga gtt ttc gat tct cct caa gac ccg atc atc ttt 307
Ile Gly Leu His Arg Val Phe Asp Ser Pro Gln Asp Pro Ile Ile Phe
                        55                        60                        65

gat act tct cac cag tcc tat gtg cat aag atc ctg acg ggt cgc gct 355
Asp Thr Ser His Gln Ser Tyr Val His Lys Ile Leu Thr Gly Arg Ala
                        70                        75                        80                        85

aaa gat ttt gat tct ttg cgt caa aaa gat ggc ctt tct ggt tac acc 403
Lys Asp Phe Asp Ser Leu Arg Gln Lys Asp Gly Leu Ser Gly Tyr Thr
                        90                        95                        100

tgc cgt gct gaa agt gag cac gat tgg act gag tct tct cat gct tct 451
Cys Arg Ala Glu Ser Glu His Asp Trp Thr Glu Ser Ser His Ala Ser
                        105                        110                        115

gcg gcc ttg tct tat gcg gat ggt ttg tct aaa gcc aag cag ttg gat 499
Ala Ala Leu Ser Tyr Ala Asp Gly Leu Ser Lys Ala Lys Gln Leu Asp
                        120                        125                        130

ggc gat acc acg cat agt gtg gtt gct gtc gtt ggt gat ggc gct cta 547
Gly Asp Thr Thr His Ser Val Val Ala Val Val Gly Asp Gly Ala Leu
                        135                        140                        145

act ggc ggc atg tgt tgg gaa gca ctg aac aat att gct gct ggt aaa 595
Thr Gly Gly Met Cys Trp Glu Ala Leu Asn Asn Ile Ala Ala Gly Lys
                        150                        155                        160                        165

gac cgc aaa gtt gtt gtc gta gtc aat gac aat ggc cgg agt tat tct 643
Asp Arg Lys Val Val Val Val Val Asn Asp Asn Gly Arg Ser Tyr Ser
                        170                        175                        180

cca acc att ggc gga ttt gcg gaa aac ctt gcg ggc ctt cgc atg cag 691
Pro Thr Ile Gly Gly Phe Ala Glu Asn Leu Ala Gly Leu Arg Met Gln
                        185                        190                        195

cct ttc tat gat 703
Pro Phe Tyr Asp

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200

<210> 408

<211> 201

<212> PRT

<213> Corynebacterium glutamicum

<400> 408

Met Gly Ile Leu Asn Ser Ile Ser Thr Pro Ala Asp Leu Lys Ala Leu
 1 5 10 15

Asn Asp Glu Asp Leu Asp Ala Leu Ala Lys Glu Ile Arg Thr Phe Leu
 20 25 30

Val Asp Lys Val Ala Ala Thr Gly Gly His Leu Gly Pro Asn Leu Gly
 35 40 45

Val Val Glu Leu Thr Ile Gly Leu His Arg Val Phe Asp Ser Pro Gln
 50 55 60

Asp Pro Ile Ile Phe Asp Thr Ser His Gln Ser Tyr Val His Lys Ile
 65 70 75 80

Leu Thr Gly Arg Ala Lys Asp Phe Asp Ser Leu Arg Gln Lys Asp Gly
 85 90 95

Leu Ser Gly Tyr Thr Cys Arg Ala Glu Ser Glu His Asp Trp Thr Glu
 100 105 110

Ser Ser His Ala Ser Ala Ala Leu Ser Tyr Ala Asp Gly Leu Ser Lys
 115 120 125

Ala Lys Gln Leu Asp Gly Asp Thr Thr His Ser Val Val Ala Val Val
 130 135 140

Gly Asp Gly Ala Leu Thr Gly Gly Met Cys Trp Glu Ala Leu Asn Asn
 145 150 155 160

Ile Ala Ala Gly Lys Asp Arg Lys Val Val Val Val Val Asn Asp Asn
 165 170 175

Gly Arg Ser Tyr Ser Pro Thr Ile Gly Gly Phe Ala Glu Asn Leu Ala
 180 185 190

Gly Leu Arg Met Gln Pro Phe Tyr Asp
 195 200

<210> 409

<211> 2241

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(2218)

<223> RXN00879

<400> 409

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				Val	Thr	Ala	Arg	Arg								
				1				5								
ttt	ttg	aat	gaa	ctc	gcc	gat	ctc	tac	ggc	gta	gca	act	tcc	tac	act	163
Phe	Leu	Asn	Glu	Leu	Ala	Asp	Leu	Tyr	Gly	Val	Ala	Thr	Ser	Tyr	Thr	
			10						15					20		
gat	tac	aaa	ggt	gcc	cat	att	gag	gtc	agc	gat	gac	aca	tta	gtg	aaa	211
Asp	Tyr	Lys	Gly	Ala	His	Ile	Glu	Val	Ser	Asp	Asp	Thr	Leu	Val	Lys	
			25					30					35			
atc	ctg	cgt	gct	ctg	ggt	gtg	aat	tta	gat	aca	agc	aac	ctc	ccc	aac	259
Ile	Leu	Arg	Ala	Leu	Gly	Val	Asn	Leu	Asp	Thr	Ser	Asn	Leu	Pro	Asn	
		40					45					50				
gat	gac	gct	atc	caa	cgc	caa	att	gcc	ctc	ttc	cat	gat	cga	gag	ttc	307
Asp	Asp	Ala	Ile	Gln	Arg	Gln	Ile	Ala	Leu	Phe	His	Asp	Arg	Glu	Phe	
	55					60					65					
act	cgc	cca	ctg	cct	cca	tcg	gtg	gtt	gca	gtt	gaa	ggt	gat	gaa	cta	355
Thr	Arg	Pro	Leu	Pro	Pro	Ser	Val	Val	Ala	Val	Glu	Gly	Asp	Glu	Leu	
	70				75				80						85	
gtt	ttc	ccg	gtg	cat	gtg	cac	gac	ggg	tcc	cct	gca	gat	gtc	cac	atc	403
Val	Phe	Pro	Val	His	Val	His	Asp	Gly	Ser	Pro	Ala	Asp	Val	His	Ile	
				90					95					100		
gaa	ttg	gaa	gac	ggc	acg	cag	cgg	gat	gtt	tct	cag	gtg	gaa	aac	tgg	451
Glu	Leu	Glu	Asp	Gly	Thr	Gln	Arg	Asp	Val	Ser	Gln	Val	Glu	Asn	Trp	
			105					110					115			
aca	gcg	cca	cgg	gaa	att	gat	ggg	att	agg	tgg	ggc	gag	gca	tcg	ttt	499
Thr	Ala	Pro	Arg	Glu	Ile	Asp	Gly	Ile	Arg	Trp	Gly	Glu	Ala	Ser	Phe	
		120					125					130				
aag	att	cct	ggt	gat	ctc	ccc	ttg	ggt	tgg	cac	aag	ctt	cac	ctt	aaa	547
Lys	Ile	Pro	Gly	Asp	Leu	Pro	Leu	Gly	Trp	His	Lys	Leu	His	Leu	Lys	
	135					140					145					
tcc	aat	gaa	cgc	tca	gct	gag	tgc	ggg	ttg	atc	atc	acc	ccg	gct	cgt	595
Ser	Asn	Glu	Arg	Ser	Ala	Glu	Cys	Gly	Leu	Ile	Ile	Thr	Pro	Ala	Arg	
	150				155				160						165	
ctg	tct	act	gct	gat	aag	tat	ctt	gat	tcc	cct	cgc	agt	ggt	gtc	atg	643
Leu	Ser	Thr	Ala	Asp	Lys	Tyr	Leu	Asp	Ser	Pro	Arg	Ser	Gly	Val	Met	
				170					175					180		
gcg	cag	atc	tac	tct	gtg	cgt	tcc	acg	ttg	tcg	tgg	ggc	atg	ggt	gat	691
Ala	Gln	Ile	Tyr	Ser	Val	Arg	Ser	Thr	Leu	Ser	Trp	Gly	Met	Gly	Asp	
			185					190					195			
ttc	aat	gat	tta	gga	aac	ttg	gca	agt	gtg	gtt	gcc	cag	gat	gga	gca	739
Phe	Asn	Asp	Leu	Gly	Asn	Leu	Ala	Ser	Val	Val	Ala	Gln	Asp	Gly	Ala	
		200					205					210				
gac	ttc	ctg	ctc	atc	aac	ccc	atg	cac	gct	gca	gag	ccg	ctg	cct	cct	787
Asp	Phe	Leu	Leu	Ile	Asn	Pro	Met	His	Ala	Ala	Glu	Pro	Leu	Pro	Pro	
	215					220					225					

act gag gac tct cct tat ctg ccc aca acc agg cgc ttt atc aac ccg	835
Thr Glu Asp Ser Pro Tyr Leu Pro Thr Thr Arg Arg Phe Ile Asn Pro	
230 235 240 245	
atc tac att cgg gta gaa gat att ccg gag ttt aat cag ctt gag att	883
Ile Tyr Ile Arg Val Glu Asp Ile Pro Glu Phe Asn Gln Leu Glu Ile	
250 255 260	
gat cta cgc gat gat atc gca gag atg gct gcg gaa ttc cgc gaa cgc	931
Asp Leu Arg Asp Asp Ile Ala Glu Met Ala Ala Glu Phe Arg Glu Arg	
265 270 275	
aat ctg acc tca gac atc att gag cgc aat gac gtc tac gct gca aag	979
Asn Leu Thr Ser Asp Ile Ile Glu Arg Asn Asp Val Tyr Ala Ala Lys	
280 285 290	
ctt caa gtg ctg cgc gcc att ttt gaa atg cct cgt tcc agc gaa cgt	1027
Leu Gln Val Leu Arg Ala Ile Phe Glu Met Pro Arg Ser Ser Glu Arg	
295 300 305	
gaa gcc aac ttt gtc tcc ttc gtg caa cgg gaa ggc caa ggt ctt att	1075
Glu Ala Asn Phe Val Ser Phe Val Gln Arg Glu Gly Gln Gly Leu Ile	
310 315 320 325	
gat ttc gcc acc tgg tgc gcg gac cgc gaa act gca cag tct gaa tct	1123
Asp Phe Ala Thr Trp Cys Ala Asp Arg Glu Thr Ala Gln Ser Glu Ser	
330 335 340	
gtc cac gga act gag cca gac cgc gat gag ctg acc atg ttc tac atg	1171
Val His Gly Thr Glu Pro Asp Arg Asp Glu Leu Thr Met Phe Tyr Met	
345 350 355	
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Trp Leu Gln Trp Leu Cys Asp Glu Gln Leu Ala Ala Ala Gln Lys Arg	
360 365 370	
gct gtc gat gcc gga atg tcg atc ggc atc atg gca gac ctg gca gtt	1267
Ala Val Asp Ala Gly Met Ser Ile Gly Ile Met Ala Asp Leu Ala Val	
375 380 385	
ggg gtg cat cca ggt ggt gct gat gcc cag aac ctc agc cac gta ctt	1315
Gly Val His Pro Gly Gly Ala Asp Ala Gln Asn Leu Ser His Val Leu	
390 395 400 405	
gct ccg gat gcg tca gtg ggc gcc cca cca gat gga tac aac cag cag	1363
Ala Pro Asp Ala Ser Val Gly Ala Pro Pro Asp Gly Tyr Asn Gln Gln	
410 415 420	
ggc caa gac tgg tcc cag cca cca tgg cat cca gtg cgt ctt gca gag	1411
Gly Gln Asp Trp Ser Gln Pro Pro Trp His Pro Val Arg Leu Ala Glu	
425 430 435	
gaa ggc tac att ccg tgg cgt aat ctg ctg cgc act gtg ctg cgt cac	1459
Glu Gly Tyr Ile Pro Trp Arg Asn Leu Leu Arg Thr Val Leu Arg His	
440 445 450	
tcc ggc gga atc cgc gtg gac cac gtt ctt ggt ttg ttc agg ctc ttt	1507
Ser Gly Gly Ile Arg Val Asp His Val Leu Gly Leu Phe Arg Leu Phe	
455 460 465	
gtc atg cca cgc atg caa tcc cct gct acg ggc acc tat atc cgc ttc	1555

Val 470	Met	Pro	Arg	Met	Gln 475	Ser	Pro	Ala	Thr	Gly 480	Thr	Tyr	Ile	Arg	Phe 485	
gac	cat	aat	gcg	ttg	gta	ggc	att	cta	gcc	cta	gaa	gca	gaa	ctc	gca	1603
Asp	His	Asn	Ala	Leu 490	Val	Gly	Ile	Leu	Ala	Leu 495	Glu	Ala	Glu	Leu	Ala 500	
ggc	gcc	gtt	gtc	att	ggg	gaa	gat	ctg	gga	acg	ttt	gag	cct	tgg	gta	1651
Gly	Ala	Val	Val 505	Ile	Gly	Glu	Asp	Leu 510	Gly	Thr	Phe	Glu	Pro	Trp	Val	
caa	gat	gca	ttg	gct	cag	cgt	ggc	atc	atg	ggc	acc	tcg	atc	cta	tgg	1699
Gln	Asp	Ala	Leu	Ala	Gln	Arg	Gly 525	Ile	Met	Gly	Thr	Ser 530	Ile	Leu	Trp	
ttc	gag	cat	tcc	cca	agc	cag	ccg	ggg	cct	cgc	cgc	cag	gaa	gag	tat	1747
Phe	Glu	His	Ser	Pro	Ser	Gln 540	Pro	Gly	Pro	Arg	Arg 545	Gln	Glu	Glu	Tyr	
cgt	ccg	ctg	gcc	ttg	acc	act	gtg	acc	act	cat	gat	ctc	cct	ccg	act	1795
Arg	Pro	Leu	Ala	Leu	Thr	Thr	Val	Thr	Thr	His 560	Asp	Leu	Pro	Pro	Thr 565	
gct	ggg	tat	ttg	gag	ggc	gag	cac	att	gct	ctt	cgt	gag	cga	ttg	ggg	1843
Ala	Gly	Tyr	Leu 570	Glu	Gly	Glu	His	Ile	Ala 575	Leu	Arg	Glu	Arg	Leu	Gly 580	
gtg	ctc	aac	act	gat	cct	gct	gca	gaa	ctc	gct	gag	gat	ctg	cag	tgg	1891
Val	Leu	Asn	Thr 585	Asp	Pro	Ala	Ala	Glu	Leu	Ala 590	Glu	Asp	Leu	Gln	Trp	
caa	gcg	gag	atc	ctt	gat	gtc	gca	gca	tct	gcc	aac	gca	ttg	cca	gcc	1939
Gln	Ala	Glu	Ile	Leu	Asp	Val	Ala 605	Ala	Ser	Ala	Asn 610	Ala	Leu	Pro	Ala	
cgg	gaa	tac	gtg	gga	ctc	gaa	cgc	gat	cag	cgc	ggg	gag	ttg	gct	gag	1987
Arg	Glu	Tyr	Val	Gly	Leu	Glu	Arg	Asp	Gln	Arg	Gly 625	Glu	Leu	Ala	Glu	
ctg	ttg	gaa	ggc	ctg	cac	act	ttc	gtt	gcg	aaa	acc	cct	tca	gca	ctg	2035
Leu	Leu	Glu	Gly	Leu	His	Thr	Phe	Val	Ala	Lys 640	Thr	Pro	Ser	Ala	Leu 645	
acc	tgt	gtc	tgc	ttg	gta	gac	atg	gtc	ggg	gaa	aag	cgg	gca	cag	aat	2083
Thr	Cys	Val	Cys	Leu 650	Val	Asp	Met	Val	Gly	Glu 655	Lys	Arg	Ala	Gln	Asn 660	
cag	ccg	ggc	aca	acg	agg	gat	atg	tat	ccc	aac	tgg	tgt	atc	cca	ctg	2131
Gln	Pro	Gly	Thr 665	Thr	Arg	Asp	Met	Tyr 670	Pro	Asn	Trp	Cys	Ile	Pro	Leu 675	
tgt	gac	agc	gaa	ggc	aac	tcc	gtg	ctc	att	gaa	tcg	ctg	cgt	gaa	aat	2179
Cys	Asp	Ser	Glu	Gly	Asn	Ser	Val 685	Leu	Ile	Glu	Ser	Leu	Arg	Glu	Asn 690	
gag	ctg	tat	cac	cgt	gtg	gca	aag	gca	agc	aag	cga	gat	taggtccgct			2228
Glu	Leu	Tyr	His	Arg	Val	Ala 700	Lys	Ala	Ser	Lys 705	Arg	Asp				
tcagttgtgg	tgg															2241

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<211> 706

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 410

Val	Thr	Ala	Arg	Arg	Phe	Leu	Asn	Glu	Leu	Ala	Asp	Leu	Tyr	Gly	Val	1	5	10	15
Ala	Thr	Ser	Tyr	Thr	Asp	Tyr	Lys	Gly	Ala	His	Ile	Glu	Val	Ser	Asp	20	25	30	
Asp	Thr	Leu	Val	Lys	Ile	Leu	Arg	Ala	Leu	Gly	Val	Asn	Leu	Asp	Thr	35	40	45	
Ser	Asn	Leu	Pro	Asn	Asp	Asp	Ala	Ile	Gln	Arg	Gln	Ile	Ala	Leu	Phe	50	55	60	
His	Asp	Arg	Glu	Phe	Thr	Arg	Pro	Leu	Pro	Pro	Ser	Val	Val	Ala	Val	65	70	75	80
Glu	Gly	Asp	Glu	Leu	Val	Phe	Pro	Val	His	Val	His	Asp	Gly	Ser	Pro	85	90	95	
Ala	Asp	Val	His	Ile	Glu	Leu	Glu	Asp	Gly	Thr	Gln	Arg	Asp	Val	Ser	100	105	110	
Gln	Val	Glu	Asn	Trp	Thr	Ala	Pro	Arg	Glu	Ile	Asp	Gly	Ile	Arg	Trp	115	120	125	
Gly	Glu	Ala	Ser	Phe	Lys	Ile	Pro	Gly	Asp	Leu	Pro	Leu	Gly	Trp	His	130	135	140	
Lys	Leu	His	Leu	Lys	Ser	Asn	Glu	Arg	Ser	Ala	Glu	Cys	Gly	Leu	Ile	145	150	155	160
Ile	Thr	Pro	Ala	Arg	Leu	Ser	Thr	Ala	Asp	Lys	Tyr	Leu	Asp	Ser	Pro	165	170	175	
Arg	Ser	Gly	Val	Met	Ala	Gln	Ile	Tyr	Ser	Val	Arg	Ser	Thr	Leu	Ser	180	185	190	
Trp	Gly	Met	Gly	Asp	Phe	Asn	Asp	Leu	Gly	Asn	Leu	Ala	Ser	Val	Val	195	200	205	
Ala	Gln	Asp	Gly	Ala	Asp	Phe	Leu	Leu	Ile	Asn	Pro	Met	His	Ala	Ala	210	215	220	
Glu	Pro	Leu	Pro	Pro	Thr	Glu	Asp	Ser	Pro	Tyr	Leu	Pro	Thr	Thr	Arg	225	230	235	240
Arg	Phe	Ile	Asn	Pro	Ile	Tyr	Ile	Arg	Val	Glu	Asp	Ile	Pro	Glu	Phe	245	250	255	
Asn	Gln	Leu	Glu	Ile	Asp	Leu	Arg	Asp	Asp	Ile	Ala	Glu	Met	Ala	Ala	260	265	270	
Glu	Phe	Arg	Glu	Arg	Asn	Leu	Thr	Ser	Asp	Ile	Ile	Glu	Arg	Asn	Asp	275	280	285	

Val Tyr Ala Ala Lys Leu Gln Val Leu Arg Ala Ile Phe Glu Met Pro
 290 295 300
 Arg Ser Ser Glu Arg Glu Ala Asn Phe Val Ser Phe Val Gln Arg Glu
 305 310 315 320
 Gly Gln Gly Leu Ile Asp Phe Ala Thr Trp Cys Ala Asp Arg Glu Thr
 325 330 335
 Ala Gln Ser Glu Ser Val His Gly Thr Glu Pro Asp Arg Asp Glu Leu
 340 345 350
 Thr Met Phe Tyr Met Trp Leu Gln Trp Leu Cys Asp Glu Gln Leu Ala
 355 360 365
 Ala Ala Gln Lys Arg Ala Val Asp Ala Gly Met Ser Ile Gly Ile Met
 370 375 380
 Ala Asp Leu Ala Val Gly Val His Pro Gly Gly Ala Asp Ala Gln Asn
 385 390 395 400
 Leu Ser His Val Leu Ala Pro Asp Ala Ser Val Gly Ala Pro Pro Asp
 405 410 415
 Gly Tyr Asn Gln Gln Gly Gln Asp Trp Ser Gln Pro Pro Trp His Pro
 420 425 430
 Val Arg Leu Ala Glu Glu Gly Tyr Ile Pro Trp Arg Asn Leu Leu Arg
 435 440 445
 Thr Val Leu Arg His Ser Gly Gly Ile Arg Val Asp His Val Leu Gly
 450 455 460
 Leu Phe Arg Leu Phe Val Met Pro Arg Met Gln Ser Pro Ala Thr Gly
 465 470 475 480
 Thr Tyr Ile Arg Phe Asp His Asn Ala Leu Val Gly Ile Leu Ala Leu
 485 490 495
 Glu Ala Glu Leu Ala Gly Ala Val Val Ile Gly Glu Asp Leu Gly Thr
 500 505 510
 Phe Glu Pro Trp Val Gln Asp Ala Leu Ala Gln Arg Gly Ile Met Gly
 515 520 525
 Thr Ser Ile Leu Trp Phe Glu His Ser Pro Ser Gln Pro Gly Pro Arg
 530 535 540
 Arg Gln Glu Glu Tyr Arg Pro Leu Ala Leu Thr Thr Val Thr Thr His
 545 550 555 560
 Asp Leu Pro Pro Thr Ala Gly Tyr Leu Glu Gly Glu His Ile Ala Leu
 565 570 575
 Arg Glu Arg Leu Gly Val Leu Asn Thr Asp Pro Ala Ala Glu Leu Ala
 580 585 590
 Glu Asp Leu Gln Trp Gln Ala Glu Ile Leu Asp Val Ala Ala Ser Ala
 595 600 605
 Asn Ala Leu Pro Ala Arg Glu Tyr Val Gly Leu Glu Arg Asp Gln Arg

610	615	620
Gly Glu Leu Ala Glu Leu Leu Glu Gly Leu His Thr Phe Val Ala Lys 625 630 635 640		
Thr Pro Ser Ala Leu Thr Cys Val Cys Leu Val Asp Met Val Gly Glu 645 650 655		
Lys Arg Ala Gln Asn Gln Pro Gly Thr Thr Arg Asp Met Tyr Pro Asn 660 665 670		
Trp Cys Ile Pro Leu Cys Asp Ser Glu Gly Asn Ser Val Leu Ile Glu 675 680 685		
Ser Leu Arg Glu Asn Glu Leu Tyr His Arg Val Ala Lys Ala Ser Lys 690 695 700		
Arg Asp 705		

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 <213> Corynebacterium glutamicum

<220>
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 <222> (101)..(2200)
 <223> FRXA00879

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 attagtggca taatgttggtg ttgtgactgc tcgcagattt ttg aat gaa ctc gcc 115
 Leu Asn Glu Leu Ala
 1 5
 gat ctc tac ggc gta gca act tcc tac act gat tac aaa ggt gcc cat 163
 Asp Leu Tyr Gly Val Ala Thr Ser Tyr Thr Asp Tyr Lys Gly Ala His
 10 15 20
 att gag gtc agc gat gac aca tta gtg aaa atc ctg cgt gct ctg ggt 211
 Ile Glu Val Ser Asp Asp Thr Leu Val Lys Ile Leu Arg Ala Leu Gly
 25 30 35
 gtg aat tta gat aca agc aac ctc ccc aac gat gac gct atc caa cgc 259
 Val Asn Leu Asp Thr Ser Asn Leu Pro Asn Asp Asp Ala Ile Gln Arg
 40 45 50
 caa att gcc ctc ttc cat gat cga gag ttc act cgc cca ctg cct cca 307
 Gln Ile Ala Leu Phe His Asp Arg Glu Phe Thr Arg Pro Leu Pro Pro
 55 60 65
 tcg gtg gtt gca gtt gaa ggt gat gaa cta gtt ttc ccg gtg cat gtg 355
 Ser Val Val Ala Val Glu Gly Asp Glu Leu Val Phe Pro Val His Val
 70 75 80 85
 cac gac ggt tcc cct gca gat gtc cac atc gaa ttg gaa gac ggc acg 403
 His Asp Gly Ser Pro Ala Asp Val His Ile Glu Leu Glu Asp Gly Thr
 90 95 100

cag cgg gat gtt tct cag gtg gaa aac tgg aca gcg cca cgg gaa att	451
Gln Arg Asp Val Ser Gln Val Glu Asn Trp Thr Ala Pro Arg Glu Ile	
105 110 115	
gat ggg att agg tgg ggc gag gca tgc ttt aag att cct ggt gat ctc	499
Asp Gly Ile Arg Trp Gly Glu Ala Ser Phe Lys Ile Pro Gly Asp Leu	
120 125 130	
ccc ttg ggt tgg cac aag ctt cac ctt aaa tcc aat gaa cgc tca gct	547
Pro Leu Gly Trp His Lys Leu His Leu Lys Ser Asn Glu Arg Ser Ala	
135 140 145	
gag tgc ggt ttg atc atc acc ccg gct cgt ctg tct act gct gat aag	595
Glu Cys Gly Leu Ile Ile Thr Pro Ala Arg Leu Ser Thr Ala Asp Lys	
150 155 160 165	
tat ctt gat tcc cct cgc agt ggt gtc atg gcg cag atc tac tct gtg	643
Tyr Leu Asp Ser Pro Arg Ser Gly Val Met Ala Gln Ile Tyr Ser Val	
170 175 180	
cgt tcc acg ttg tgc tgg ggc atg ggt gat ttc aat gat tta gga aac	691
Arg Ser Thr Leu Ser Trp Gly Met Gly Asp Phe Asn Asp Leu Gly Asn	
185 190 195	
ttg gca agt gtg gtt gcc cag gat gga gca gac ttc ctg ctc atc aac	739
Leu Ala Ser Val Val Ala Gln Asp Gly Ala Asp Phe Leu Leu Ile Asn	
200 205 210	
ccc atg cac gct gca gag ccg ctg cct cct act gag gac tct cct tat	787
Pro Met His Ala Ala Glu Pro Leu Pro Pro Thr Glu Asp Ser Pro Tyr	
215 220 225	
ctg ccc aca acc agg cgc ttt atc aac ccg atc tac att cgg gta gaa	835
Leu Pro Thr Thr Arg Arg Phe Ile Asn Pro Ile Tyr Ile Arg Val Glu	
230 235 240 245	
gat att ccg gag ttt aat cag ctt gag att gat cta cgc gat gat atc	883
Asp Ile Pro Glu Phe Asn Gln Leu Glu Ile Asp Leu Arg Asp Asp Ile	
250 255 260	
gca gag atg gct gcg gaa ttc cgc gaa cgc aat ctg acc tca gac atc	931
Ala Glu Met Ala Ala Glu Phe Arg Glu Arg Asn Leu Thr Ser Asp Ile	
265 270 275	
att gag cgc aat gac gtc tac gct gca aag ctt caa gtg ctg cgc gcc	979
Ile Glu Arg Asn Asp Val Tyr Ala Ala Lys Leu Gln Val Leu Arg Ala	
280 285 290	
att ttt gaa atg cct cgt tcc agc gaa cgt gaa gcc aac ttt gtc tcc	1027
Ile Phe Glu Met Pro Arg Ser Ser Glu Arg Glu Ala Asn Phe Val Ser	
295 300 305	
ttc gtg caa cgg gaa ggc caa ggt ctt att gat ttc gcc acc tgg tgc	1075
Phe Val Gln Arg Glu Gly Gln Gly Leu Ile Asp Phe Ala Thr Trp Cys	
310 315 320 325	
gcg gac cgc gaa act gca cag tct gaa tct gtc cac gga act gag cca	1123
Ala Asp Arg Glu Thr Ala Gln Ser Glu Ser Val His Gly Thr Glu Pro	
330 335 340	

gac cgc gat gag ctg acc atg ttc tac atg tgg ttg cag tgg cta tgt	1171
Asp Arg Asp Glu Leu Thr Met Phe Tyr Met Trp Leu Gln Trp Leu Cys	
345 350 355	
gat gag cag ctg gcg gca gct caa aag cgc gct gtc gat gcc gga atg	1219
Asp Glu Gln Leu Ala Ala Ala Gln Lys Arg Ala Val Asp Ala Gly Met	
360 365 370	
tcg atc ggc atc atg gca gac ctg gca gtt ggt gtg cat cca ggt ggt	1267
Ser Ile Gly Ile Met Ala Asp Leu Ala Val Gly Val His Pro Gly Gly	
375 380 385	
gct gat gcc cag aac ctc agc cac gta ctt gct ccg gat gcg tca gtg	1315
Ala Asp Ala Gln Asn Leu Ser His Val Leu Ala Pro Asp Ala Ser Val	
390 395 400 405	
ggc gcc cca cca gat gga tac aac cag cag ggc caa gac tgg tcc cag	1363
Gly Ala Pro Pro Asp Gly Tyr Asn Gln Gln Gly Gln Asp Trp Ser Gln	
410 415 420	
cca cca tgg cat cca gtg cgt ctt gca gag gaa ggc tac att ccg tgg	1411
Pro Pro Trp His Pro Val Arg Leu Ala Glu Glu Gly Tyr Ile Pro Trp	
425 430 435	
cgt aat ctg ctg cgc act gtg ctg cgt cac tcc ggc gga atc cgc gtg	1459
Arg Asn Leu Leu Arg Thr Val Leu Arg His Ser Gly Gly Ile Arg Val	
440 445 450	
gac cac gtt ctt ggt ttg ttc agg ctc ttt gtc atg cca cgc atg caa	1507
Asp His Val Leu Gly Leu Phe Arg Leu Phe Val Met Pro Arg Met Gln	
455 460 465	
tcc cct gct acg ggc acc tat atc cgc ttc gac cat aat gcg ttg gta	1555
Ser Pro Ala Thr Gly Thr Tyr Ile Arg Phe Asp His Asn Ala Leu Val	
470 475 480 485	
ggc att cta gcc cta gaa gca gaa ctc gca ggc gcc gtt gtc att ggt	1603
Gly Ile Leu Ala Leu Glu Ala Glu Leu Ala Gly Ala Val Val Ile Gly	
490 495 500	
gaa gat ctg gga acg ttt gag cct tgg gta caa gat gca ttg gct cag	1651
Glu Asp Leu Gly Thr Phe Glu Pro Trp Val Gln Asp Ala Leu Ala Gln	
505 510 515	
cgt ggc atc atg ggc acc tcg atc cta tgg ttc gag cat tcc cca agc	1699
Arg Gly Ile Met Gly Thr Ser Ile Leu Trp Phe Glu His Ser Pro Ser	
520 525 530	
cag ccg ggt cct cgc cgc cag gaa gag tat cgt ccg ctg gcc ttg acc	1747
Gln Pro Gly Pro Arg Arg Gln Glu Glu Tyr Arg Pro Leu Ala Leu Thr	
535 540 545	
act gtg acc act cat gat ctc cct ccg act gct ggt tat ttg gag ggc	1795
Thr Val Thr Thr His Asp Leu Pro Pro Thr Ala Gly Tyr Leu Glu Gly	
550 555 560 565	
gag cac att gct ctt cgt gag cga ttg ggg gtg ctc aac act gat cct	1843
Glu His Ile Ala Leu Arg Glu Arg Leu Gly Val Leu Asn Thr Asp Pro	
570 575 580	
gct gca gaa ctc gct gag gat ctg cag tgg caa gcg gag atc ctt gat	1891

Ala Ala Glu Leu Ala Glu Asp Leu Gln Trp Gln Ala Glu Ile Leu Asp
 585 590 595

gtc gca gca tct gcc aac gca ttg cca gcc cgg gaa tac gtg gga ctc 1939
 Val Ala Ala Ser Ala Asn Ala Leu Pro Ala Arg Glu Tyr Val Gly Leu
 600 605 610

gaa cgc gat cag cgc ggt gag ttg gct gag ctg ttg gaa ggc ctg cac 1987
 Glu Arg Asp Gln Arg Gly Glu Leu Ala Glu Leu Leu Glu Gly Leu His
 615 620 625

act ttc gtt gcg aaa acc cct tca gca ctg acc tgt gtc tgc ttg gta 2035
 Thr Phe Val Ala Lys Thr Pro Ser Ala Leu Thr Cys Val Cys Leu Val
 630 635 640 645

gac atg gtc ggt gaa aag cgg gca cag aat cag ccg ggc aca acg agg 2083
 Asp Met Val Gly Glu Lys Arg Ala Gln Asn Gln Pro Gly Thr Thr Arg
 650 655 660

gat atg tat ccc aac tgg tgt atc cca ctg tgt gac agc gaa ggc aac 2131
 Asp Met Tyr Pro Asn Trp Cys Ile Pro Leu Cys Asp Ser Glu Gly Asn
 665 670 675

tcc gtg ctc att gaa tcg ctg cgt gaa aat gag ctg tat cac cgt gtg 2179
 Ser Val Leu Ile Glu Ser Leu Arg Glu Asn Glu Leu Tyr His Arg Val
 680 685 690

gca aag gca agc aag cga gat taggtccgct tcagttgtgg tgg 2223
 Ala Lys Ala Ser Lys Arg Asp
 695 700

<210> 412

<211> 700

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 412

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Tyr Lys Gly Ala His Ile Glu Val Ser Asp Asp Thr Leu Val Lys Ile
 20 25 30

Leu Arg Ala Leu Gly Val Asn Leu Asp Thr Ser Asn Leu Pro Asn Asp
 35 40 45

Asp Ala Ile Gln Arg Gln Ile Ala Leu Phe His Asp Arg Glu Phe Thr
 50 55 60

Arg Pro Leu Pro Pro Ser Val Val Ala Val Glu Gly Asp Glu Leu Val
 65 70 75 80

Phe Pro Val His Val His Asp Gly Ser Pro Ala Asp Val His Ile Glu
 85 90 95

Leu Glu Asp Gly Thr Gln Arg Asp Val Ser Gln Val Glu Asn Trp Thr
 100 105 110

Ala Pro Arg Glu Ile Asp Gly Ile Arg Trp Gly Glu Ala Ser Phe Lys
 115 120 125

Ile Pro Gly Asp Leu Pro Leu Gly Trp His Lys Leu His Leu Lys Ser
 130 135 140
 Asn Glu Arg Ser Ala Glu Cys Gly Leu Ile Ile Thr Pro Ala Arg Leu
 145 150 155 160
 Ser Thr Ala Asp Lys Tyr Leu Asp Ser Pro Arg Ser Gly Val Met Ala
 165 170 175
 Gln Ile Tyr Ser Val Arg Ser Thr Leu Ser Trp Gly Met Gly Asp Phe
 180 185 190
 Asn Asp Leu Gly Asn Leu Ala Ser Val Val Ala Gln Asp Gly Ala Asp
 195 200 205
 Phe Leu Leu Ile Asn Pro Met His Ala Ala Glu Pro Leu Pro Pro Thr
 210 215 220
 Glu Asp Ser Pro Tyr Leu Pro Thr Thr Arg Arg Phe Ile Asn Pro Ile
 225 230 235 240
 Tyr Ile Arg Val Glu Asp Ile Pro Glu Phe Asn Gln Leu Glu Ile Asp
 245 250 255
 Leu Arg Asp Asp Ile Ala Glu Met Ala Ala Glu Phe Arg Glu Arg Asn
 260 265 270
 Leu Thr Ser Asp Ile Ile Glu Arg Asn Asp Val Tyr Ala Ala Lys Leu
 275 280 285
 Gln Val Leu Arg Ala Ile Phe Glu Met Pro Arg Ser Ser Glu Arg Glu
 290 295 300
 Ala Asn Phe Val Ser Phe Val Gln Arg Glu Gly Gln Gly Leu Ile Asp
 305 310 315 320
 Phe Ala Thr Trp Cys Ala Asp Arg Glu Thr Ala Gln Ser Glu Ser Val
 325 330 335
 His Gly Thr Glu Pro Asp Arg Asp Glu Leu Thr Met Phe Tyr Met Trp
 340 345 350
 Leu Gln Trp Leu Cys Asp Glu Gln Leu Ala Ala Ala Gln Lys Arg Ala
 355 360 365
 Val Asp Ala Gly Met Ser Ile Gly Ile Met Ala Asp Leu Ala Val Gly
 370 375 380
 Val His Pro Gly Gly Ala Asp Ala Gln Asn Leu Ser His Val Leu Ala
 385 390 395 400
 Pro Asp Ala Ser Val Gly Ala Pro Pro Asp Gly Tyr Asn Gln Gln Gly
 405 410 415
 Gln Asp Trp Ser Gln Pro Pro Trp His Pro Val Arg Leu Ala Glu Glu
 420 425 430
 Gly Tyr Ile Pro Trp Arg Asn Leu Leu Arg Thr Val Leu Arg His Ser
 435 440 445

Gly Gly Ile Arg Val Asp His Val Leu Gly Leu Phe Arg Leu Phe Val
 450 455 460
 Met Pro Arg Met Gln Ser Pro Ala Thr Gly Thr Tyr Ile Arg Phe Asp
 465 470 475 480
 His Asn Ala Leu Val Gly Ile Leu Ala Leu Glu Ala Glu Leu Ala Gly
 485 490 495
 Ala Val Val Ile Gly Glu Asp Leu Gly Thr Phe Glu Pro Trp Val Gln
 500 505 510
 Asp Ala Leu Ala Gln Arg Gly Ile Met Gly Thr Ser Ile Leu Trp Phe
 515 520 525
 Glu His Ser Pro Ser Gln Pro Gly Pro Arg Arg Gln Glu Glu Tyr Arg
 530 535 540
 Pro Leu Ala Leu Thr Thr Val Thr Thr His Asp Leu Pro Pro Thr Ala
 545 550 555 560
 Gly Tyr Leu Glu Gly Glu His Ile Ala Leu Arg Glu Arg Leu Gly Val
 565 570 575
 Leu Asn Thr Asp Pro Ala Ala Glu Leu Ala Glu Asp Leu Gln Trp Gln
 580 585 590
 Ala Glu Ile Leu Asp Val Ala Ala Ser Ala Asn Ala Leu Pro Ala Arg
 595 600 605
 Glu Tyr Val Gly Leu Glu Arg Asp Gln Arg Gly Glu Leu Ala Glu Leu
 610 615 620
 Leu Glu Gly Leu His Thr Phe Val Ala Lys Thr Pro Ser Ala Leu Thr
 625 630 635 640
 Cys Val Cys Leu Val Asp Met Val Gly Glu Lys Arg Ala Gln Asn Gln
 645 650 655
 Pro Gly Thr Thr Arg Asp Met Tyr Pro Asn Trp Cys Ile Pro Leu Cys
 660 665 670
 Asp Ser Glu Gly Asn Ser Val Leu Ile Glu Ser Leu Arg Glu Asn Glu
 675 680 685
 Leu Tyr His Arg Val Ala Lys Ala Ser Lys Arg Asp
 690 695 700

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 <213> Corynebacterium glutamicum

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 <222> (101)..(1264)
 <223> RXN00043

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	Met Ala Glu Val Val	
	1 5	
cat tat caa gaa aat gca ggt caa gca gtt aaa aaa att gaa gga aga	163	
His Tyr Gln Glu Asn Ala Gly Gln Ala Val Lys Lys Ile Glu Gly Arg		
	10 15 20	
att gtt acc ccc cac ggg gtg att gat ggc ttt ctc caa ctc gaa aac	211	
Ile Val Thr Pro His Gly Val Ile Asp Gly Phe Leu Gln Leu Glu Asn		
	25 30 35	
ggc atc atc acg gaa ctc tct gga gaa cca gca cct aaa aac gca gga	259	
Gly Ile Ile Thr Glu Leu Ser Gly Glu Pro Ala Pro Lys Asn Ala Gly		
	40 45 50	
ttc cac ccc gaa ctc ccc acg att gtt ccc agt ttt att gat ctt cat	307	
Phe His Pro Glu Leu Pro Thr Ile Val Pro Ser Phe Ile Asp Leu His		
	55 60 65	
aat cac ggt gga aac ggt ggc gcg ttt cct acg gga acg cag gac cag	355	
Asn His Gly Gly Asn Gly Gly Ala Phe Pro Thr Gly Thr Gln Asp Gln		
	70 75 80 85	
gcg agg aat gcc gcg cag tat cac cgc gaa cat ggc acg acc gtg atg	403	
Ala Arg Asn Ala Ala Gln Tyr His Arg Glu His Gly Thr Thr Val Met		
	90 95 100	
ttg gca agc atg gtt tcg gcg ccg gct gac gca ctg gca gcg cag gtg	451	
Leu Ala Ser Met Val Ser Ala Pro Ala Asp Ala Leu Ala Ala Gln Val		
	105 110 115	
gaa aac ctt att ccc ttg tgt gaa gag ggc ctg ctg tgc ggc att cac	499	
Glu Asn Leu Ile Pro Leu Cys Glu Glu Gly Leu Leu Cys Gly Ile His		
	120 125 130	
ctc gag ggt cct ttc atc aac gca tgc cgt tgt ggt gct caa aac ccg	547	
Leu Glu Gly Pro Phe Ile Asn Ala Cys Arg Cys Gly Ala Gln Asn Pro		
	135 140 145	
gat ttt att ttt ccc ggc aac cca aca gat ctt gcc cag gtg atc cat	595	
Asp Phe Ile Phe Pro Gly Asn Pro Thr Asp Leu Ala Gln Val Ile His		
	150 155 160 165	
gcg gga aaa ggt tgg atc aaa tcg atc aca gta gcg ccg gaa act gac	643	
Ala Gly Lys Gly Trp Ile Lys Ser Ile Thr Val Ala Pro Glu Thr Asp		
	170 175 180	
aat ctt act gag ctt ctc gat ctc tgc gca gcg cac cac atc att gct	691	
Asn Leu Thr Glu Leu Leu Asp Leu Cys Ala Ala His His Ile Ile Ala		
	185 190 195	
tcc ttc ggg cac act gat gca gat ttt gat acc act acc agc gca att	739	
Ser Phe Gly His Thr Asp Ala Asp Phe Asp Thr Thr Thr Ser Ala Ile		
	200 205 210	
gcc ttg gct aaa gag aaa aat gtg acg gtc acg gct acg cat ttg ttc	787	
Ala Leu Ala Lys Glu Lys Asn Val Thr Val Thr Ala Thr His Leu Phe		
	215 220 225	

aat gcg atg cct ccg ctg cat cat agg gat ccc ggc agc gtg ggc gct 835
 Asn Ala Met Pro Pro Leu His His Arg Asp Pro Gly Ser Val Gly Ala
 230 235 240 245

 ttg ctt gct gcg gca cgt gcc ggg gac gca tat gtt gag ttg atc gcc 883
 Leu Leu Ala Ala Ala Arg Ala Gly Asp Ala Tyr Val Glu Leu Ile Ala
 250 255 260

 gac ggc gtg cat ttg gcc gat gga acg gtc gat cta gct cgt tcc aac 931
 Asp Gly Val His Leu Ala Asp Gly Thr Val Asp Leu Ala Arg Ser Asn
 265 270 275

 aac gcc ttt ttc atc acg gac gcc atg gaa gcc gcc gga atg cca gac 979
 Asn Ala Phe Phe Ile Thr Asp Ala Met Glu Ala Ala Gly Met Pro Asp
 280 285 290

 ggt gag tac att ttg ggc gtt ttg aac gtc acc gtc acc gat ggc gtc 1027
 Gly Glu Tyr Ile Leu Gly Val Leu Asn Val Thr Val Thr Asp Gly Val
 295 300 305

 gcc cgt ctg cgc gat ggc ggc gcc atc gcc ggg ggt acc agc aca cta 1075
 Ala Arg Leu Arg Asp Gly Gly Ala Ile Ala Gly Gly Thr Ser Thr Leu
 310 315 320 325

 gcg agt cag ttc gtg cac cac gtg cgc agg ggt atg acg ctt atc gac 1123
 Ala Ser Gln Phe Val His His Val Arg Arg Gly Met Thr Leu Ile Asp
 330 335 340

 gcg acc ctc cac acc tca acc gtc gcc gcc aaa att ctc gga ctt agc 1171
 Ala Thr Leu His Thr Ser Thr Val Ala Ala Lys Ile Leu Gly Leu Ser
 345 350 355

 gat cac gaa atc gtt aaa tcc aac cct gta aat ttt gtg gtc ttt gac 1219
 Asp His Glu Ile Val Lys Ser Asn Pro Val Asn Phe Val Val Phe Asp
 360 365 370

 tca aac ggc cag tta caa cag gtc cat tta gac cat caa gta att 1264
 Ser Asn Gly Gln Leu Gln Gln Val His Leu Asp His Gln Val Ile
 375 380 385

 taaatacgag caaaactttc ctg 1287

<210> 414

<211> 388

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 414

Met Ala Glu Val Val His Tyr Gln Glu Asn Ala Gly Gln Ala Val Lys
 1 5 10 15

 Lys Ile Glu Gly Arg Ile Val Thr Pro His Gly Val Ile Asp Gly Phe
 20 25 30

 Leu Gln Leu Glu Asn Gly Ile Ile Thr Glu Leu Ser Gly Glu Pro Ala
 35 40 45

 Pro Lys Asn Ala Gly Phe His Pro Glu Leu Pro Thr Ile Val Pro Ser
 50 55 60

Phe Ile Asp Leu His Asn His Gly Gly Asn Gly Gly Ala Phe Pro Thr
 65 70 75 80
 Gly Thr Gln Asp Gln Ala Arg Asn Ala Ala Gln Tyr His Arg Glu His
 85 90 95
 Gly Thr Thr Val Met Leu Ala Ser Met Val Ser Ala Pro Ala Asp Ala
 100 105 110
 Leu Ala Ala Gln Val Glu Asn Leu Ile Pro Leu Cys Glu Glu Gly Leu
 115 120 125
 Leu Cys Gly Ile His Leu Glu Gly Pro Phe Ile Asn Ala Cys Arg Cys
 130 135 140
 Gly Ala Gln Asn Pro Asp Phe Ile Phe Pro Gly Asn Pro Thr Asp Leu
 145 150 155 160
 Ala Gln Val Ile His Ala Gly Lys Gly Trp Ile Lys Ser Ile Thr Val
 165 170 175
 Ala Pro Glu Thr Asp Asn Leu Thr Glu Leu Leu Asp Leu Cys Ala Ala
 180 185 190
 His His Ile Ile Ala Ser Phe Gly His Thr Asp Ala Asp Phe Asp Thr
 195 200 205
 Thr Thr Ser Ala Ile Ala Leu Ala Lys Glu Lys Asn Val Thr Val Thr
 210 215 220
 Ala Thr His Leu Phe Asn Ala Met Pro Pro Leu His His Arg Asp Pro
 225 230 235 240
 Gly Ser Val Gly Ala Leu Leu Ala Ala Ala Arg Ala Gly Asp Ala Tyr
 245 250 255
 Val Glu Leu Ile Ala Asp Gly Val His Leu Ala Asp Gly Thr Val Asp
 260 265 270
 Leu Ala Arg Ser Asn Asn Ala Phe Phe Ile Thr Asp Ala Met Glu Ala
 275 280 285
 Ala Gly Met Pro Asp Gly Glu Tyr Ile Leu Gly Val Leu Asn Val Thr
 290 295 300
 Val Thr Asp Gly Val Ala Arg Leu Arg Asp Gly Gly Ala Ile Ala Gly
 305 310 315 320
 Gly Thr Ser Thr Leu Ala Ser Gln Phe Val His His Val Arg Arg Gly
 325 330 335
 Met Thr Leu Ile Asp Ala Thr Leu His Thr Ser Thr Val Ala Ala Lys
 340 345 350
 Ile Leu Gly Leu Ser Asp His Glu Ile Val Lys Ser Asn Pro Val Asn
 355 360 365
 Phe Val Val Phe Asp Ser Asn Gly Gln Leu Gln Gln Val His Leu Asp
 370 375 380
 His Gln Val Ile

Ala Gly Lys Gly Trp Ile Lys Ser Ile Thr Val Ala Pro Glu Thr Asp	
170 175 180	
aat ctt act gag ctt ctc gat ctc tgc gca gcg cac cac atc att gct	691
Asn Leu Thr Glu Leu Leu Asp Leu Cys Ala Ala His His Ile Ile Ala	
185 190 195	
tcc ttc ggg cac act gat gca gat ttt gat acc act acc agc gca att	739
Ser Phe Gly His Thr Asp Ala Asp Phe Asp Thr Thr Thr Ser Ala Ile	
200 205 210	
gcc ttg gct aaa gag aaa aat gtg acg gtc acg gct acg cat ttg ttc	787
Ala Leu Ala Lys Glu Lys Asn Val Thr Val Thr Ala Thr His Leu Phe	
215 220 225	
aat gcg atg cct ccg ctg cat cat agg gat ccc ggc agc gtg ggc gct	835
Asn Ala Met Pro Pro Leu His His Arg Asp Pro Gly Ser Val Gly Ala	
230 235 240 245	
ttg ctt gct gcg gca cgt gcc ggg gac gca tat gtt gag ttg atc gcc	883
Leu Leu Ala Ala Ala Arg Ala Gly Asp Ala Tyr Val Glu Leu Ile Ala	
250 255 260	
gac ggc gtg cat ttg gcc gat gga acg gtc gat cta gct cgt tcc aac	931
Asp Gly Val His Leu Ala Asp Gly Thr Val Asp Leu Ala Arg Ser Asn	
265 270 275	
aac gcc ttt ttc atc acg gac gcc atg gaa gcc gcc gga atg cca gac	979
Asn Ala Phe Phe Ile Thr Asp Ala Met Glu Ala Ala Gly Met Pro Asp	
280 285 290	
ggt gag tac att ttg ggc gtt ttg aac gtc acc gtc acc gat ggc gtc	1027
Gly Glu Tyr Ile Leu Gly Val Leu Asn Val Thr Val Thr Asp Gly Val	
295 300 305	
gcc cgt ctg cgc gat ggc ggc gcc atc gcc ggg ggt acc agc aca cta	1075
Ala Arg Leu Arg Asp Gly Gly Ala Ile Ala Gly Gly Thr Ser Thr Leu	
310 315 320 325	
gcg agt cag ttc gtg cac cac gtg cgc agg ggt atg acg ctt atc gac	1123
Ala Ser Gln Phe Val His His Val Arg Arg Gly Met Thr Leu Ile Asp	
330 335 340	
gcg acc ctc cac acc tca acc gtc gcc gcc aaa att ctc gga ctt agc	1171
Ala Thr Leu His Thr Ser Thr Val Ala Ala Lys Ile Leu Gly Leu Ser	
345 350 355	
gat cac gaa atc gtt aaa tcc aac cct gta aat ttt gtg gtc ttt gac	1219
Asp His Glu Ile Val Lys Ser Asn Pro Val Asn Phe Val Val Phe Asp	
360 365 370	
tca aac ggc cag tta caa cag gtc cat tta gac cat caa gta att	1264
Ser Asn Gly Gln Leu Gln Gln Val His Leu Asp His Gln Val Ile	
375 380 385	
taaatacgag caaaactttc ctg	1287

<210> 416

<211> 388

<212> PRT

<213> Corynebacterium glutamicum

<400> 416

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Met Ala Glu Val Val His Tyr Gln Glu Asn Ala Gly Gln Ala Val Lys
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Lys Ile Glu Gly Arg Ile Val Thr Pro His Gly Val Ile Asp Gly Phe
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Leu Gln Leu Glu Asn Gly Ile Ile Thr Glu Leu Ser Gly Glu Pro Ala
      35              40              45

Pro Lys Asn Ala Gly Phe His Pro Glu Leu Pro Thr Ile Val Pro Ser
      50              55              60

Phe Ile Asp Leu His Asn His Gly Gly Asn Gly Gly Ala Phe Pro Thr
      65              70              75              80

Gly Thr Gln Asp Gln Ala Arg Asn Ala Ala Gln Tyr His Arg Glu His
              85              90              95

Gly Thr Thr Val Met Leu Ala Ser Met Val Ser Ala Pro Ala Asp Ala
      100              105              110

Leu Ala Ala Gln Val Glu Asn Leu Ile Pro Leu Cys Glu Glu Gly Leu
      115              120              125

Leu Cys Gly Ile His Leu Glu Gly Pro Phe Ile Asn Ala Cys Arg Cys
      130              135              140

Gly Ala Gln Asn Pro Asp Phe Ile Phe Pro Gly Asn Pro Thr Asp Leu
      145              150              155              160

Ala Gln Val Ile His Ala Gly Lys Gly Trp Ile Lys Ser Ile Thr Val
              165              170              175

Ala Pro Glu Thr Asp Asn Leu Thr Glu Leu Leu Asp Leu Cys Ala Ala
      180              185              190

His His Ile Ile Ala Ser Phe Gly His Thr Asp Ala Asp Phe Asp Thr
      195              200              205

Thr Thr Ser Ala Ile Ala Leu Ala Lys Glu Lys Asn Val Thr Val Thr
      210              215              220

Ala Thr His Leu Phe Asn Ala Met Pro Pro Leu His His Arg Asp Pro
      225              230              235              240

Gly Ser Val Gly Ala Leu Leu Ala Ala Ala Arg Ala Gly Asp Ala Tyr
              245              250              255

Val Glu Leu Ile Ala Asp Gly Val His Leu Ala Asp Gly Thr Val Asp
      260              265              270

Leu Ala Arg Ser Asn Asn Ala Phe Phe Ile Thr Asp Ala Met Glu Ala
      275              280              285

Ala Gly Met Pro Asp Gly Glu Tyr Ile Leu Gly Val Leu Asn Val Thr
      290              295              300

Val Thr Asp Gly Val Ala Arg Leu Arg Asp Gly Gly Ala Ile Ala Gly

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305		310		315		320
Gly Thr Ser Thr	Leu Ala Ser Gln Phe Val His His Val Arg Arg Gly					
	325		330		335	
Met Thr Leu Ile Asp Ala Thr Leu His Thr Ser Thr Val Ala Ala Lys						
	340		345		350	
Ile Leu Gly Leu Ser Asp His Glu Ile Val Lys Ser Asn Pro Val Asn						
	355		360		365	
Phe Val Val Phe Asp Ser Asn Gly Gln Leu Gln Gln Val His Leu Asp						
	370		375		380	
His Gln Val Ile						
385						

<210> 417
 <211> 1584
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1561)
 <223> RXN01752

<400> 417
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ttggccgtca gatcgtggca gaacaacagg tggggaggtc	atg atg gaa caa gat	115
	Met Met Glu Gln Asp	
	1 5	
ctc agc tac cgt gaa att ctt ccc ctc aac gcg agt gag gag aag aaa		163
Leu Ser Tyr Arg Glu Ile Leu Pro Leu Asn Ala Ser Glu Glu Lys Lys		
	10 15 20	
aag gct gca ctg att gat gcc att gaa ggg tta agg gtg cgc gat ccg		211
Lys Ala Ala Leu Ile Asp Ala Ile Glu Gly Leu Arg Val Arg Asp Pro		
	25 30 35	
cta ctc tct gcc tcg att gca ttt act aga ggg cag aaa gtc gcc ttc		259
Leu Leu Ser Ala Ser Ile Ala Phe Thr Arg Gly Gln Lys Val Ala Phe		
	40 45 50	
att gct gtg gtg gtg ggc ttt atc ttg atg ctc att ttt gct cgg caa		307
Ile Ala Val Val Val Gly Phe Ile Leu Met Leu Ile Phe Ala Arg Gln		
	55 60 65	
gca gca ctt att gga ctg tca gca acg tgt acg ttc atg tac ctc att		355
Ala Ala Leu Ile Gly Leu Ser Ala Thr Cys Thr Phe Met Tyr Leu Ile		
	70 75 80 85	
aca ttg ttg gac aga ttt atc atg ttt tcc aga ggt atc cgc gcg gaa		403
Thr Leu Leu Asp Arg Phe Ile Met Phe Ser Arg Gly Ile Arg Ala Glu		
	90 95 100	
tcc atc atc cag gta tcg gat gaa gat gcg ctg gct ttc cct gag gac		451
Ser Ile Ile Gln Val Ser Asp Glu Asp Ala Leu Ala Phe Pro Glu Asp		

105					110					115						
aag	ctg	aaa	acc	tac	acg	gtg	ttg	gtg	ccc	gcc	tat	ggc	gaa	cct	gag	499
Lys	Leu	Lys	Thr	Tyr	Thr	Val	Leu	Val	Pro	Ala	Tyr	Gly	Glu	Pro	Glu	
		120					125					130				
gtg	att	gcg	cag	ctg	ctg	gca	tcc	atg	cac	gct	ttt	gat	tac	ccc	aag	547
Val	Ile	Ala	Gln	Leu	Leu	Ala	Ser	Met	His	Ala	Phe	Asp	Tyr	Pro	Lys	
		135				140					145					
cat	ctt	ctg	cag	gta	ttg	ctc	atg	ttg	gag	gaa	gat	gat	ctg	ccc	acg	595
His	Leu	Leu	Gln	Val	Leu	Leu	Met	Leu	Glu	Glu	Asp	Asp	Leu	Pro	Thr	
150					155					160					165	
atc	gcc	gcg	gca	gag	gca	gcg	gga	gtg	gat	cag	gtg	gca	acg	atc	att	643
Ile	Ala	Ala	Ala	Glu	Ala	Ala	Gly	Val	Asp	Gln	Val	Ala	Thr	Ile	Ile	
				170					175						180	
aag	gtg	ccg	cca	gcg	cag	ccc	cgc	acc	aag	ccg	aag	gcc	tgt	aac	tat	691
Lys	Val	Pro	Pro	Ala	Gln	Pro	Arg	Thr	Lys	Pro	Lys	Ala	Cys	Asn	Tyr	
			185					190					195			
gga	ttg	cac	ttt	gcc	acg	ggg	gaa	att	gtc	acg	atc	ttt	gac	gcg	gaa	739
Gly	Leu	His	Phe	Ala	Thr	Gly	Glu	Ile	Val	Thr	Ile	Phe	Asp	Ala	Glu	
		200					205					210				
gac	atg	cca	gat	ccc	ctc	caa	ctg	cgt	cgc	gtg	gtg	gtg	gca	ttt	gaa	787
Asp	Met	Pro	Asp	Pro	Leu	Gln	Leu	Arg	Arg	Val	Val	Val	Ala	Phe	Glu	
		215				220					225					
cgc	tcg	gct	tcc	aat	acg	gtg	tgc	gtc	cag	tca	agg	ttg	tcg	tat	cga	835
Arg	Ser	Ala	Ser	Asn	Thr	Val	Cys	Val	Gln	Ser	Arg	Leu	Ser	Tyr	Arg	
230					235					240					245	
aac	gcc	agg	cag	aat	ctg	cta	act	gcg	tgg	ttc	acc	att	gaa	tat	gac	883
Asn	Ala	Arg	Gln	Asn	Leu	Leu	Thr	Ala	Trp	Phe	Thr	Ile	Glu	Tyr	Asp	
				250					255					260		
gtg	tgg	ttt	aac	ttc	ctg	ctg	cca	ggc	gtc	atg	cgc	atg	aac	gca	cct	931
Val	Trp	Phe	Asn	Phe	Leu	Leu	Pro	Gly	Val	Met	Arg	Met	Asn	Ala	Pro	
			265					270					275			
gtc	cca	ttg	ggc	ggg	acc	tcc	aac	cat	ctg	ctc	acg	ggg	gtc	ctg	aaa	979
Val	Pro	Leu	Gly	Gly	Thr	Ser	Asn	His	Leu	Leu	Thr	Gly	Val	Leu	Lys	
		280					285					290				
gat	ctc	ggc	gcg	tgg	gat	cct	ttc	aat	gtc	aca	gaa	aat	gcc	gac	ctc	1027
Asp	Leu	Gly	Ala	Trp	Asp	Pro	Phe	Asn	Val	Thr	Glu	Asn	Ala	Asp	Leu	
		295				300					305					
ggc	gta	ccc	atc	gcg	gca	aaa	gga	tat	tcc	acc	gcg	gtg	ttg	gat	tcg	1075
Gly	Val	Pro	Ile	Ala	Ala	Lys	Gly	Tyr	Ser	Thr	Ala	Val	Leu	Asp	Ser	
310					315					320					325	
gtg	acg	tgg	gag	gaa	gca	aac	tcc	gac	acc	atc	aac	tgg	ttg	cgc	cag	1123
Val	Thr	Trp	Glu	Glu	Ala	Asn	Ser	Asp	Thr	Ile	Asn	Trp	Leu	Arg	Gln	
				330					335					340		
cgt	tct	cgc	tgg	tac	aag	ggc	tat	ctg	caa	aca	tgg	ctt	gtg	tat	atg	1171
Arg	Ser	Arg	Trp	Tyr	Lys	Gly	Tyr	Leu	Gln	Thr	Trp	Leu	Val	Tyr	Met	
			345					350					355			

cgc agg cca aag tgg tta gtc caa gag ctt ggc atc att cct gct gtg 1219
 Arg Arg Pro Lys Trp Leu Val Gln Glu Leu Gly Ile Ile Pro Ala Val
 360 365 370
 cgt ttt acc ttc ctc atg gca ggc acc ccg atc att gcg gtg ctc aat 1267
 Arg Phe Thr Phe Leu Met Ala Gly Thr Pro Ile Ile Ala Val Leu Asn
 375 380 385
 ctg ctc ttt tgg tac ttg tcg ctc acg tgg att ctg ggc cag ccc ggc 1315
 Leu Leu Phe Trp Tyr Leu Ser Leu Thr Trp Ile Leu Gly Gln Pro Gly
 390 395 400 405
 acc att gag cag atg ttc cca cct gcg gtg tac tac cca gcg ttg gtg 1363
 Thr Ile Glu Gln Met Phe Pro Pro Ala Val Tyr Tyr Pro Ala Leu Val
 410 415 420
 tgt ttg gtg gtg gcc aat gct gcg acc atc ttt atg aat ctc att ggc 1411
 Cys Leu Val Val Ala Asn Ala Ala Thr Ile Phe Met Asn Leu Ile Gly
 425 430 435
 tgc cgg gaa ggc cgc gac ccc ttg ctg ctc atc gcg gtt ctc acg ttc 1459
 Cys Arg Glu Gly Arg Asp Pro Leu Leu Leu Ile Ala Val Leu Thr Phe
 440 445 450
 ccg ctg tat tgg ctg ctc atg agc att gca gcg ttg aaa ggc acg tgg 1507
 Pro Leu Tyr Trp Leu Leu Met Ser Ile Ala Ala Leu Lys Gly Thr Trp
 455 460 465
 caa ttg atc acg cga cca tcc tat tgg gag aaa act gcc cac gga ttg 1555
 Gln Leu Ile Thr Arg Pro Ser Tyr Trp Glu Lys Thr Ala His Gly Leu
 470 475 480 485
 gag gcg taagcgggtgc ccatcggtcaa acc 1584
 Glu Ala

<210> 418

<211> 487

<212> PRT

<213> Corynebacterium glutamicum

<400> 418

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 20 25 30
 Arg Val Arg Asp Pro Leu Leu Ser Ala Ser Ile Ala Phe Thr Arg Gly
 35 40 45
 Gln Lys Val Ala Phe Ile Ala Val Val Val Gly Phe Ile Leu Met Leu
 50 55 60
 Ile Phe Ala Arg Gln Ala Ala Leu Ile Gly Leu Ser Ala Thr Cys Thr
 65 70 75 80
 Phe Met Tyr Leu Ile Thr Leu Leu Asp Arg Phe Ile Met Phe Ser Arg
 85 90 95

Gly Ile Arg Ala Glu Ser Ile Ile Gln Val Ser Asp Glu Asp Ala Leu
 100 105 110
 Ala Phe Pro Glu Asp Lys Leu Lys Thr Tyr Thr Val Leu Val Pro Ala
 115 120 125
 Tyr Gly Glu Pro Glu Val Ile Ala Gln Leu Leu Ala Ser Met His Ala
 130 135 140
 Phe Asp Tyr Pro Lys His Leu Leu Gln Val Leu Leu Met Leu Glu Glu
 145 150 155 160
 Asp Asp Leu Pro Thr Ile Ala Ala Ala Glu Ala Ala Gly Val Asp Gln
 165 170 175
 Val Ala Thr Ile Ile Lys Val Pro Pro Ala Gln Pro Arg Thr Lys Pro
 180 185 190
 Lys Ala Cys Asn Tyr Gly Leu His Phe Ala Thr Gly Glu Ile Val Thr
 195 200 205
 Ile Phe Asp Ala Glu Asp Met Pro Asp Pro Leu Gln Leu Arg Arg Val
 210 215 220
 Val Val Ala Phe Glu Arg Ser Ala Ser Asn Thr Val Cys Val Gln Ser
 225 230 235 240
 Arg Leu Ser Tyr Arg Asn Ala Arg Gln Asn Leu Leu Thr Ala Trp Phe
 245 250 255
 Thr Ile Glu Tyr Asp Val Trp Phe Asn Phe Leu Leu Pro Gly Val Met
 260 265 270
 Arg Met Asn Ala Pro Val Pro Leu Gly Gly Thr Ser Asn His Leu Leu
 275 280 285
 Thr Gly Val Leu Lys Asp Leu Gly Ala Trp Asp Pro Phe Asn Val Thr
 290 295 300
 Glu Asn Ala Asp Leu Gly Val Pro Ile Ala Ala Lys Gly Tyr Ser Thr
 305 310 315 320
 Ala Val Leu Asp Ser Val Thr Trp Glu Glu Ala Asn Ser Asp Thr Ile
 325 330 335
 Asn Trp Leu Arg Gln Arg Ser Arg Trp Tyr Lys Gly Tyr Leu Gln Thr
 340 345 350
 Trp Leu Val Tyr Met Arg Arg Pro Lys Trp Leu Val Gln Glu Leu Gly
 355 360 365
 Ile Ile Pro Ala Val Arg Phe Thr Phe Leu Met Ala Gly Thr Pro Ile
 370 375 380
 Ile Ala Val Leu Asn Leu Leu Phe Trp Tyr Leu Ser Leu Thr Trp Ile
 385 390 395 400
 Leu Gly Gln Pro Gly Thr Ile Glu Gln Met Phe Pro Pro Ala Val Tyr
 405 410 415

Tyr Pro Ala Leu Val Cys Leu Val Val Ala Asn Ala Ala Thr Ile Phe
 420 425 430
 Met Asn Leu Ile Gly Cys Arg Glu Gly Arg Asp Pro Leu Leu Leu Ile
 435 440 445
 Ala Val Leu Thr Phe Pro Leu Tyr Trp Leu Leu Met Ser Ile Ala Ala
 450 455 460
 Leu Lys Gly Thr Trp Gln Leu Ile Thr Arg Pro Ser Tyr Trp Glu Lys
 465 470 475 480
 Thr Ala His Gly Leu Glu Ala
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<210> 419
 <211> 689
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (19)..(666)
 <223> FRXA01839

<400> 419
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 Met Arg Met Asn Ala Pro Val Pro Leu Gly Gly
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 acc tcc aac cat ctg ctc acg ggt gtc ctg aaa gat ctc ggc gcg tgg 99
 Thr Ser Asn His Leu Leu Thr Gly Val Leu Lys Asp Leu Gly Ala Trp
 15 20 25
 gat cct ttc aat gtc aca gaa gat gcg gac ctc ggc gta cgc atc gcg 147
 Asp Pro Phe Asn Val Thr Glu Asp Ala Asp Leu Gly Val Arg Ile Ala
 30 35 40
 gca aag gga tat tcc acc gcg gtg ttg gat tcg gtg acg tgg gag gaa 195
 Ala Lys Gly Tyr Ser Thr Ala Val Leu Asp Ser Val Thr Trp Glu Glu
 45 50 55
 gca aac tcc gac acc atc aac tgg ttg cgc cag cgt tct cgc tgg tac 243
 Ala Asn Ser Asp Thr Ile Asn Trp Leu Arg Gln Arg Ser Arg Trp Tyr
 60 65 70 75
 aag ggc tat ctg caa aca tgg ctt gtg tat atg cgc agg cca aag tgg 291
 Lys Gly Tyr Leu Gln Thr Trp Leu Val Tyr Met Arg Arg Pro Lys Trp
 80 85 90
 tta gtc caa gag ctt ggc atc att cct gct gtg cgt ttt acc ttc ctc 339
 Leu Val Gln Glu Leu Gly Ile Ile Pro Ala Val Arg Phe Thr Phe Leu
 95 100 105
 atg gca ggc acc ccg atc att gcg gtg ctc aat ctg ctc ttt tgg tac 387
 Met Ala Gly Thr Pro Ile Ile Ala Val Leu Asn Leu Leu Phe Trp Tyr
 110 115 120
 ttg tcg ctc acg tgg att ctg ggc cag ccc ggc acc att gag cag atg 435
 Leu Ser Leu Thr Trp Ile Leu Gly Gln Pro Gly Thr Ile Glu Gln Met

125	130	135	
ttc cca cct gcg gtg tac	tac cca gcg ttg gtg	tgt ttg gtg gtg gcc	483
Phe Pro Pro Ala Val Tyr	Tyr Pro Ala Leu Val Cys	Leu Val Val Ala	
140	145	150	155
aat gct gcg acc atc ttt atg	aat ctc att ggc tgc	cgg gaa ggc cgc	531
Asn Ala Ala Thr	Ile Phe Met Asn Leu	Ile Gly Cys Arg Glu Gly Arg	
160	165	170	
gac ccc ttg ctg ctc atc gcg	gtt ctc acg ttc ccg	ctg tat tgg ctg	579
Asp Pro Leu Leu Leu Ile	Ala Val Leu Thr Phe	Pro Leu Tyr Trp Leu	
175	180	185	
ctc atg agc att gca gcg	ttg aaa ggc acg tgg	caa ttg atc acg cga	627
Leu Met Ser Ile Ala Ala	Leu Lys Gly Thr Trp	Gln Leu Ile Thr Arg	
190	195	200	
cca tcc tat tgg gag aaa act	gcc cac gga ttg gag	gcg taagcgggtgc	676
Pro Ser Tyr Trp Glu Lys	Thr Ala His Gly Leu	Glu Ala	
205	210	215	
ccatcggtcaa acc			689
<210> 420			
<211> 216			
<212> PRT			
<213> Corynebacterium glutamicum			
<400> 420			
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Leu Thr Gly Val Leu Lys Asp	Leu Gly Ala Trp Asp	Pro Phe Asn Val	
20	25	30	
Thr Glu Asp Ala Asp Leu Gly	Val Arg Ile Ala Ala	Lys Gly Tyr Ser	
35	40	45	
Thr Ala Val Leu Asp Ser Val	Thr Trp Glu Glu Ala	Asn Ser Asp Thr	
50	55	60	
Ile Asn Trp Leu Arg Gln Arg	Ser Arg Trp Tyr Lys	Gly Tyr Leu Gln	
65	70	75	80
Thr Trp Leu Val Tyr Met Arg	Arg Pro Lys Trp Leu	Val Gln Glu Leu	
85	90	95	
Gly Ile Ile Pro Ala Val Arg	Phe Thr Phe Leu Met	Ala Gly Thr Pro	
100	105	110	
Ile Ile Ala Val Leu Asn Leu	Leu Phe Trp Tyr Leu	Ser Leu Thr Trp	
115	120	125	
Ile Leu Gly Gln Pro Gly Thr	Ile Glu Gln Met Phe	Pro Pro Ala Val	
130	135	140	
Tyr Tyr Pro Ala Leu Val Cys	Leu Val Val Ala	Asn Ala Ala Thr Ile	
145	150	155	160

Phe	Met	Asn	Leu	Ile	Gly	Cys	Arg	Glu	Gly	Arg	Asp	Pro	Leu	Leu	Leu
				165					170					175	
Ile	Ala	Val	Leu	Thr	Phe	Pro	Leu	Tyr	Trp	Leu	Leu	Met	Ser	Ile	Ala
			180					185					190		
Ala	Leu	Lys	Gly	Thr	Trp	Gln	Leu	Ile	Thr	Arg	Pro	Ser	Tyr	Trp	Glu
		195					200					205			
Lys	Thr	Ala	His	Gly	Leu	Glu	Ala								
	210					215									

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<211> 1050
<212> DNA
<213> Corynebacterium glutamicum
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<220>  
<221> CDS  
<222> (101)..(1027)  
<223> RXA01859
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ctcgcagacga accaaaccgc tacctggggg taggaagaat atg aaa aag aag agc															115	
												Met	Lys	Lys	Lys	Ser
												1				5
ttt cca atc gca aga gtc atc ggt atc ggc gtc ctt ggc atc gcc ggg															163	
Phe	Pro	Ile	Ala	Arg	Val	Ile	Gly	Ile	Gly	Val	Leu	Gly	Ile	Ala	Gly	
				10					15					20		
atg gga ata ttg ttg cta tgg ctt gca gtt acc ctg tct gat cca gca															211	
Met	Gly	Ile	Leu	Leu	Leu	Trp	Leu	Ala	Val	Thr	Leu	Ser	Asp	Pro	Ala	
			25					30					35			
tca ccg ggt gcc aaa gaa acc gaa gtc ttt gat agg tgg aaa gtg ctc															259	
Ser	Pro	Gly	Ala	Lys	Glu	Thr	Glu	Val	Phe	Asp	Arg	Trp	Lys	Val	Leu	
		40					45					50				
ttt gat gac tat att cca cca gtc agg gta ttg gtt gct gcg att atc															307	
Phe	Asp	Asp	Tyr	Ile	Pro	Pro	Val	Arg	Val	Leu	Val	Ala	Ala	Ile	Ile	
	55					60					65					
gtt gca tta att ttc gtc ttt atc gct gcc aca gtg gaa cga acc gta															355	
Val	Ala	Leu	Ile	Phe	Val	Phe	Ile	Ala	Ala	Thr	Val	Glu	Arg	Thr	Val	
70					75					80				85		
acc aac cgc tac cga agc tcc gta gac ggc gaa aga gtg cca tta gcg															403	
Thr	Asn	Arg	Tyr	Arg	Ser	Ser	Val	Asp	Gly	Glu	Arg	Val	Pro	Leu	Ala	
				90					95					100		
ccg aag att gtg atg gca gaa acc cga ggg gta ttt cat gga ccg att															451	
Pro	Lys	Ile	Val	Met	Ala	Glu	Thr	Arg	Gly	Val	Phe	His	Gly	Pro	Ile	
			105					110					115			
acc att aac gtg ctc gtg cca gca cac aat gag gcg gaa aga att act															499	
Thr	Ile	Asn	Val	Leu	Val	Pro	Ala	His	Asn	Glu	Ala	Glu	Arg	Ile	Thr	
		120					125					130				

gga aca att cag gca ttg aaa tca caa cat gag cct cca gaa cgc atc 547
 Gly Thr Ile Gln Ala Leu Lys Ser Gln His Glu Pro Pro Glu Arg Ile
 135 140 145
 gtt gta gtt gcc gat aat tgc act gat gaa act acg gaa tta gcc cgt 595
 Val Val Val Ala Asp Asn Cys Thr Asp Glu Thr Thr Glu Leu Ala Arg
 150 155 160 165
 gct gag gga gtg gag gtc ttg gaa aca gtc aat aat aag ttt aag aag 643
 Ala Glu Gly Val Glu Val Leu Glu Thr Val Asn Asn Lys Phe Lys Lys
 170 175 180
 gcc gga gga ctc aat cag gct ttg agc cgg atg ctt ccc aca ttg ggg 691
 Ala Gly Gly Leu Asn Gln Ala Leu Ser Arg Met Leu Pro Thr Leu Gly
 185 190 195
 gag aat gac att gtg atg atc gtt gac gct gat aca gca ctt gat caa 739
 Glu Asn Asp Ile Val Met Ile Val Asp Ala Asp Thr Ala Leu Asp Gln
 200 205 210
 ggt ttc ctc aag gaa gca cgg cgc cgc ttt gag tct gat cgc gct cta 787
 Gly Phe Leu Lys Glu Ala Arg Arg Arg Phe Glu Ser Asp Arg Ala Leu
 215 220 225
 atg gcc gtg ggc gga ttg ttc tac ggt gag tca ggc tcc gga tgg ctt 835
 Met Ala Val Gly Gly Leu Phe Tyr Gly Glu Ser Gly Ser Gly Trp Leu
 230 235 240 245
 ggc caa tat cag cgc aac gaa tac acc cgt tat agc cgt gac atc tat 883
 Gly Gln Tyr Gln Arg Asn Glu Tyr Thr Arg Tyr Ser Arg Asp Ile Tyr
 250 255 260
 cga cgc cgc gga cgt gtg ttt gtt ttg act gga aca gcg tcg gct ttt 931
 Arg Arg Arg Gly Arg Val Phe Val Leu Thr Gly Thr Ala Ser Ala Phe
 265 270 275
 cgg cca cgc ggc ctg cgg aca gta gcg gaa tca cgc ggg aca ttg atc 979
 Arg Pro Arg Gly Leu Arg Thr Val Ala Glu Ser Arg Gly Thr Leu Ile
 280 285 290
 ccc gga cgt aaa gcc gat gtt tat gac acc gcg ggc gtt gac cga aga 1027
 Pro Gly Arg Lys Ala Asp Val Tyr Asp Thr Ala Gly Val Asp Arg Arg
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 taatgagttg accctggctt tga 1050

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<211> 309

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 422

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Leu Gly Ile Ala Gly Met Gly Ile Leu Leu Leu Trp Leu Ala Val Thr
 20 25 30

Leu Ser Asp Pro Ala Ser Pro Gly Ala Lys Glu Thr Glu Val Phe Asp

35	40	45
Arg Trp Lys Val Leu Phe Asp Asp Tyr Ile Pro Pro Val Arg Val Leu		
50	55	60
Val Ala Ala Ile Ile Val Ala Leu Ile Phe Val Phe Ile Ala Ala Thr		
65	70	75 80
Val Glu Arg Thr Val Thr Asn Arg Tyr Arg Ser Ser Val Asp Gly Glu		
	85	90 95
Arg Val Pro Leu Ala Pro Lys Ile Val Met Ala Glu Thr Arg Gly Val		
	100	105 110
Phe His Gly Pro Ile Thr Ile Asn Val Leu Val Pro Ala His Asn Glu		
	115	120 125
Ala Glu Arg Ile Thr Gly Thr Ile Gln Ala Leu Lys Ser Gln His Glu		
	130	135 140
Pro Pro Glu Arg Ile Val Val Val Ala Asp Asn Cys Thr Asp Glu Thr		
145	150	155 160
Thr Glu Leu Ala Arg Ala Glu Gly Val Glu Val Leu Glu Thr Val Asn		
	165	170 175
Asn Lys Phe Lys Lys Ala Gly Gly Leu Asn Gln Ala Leu Ser Arg Met		
	180	185 190
Leu Pro Thr Leu Gly Glu Asn Asp Ile Val Met Ile Val Asp Ala Asp		
	195	200 205
Thr Ala Leu Asp Gln Gly Phe Leu Lys Glu Ala Arg Arg Arg Phe Glu		
	210	215 220
Ser Asp Arg Ala Leu Met Ala Val Gly Gly Leu Phe Tyr Gly Glu Ser		
225	230	235 240
Gly Ser Gly Trp Leu Gly Gln Tyr Gln Arg Asn Glu Tyr Thr Arg Tyr		
	245	250 255
Ser Arg Asp Ile Tyr Arg Arg Arg Gly Arg Val Phe Val Leu Thr Gly		
	260	265 270
Thr Ala Ser Ala Phe Arg Pro Arg Gly Leu Arg Thr Val Ala Glu Ser		
	275	280 285
Arg Gly Thr Leu Ile Pro Gly Arg Lys Ala Asp Val Tyr Asp Thr Ala		
	290	295 300
Gly Val Asp Arg Arg		
305		

<210> 423

<211> 882

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(859)

<223> RXA00042

<400> 423

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atacgagcaa aactttcctg ataataaaag gagtccgacc atg gac atc atc atc 115
                                         Met Asp Ile Ile Ile
                                         1           5

tgc aaa gac gag caa gaa gtc ggc aaa gca gcg gca gcc ctg atc gca 163
Cys Lys Asp Glu Gln Glu Val Gly Lys Ala Ala Ala Ala Leu Ile Ala
              10              15              20

ccc ttc gca act aag ggc gga acc ttg ggg ctt gca act gga tcg tca 211
Pro Phe Ala Thr Lys Gly Gly Thr Leu Gly Leu Ala Thr Gly Ser Ser
              25              30              35

cct ttg agc acc tac caa gag ctc att cgc atg tat gaa gct ggg gaa 259
Pro Leu Ser Thr Tyr Gln Glu Leu Ile Arg Met Tyr Glu Ala Gly Glu
              40              45              50

gtg tca ttc aag aac tgc aag gca ttc ttg ttg gat gaa tac gtg gga 307
Val Ser Phe Lys Asn Cys Lys Ala Phe Leu Leu Asp Glu Tyr Val Gly
              55              60              65

tta acg cgc gac gat gaa aac agc tac ttc aaa acc att cgt aaa gag 355
Leu Thr Arg Asp Asp Glu Asn Ser Tyr Phe Lys Thr Ile Arg Lys Glu
              70              75              80              85

ttc act gac cac atc gac atc gtt gat gaa gag gtc tac agc cca gat 403
Phe Thr Asp His Ile Asp Ile Val Asp Glu Glu Val Tyr Ser Pro Asp
              90              95              100

ggg gca aac cct gat cca tac gaa gca gct gca gag tat gag gca aag 451
Gly Ala Asn Pro Asp Pro Tyr Glu Ala Ala Ala Glu Tyr Glu Ala Lys
              105              110              115

atc gct gca gaa tcc gtt gat gtt caa atc ctt ggc atc ggc gga aac 499
Ile Ala Ala Glu Ser Val Asp Val Gln Ile Leu Gly Ile Gly Gly Asn
              120              125              130

ggc cac atc gct ttc aat gag cca tca tct tct ctg tca gga ctg aca 547
Gly His Ile Ala Phe Asn Glu Pro Ser Ser Ser Leu Ser Gly Leu Thr
              135              140              145

aag gtc cag gcg ctg cac cct aaa act gtg gag gac aac gct cga ttc 595
Lys Val Gln Ala Leu His Pro Lys Thr Val Glu Asp Asn Ala Arg Phe
              150              155              160              165

ttc aac acc atc gaa gag gtc cca acc cac gcc ctg acc cag ggt ttg 643
Phe Asn Thr Ile Glu Glu Val Pro Thr His Ala Leu Thr Gln Gly Leu
              170              175              180

ggc act ttg tcc cgc gcg caa aac atc gtg ttg gtg gca act ggt gaa 691
Gly Thr Leu Ser Arg Ala Gln Asn Ile Val Leu Val Ala Thr Gly Glu
              185              190              195

gga aaa gcc gac gcc atc cgc gga act gtg gaa ggc cca ctg acc gcc 739
Gly Lys Ala Asp Ala Ile Arg Gly Thr Val Glu Gly Pro Leu Thr Ala
              200              205              210

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atg tgc cca ggt tcc atc ctg cag atg cac aac aat gcc acc atc atc 787
 Met Cys Pro Gly Ser Ile Leu Gln Met His Asn Asn Ala Thr Ile Ile
 215 220 225

gtt gat gaa gca gca gca tcc aag ctg gaa aac gct gat cac tac cgt 835
 Val Asp Glu Ala Ala Ala Ser Lys Leu Glu Asn Ala Asp His Tyr Arg
 230 235 240 245

ctc atg gag caa tta aag ctg cgc tagaaacaaa aaggaaagta gtg 882
 Leu Met Glu Gln Leu Lys Leu Arg
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<213> Corynebacterium glutamicum

<400> 424

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 20 25 30

Ala Thr Gly Ser Ser Pro Leu Ser Thr Tyr Gln Glu Leu Ile Arg Met
 35 40 45

Tyr Glu Ala Gly Glu Val Ser Phe Lys Asn Cys Lys Ala Phe Leu Leu
 50 55 60

Asp Glu Tyr Val Gly Leu Thr Arg Asp Asp Glu Asn Ser Tyr Phe Lys
 65 70 75 80

Thr Ile Arg Lys Glu Phe Thr Asp His Ile Asp Ile Val Asp Glu Glu
 85 90 95

Val Tyr Ser Pro Asp Gly Ala Asn Pro Asp Pro Tyr Glu Ala Ala Ala
 100 105 110

Glu Tyr Glu Ala Lys Ile Ala Ala Glu Ser Val Asp Val Gln Ile Leu
 115 120 125

Gly Ile Gly Gly Asn Gly His Ile Ala Phe Asn Glu Pro Ser Ser Ser
 130 135 140

Leu Ser Gly Leu Thr Lys Val Gln Ala Leu His Pro Lys Thr Val Glu
 145 150 155 160

Asp Asn Ala Arg Phe Phe Asn Thr Ile Glu Glu Val Pro Thr His Ala
 165 170 175

Leu Thr Gln Gly Leu Gly Thr Leu Ser Arg Ala Gln Asn Ile Val Leu
 180 185 190

Val Ala Thr Gly Glu Gly Lys Ala Asp Ala Ile Arg Gly Thr Val Glu
 195 200 205

Gly Pro Leu Thr Ala Met Cys Pro Gly Ser Ile Leu Gln Met His Asn
 210 215 220

gca aac ggt gac ctc acc ctt gct atg cag ctg acc ggt cag cgc ctt	595
Ala Asn Gly Asp Leu Thr Leu Ala Met Gln Leu Thr Gly Gln Arg Leu	
150 155 160 165	
gag ggt gct ttc acc ctg cta gct att cat gct gat cac gat gac cgc	643
Glu Gly Ala Phe Thr Leu Leu Ala Ile His Ala Asp His Asp Asp Arg	
170 175 180	
atc gtt gca gct cgt cgt aac tct cct ttg gtt atc ggc gtc ggc gag	691
Ile Val Ala Ala Arg Arg Asn Ser Pro Leu Val Ile Gly Val Gly Glu	
185 190 195	
ggc gag aac ttc ctc gga tct gac gtt tct ggc ttt att gat tac acc	739
Gly Glu Asn Phe Leu Gly Ser Asp Val Ser Gly Phe Ile Asp Tyr Thr	
200 205 210	
cgc aag gct gta gag ctg gct aat gac cag gtt gtt acc atc acc gct	787
Arg Lys Ala Val Glu Leu Ala Asn Asp Gln Val Val Thr Ile Thr Ala	
215 220 225	
gat gat tac gcc atc acc aac ttt gat gga tca gaa gca gtt ggc aag	835
Asp Asp Tyr Ala Ile Thr Asn Phe Asp Gly Ser Glu Ala Val Gly Lys	
230 235 240 245	
cct ttc gac gtg gag tgg gac gct gca gct gct gaa aag ggt ggc ttc	883
Pro Phe Asp Val Glu Trp Asp Ala Ala Ala Glu Lys Gly Gly Phe	
250 255 260	
ggt tcc ttc atg gag aag gaa atc cac gat cag cca gca gct gtt cgc	931
Gly Ser Phe Met Glu Lys Glu Ile His Asp Gln Pro Ala Ala Val Arg	
265 270 275	
gat acc ctg atg ggc cgt ctt gat gaa gat ggc aag ctc gtt ctt gat	979
Asp Thr Leu Met Gly Arg Leu Asp Glu Asp Gly Lys Leu Val Leu Asp	
280 285 290	
gag ctg cgc atc gat gaa gct att ctg cgt agt gtc gac aag atc gtc	1027
Glu Leu Arg Ile Asp Glu Ala Ile Leu Arg Ser Val Asp Lys Ile Val	
295 300 305	
att gtt gct tgt ggt act gca gct tat gca ggc cag gtt gct cgt tac	1075
Ile Val Ala Cys Gly Thr Ala Ala Tyr Ala Gly Gln Val Ala Arg Tyr	
310 315 320 325	
gcc att gag cac tgg tgc cgc atc cca acc gag gtg gag ctg gct cac	1123
Ala Ile Glu His Trp Cys Arg Ile Pro Thr Glu Val Glu Leu Ala His	
330 335 340	
gag ttc cgt tac cgc gac cca atc ctc aac gag aag acc ctt gtt gtg	1171
Glu Phe Arg Tyr Arg Asp Pro Ile Leu Asn Glu Lys Thr Leu Val Val	
345 350 355	
gca ttg tcc cag tcc ggc gag acc atg gat acc ctc atg gct gtt cgc	1219
Ala Leu Ser Gln Ser Gly Glu Thr Met Asp Thr Leu Met Ala Val Arg	
360 365 370	
cac gca cgt gag cag ggt gcc aag gtt gtt gct att tgt aac act gtt	1267
His Ala Arg Glu Gln Gly Ala Lys Val Val Ala Ile Cys Asn Thr Val	
375 380 385	
gga tcc act ctt cca cgt gaa gca gat gcg tcc ctg tac acc tac gct	1315

Gly 390	Ser	Thr	Leu	Pro	Arg 395	Glu	Ala	Asp	Ala	Ser 400	Leu	Tyr	Thr	Tyr	Ala 405	
ggc	cct	gag	atc	gct	gtg	gcg	tcc	acc	aag	gcg	ttc	ttg	gct	cag	atc	1363
Gly	Pro	Glu	Ile	Ala 410	Val	Ala	Ser	Thr	Lys 415	Ala	Phe	Leu	Ala	Gln	Ile 420	
act	gct	tct	tac	ttg	ctt	ggc	ctg	tac	ttg	gct	cag	ctg	cgc	ggc	aac	1411
Thr	Ala	Ser	Tyr 425	Leu	Leu	Gly	Leu	Tyr 430	Leu	Ala	Gln	Leu	Arg	Gly	Asn 435	
aag	ttc	gct	gat	gag	gtt	tct	tcc	att	ctg	gac	agc	ctg	cgt	gag	atg	1459
Lys	Phe	Ala 440	Asp	Glu	Val	Ser	Ser 445	Ile	Leu	Asp	Ser	Leu	Arg	Glu	Met 450	
cct	gag	aag	att	cag	cag	gtc	atc	gat	gca	gaa	gag	cag	atc	aag	aag	1507
Pro	Glu	Lys 455	Ile	Gln	Gln	Val 460	Ile	Asp	Ala	Glu	Glu 465	Gln	Ile	Lys	Lys	
ctt	ggc	caa	gat	atg	gca	gat	gct	aag	tct	gtg	ctg	ttc	ctg	ggc	cgc	1555
Leu 470	Gly	Gln	Asp	Met	Ala 475	Asp	Ala	Lys	Ser	Val 480	Leu	Phe	Leu	Gly	Arg 485	
cac	gtt	ggt	ttc	cca	gtt	gcg	ctt	gag	ggt	gcg	ttg	aag	ctc	aag	gag	1603
His	Val	Gly	Phe 490	Pro	Val	Ala	Leu	Glu	Gly 495	Ala	Leu	Lys	Leu	Lys	Glu 500	
atc	gca	tac	ctg	cac	gct	gaa	ggt	ttc	gct	gca	ggc	gag	ctc	aag	cac	1651
Ile	Ala	Tyr 505	Leu	His	Ala	Glu	Gly	Phe 510	Ala	Ala	Gly	Glu	Leu	Lys	His 515	
ggc	cca	att	gct	ttg	gtt	gag	gaa	ggc	cag	ccg	atc	ttc	gtt	atc	gtg	1699
Gly	Pro	Ile 520	Ala	Leu	Val	Glu	Glu 525	Gly	Gln	Pro	Ile	Phe 530	Val	Ile	Val	
cct	tca	cct	cgt	ggt	cgc	gat	tcc	ctg	cac	tcc	aag	gtt	gtc	tcc	aac	1747
Pro	Ser	Pro	Arg	Gly	Arg	Asp 540	Ser	Leu	His	Ser	Lys 545	Val	Val	Ser	Asn	
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Ile 550	Gln	Glu	Ile	Arg	Ala 555	Arg	Gly	Ala	Val	Thr 560	Ile	Val	Ile	Ala	Glu 565	
gaa	ggc	gat	gag	gct	gtc	aac	gat	tac	gcc	aac	ttc	atc	atc	cgc	att	1843
Glu	Gly	Asp	Glu	Ala 570	Val	Asn	Asp	Tyr	Ala 575	Asn	Phe	Ile	Ile	Arg	Ile 580	
cct	cag	gcc	cca	acc	ctg	atg	cag	cct	ctg	ctg	tcc	acc	gtg	cct	ctg	1891
Pro	Gln	Ala 585	Pro	Thr	Leu	Met	Gln	Pro 590	Leu	Leu	Ser	Thr	Val	Pro	Leu 595	
cag	atc	ttt	gcg	tgc	gct	gtg	gca	acc	gca	aag	ggc	tac	aac	gtg	gat	1939
Gln	Ile	Phe 600	Ala	Cys	Ala	Val	Ala 605	Thr	Ala	Lys	Gly	Tyr	Asn	Val	Asp 610	
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Gln	Pro	Arg	Asn	Leu	Ala	Lys 620	Ser	Val	Thr	Val	Glu 625					
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 <213> Corynebacterium glutamicum

<400> 426

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Glu Tyr Arg Gly Tyr Asp Ser Ala Gly Ile Ala Ile His Ala Asn Gly
      35           40           45

Glu Ile Ser Tyr Arg Lys Lys Ala Gly Lys Val Ala Ala Leu Asp Ala
      50           55           60

Glu Ile Ala Lys Ala Pro Leu Pro Asp Ser Ile Leu Gly Ile Gly His
      65           70           75           80

Thr Arg Trp Ala Thr His Gly Gly Pro Thr Asp Val Asn Ala His Pro
      85           90           95

His Val Val Ser Asn Gly Lys Leu Ala Val Val His Asn Gly Ile Ile
      100          105          110

Glu Asn Phe Ala Glu Leu Arg Ser Glu Leu Ser Ala Lys Gly Tyr Asn
      115          120          125

Phe Val Ser Asp Thr Asp Thr Glu Val Ala Ala Ser Leu Leu Ala Glu
      130          135          140

Ile Tyr Asn Thr Gln Ala Asn Gly Asp Leu Thr Leu Ala Met Gln Leu
      145          150          155          160

Thr Gly Gln Arg Leu Glu Gly Ala Phe Thr Leu Leu Ala Ile His Ala
      165          170          175

Asp His Asp Asp Arg Ile Val Ala Ala Arg Arg Asn Ser Pro Leu Val
      180          185          190

Ile Gly Val Gly Glu Gly Glu Asn Phe Leu Gly Ser Asp Val Ser Gly
      195          200          205

Phe Ile Asp Tyr Thr Arg Lys Ala Val Glu Leu Ala Asn Asp Gln Val
      210          215          220

Val Thr Ile Thr Ala Asp Asp Tyr Ala Ile Thr Asn Phe Asp Gly Ser
      225          230          235          240

Glu Ala Val Gly Lys Pro Phe Asp Val Glu Trp Asp Ala Ala Ala Ala
      245          250          255

Glu Lys Gly Gly Phe Gly Ser Phe Met Glu Lys Glu Ile His Asp Gln
      260          265          270

Pro Ala Ala Val Arg Asp Thr Leu Met Gly Arg Leu Asp Glu Asp Gly
      275          280          285

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Lys Leu Val Leu Asp Glu Leu Arg Ile Asp Glu Ala Ile Leu Arg Ser
 290 295 300
 Val Asp Lys Ile Val Ile Val Ala Cys Gly Thr Ala Ala Tyr Ala Gly
 305 310 315 320
 Gln Val Ala Arg Tyr Ala Ile Glu His Trp Cys Arg Ile Pro Thr Glu
 325 330 335
 Val Glu Leu Ala His Glu Phe Arg Tyr Arg Asp Pro Ile Leu Asn Glu
 340 345 350
 Lys Thr Leu Val Val Ala Leu Ser Gln Ser Gly Glu Thr Met Asp Thr
 355 360 365
 Leu Met Ala Val Arg His Ala Arg Glu Gln Gly Ala Lys Val Val Ala
 370 375 380
 Ile Cys Asn Thr Val Gly Ser Thr Leu Pro Arg Glu Ala Asp Ala Ser
 385 390 395 400
 Leu Tyr Thr Tyr Ala Gly Pro Glu Ile Ala Val Ala Ser Thr Lys Ala
 405 410 415
 Phe Leu Ala Gln Ile Thr Ala Ser Tyr Leu Leu Gly Leu Tyr Leu Ala
 420 425 430
 Gln Leu Arg Gly Asn Lys Phe Ala Asp Glu Val Ser Ser Ile Leu Asp
 435 440 445
 Ser Leu Arg Glu Met Pro Glu Lys Ile Gln Gln Val Ile Asp Ala Glu
 450 455 460
 Glu Gln Ile Lys Lys Leu Gly Gln Asp Met Ala Asp Ala Lys Ser Val
 465 470 475 480
 Leu Phe Leu Gly Arg His Val Gly Phe Pro Val Ala Leu Glu Gly Ala
 485 490 495
 Leu Lys Leu Lys Glu Ile Ala Tyr Leu His Ala Glu Gly Phe Ala Ala
 500 505 510
 Gly Glu Leu Lys His Gly Pro Ile Ala Leu Val Glu Glu Gly Gln Pro
 515 520 525
 Ile Phe Val Ile Val Pro Ser Pro Arg Gly Arg Asp Ser Leu His Ser
 530 535 540
 Lys Val Val Ser Asn Ile Gln Glu Ile Arg Ala Arg Gly Ala Val Thr
 545 550 555 560
 Ile Val Ile Ala Glu Glu Gly Asp Glu Ala Val Asn Asp Tyr Ala Asn
 565 570 575
 Phe Ile Ile Arg Ile Pro Gln Ala Pro Thr Leu Met Gln Pro Leu Leu
 580 585 590
 Ser Thr Val Pro Leu Gln Ile Phe Ala Cys Ala Val Ala Thr Ala Lys
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 Gly Tyr Asn Val Asp Gln Pro Arg Asn Leu Ala Lys Ser Val Thr Val

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625			
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gga acc gca act ggc tac tgg gtg gag cag gaa ttt gag cac gtt ttc			96
Gly Thr Ala Thr Gly Tyr Trp Val Glu Gln Glu Phe His Val Phe			
20 25 30			
ggc atc aac gcg gag cgc ctg aat gtt ggc acc cca gaa cat gct gac			144
Gly Ile Asn Ala Glu Arg Leu Asn Val Gly Thr Pro Glu His Ala Asp			
35 40 45			
gcc atc ttt gat gag ctg acc gat att ctt gcc aag cca gat ttc cga			192
Ala Ile Phe Asp Glu Leu Thr Asp Ile Leu Ala Lys Pro Asp Phe Arg			
50 55 60			
cca cgc gca ctg gct gag cag ttc aac ttg gaa gtt cta gcc acc acc			240
Pro Arg Ala Leu Ala Glu Gln Phe Asn Leu Glu Val Leu Ala Thr Thr			
65 70 75 80			
gac gat ccg ctc gat gac ctg gca gat cac aag gca ctg gca gat gat			288
Asp Asp Pro Leu Asp Asp Leu Ala Asp His Lys Ala Leu Ala Asp Asp			
85 90 95			
cca acc ttc tcc cct cgt gtg ctc cct acc ttc cgc cca gac gca tac			336
Pro Thr Phe Ser Pro Arg Val Leu Pro Thr Phe Arg Pro Asp Ala Tyr			
100 105 110			
acc aag atg tac aac gct ggt tgg gca gaa aaa acc acc aag ctt atc			384
Thr Lys Met Tyr Asn Ala Gly Trp Ala Glu Lys Thr Thr Lys Leu Ile			
115 120 125			
gat acc gca ggt gac ggc aag gca ggc tgg gag ggt tac ctt cag gca			432
Asp Thr Ala Gly Asp Gly Lys Ala Gly Trp Glu Gly Tyr Leu Gln Ala			
130 135 140			
atg cgc aac cgc cgc cag tac ttc atc aat cac ggt gca acc tcc gcg			480
Met Arg Asn Arg Arg Gln Tyr Phe Ile Asn His Gly Ala Thr Ser Ala			
145 150 155 160			
gac cac ggt ctc cac gac acc gac acc acc cca ctg agc cac aaa gat			528
Asp His Gly Leu His Asp Thr Asp Thr Thr Pro Leu Ser His Lys Asp			
165 170 175			

gcc cag aag atc ttg gac aag ggt ctc gct ggc aca gca acc ttg gct 576
 Ala Gln Lys Ile Leu Asp Lys Gly Leu Ala Gly Thr Ala Thr Leu Ala
 180 185 190

gaa atg cat gcc ttc gaa gcc aac acc acc tac cgt tcg cgg aaa tgt 624
 Glu Met His Ala Phe Glu Ala Asn Thr Thr Tyr Arg Ser Arg Lys Cys
 195 200 205

cca aga aga cgg ctg gtc atg acc atc cac cag gtg tgt acc 666
 Pro Arg Arg Arg Leu Val Met Thr Ile His Gln Val Cys Thr
 210 215 220

<210> 428

<211> 222

<212> PRT

<213> Corynebacterium glutamicum

<400> 428

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Gly Thr Ala Thr Gly Tyr Trp Val Glu Gln Glu Phe Glu His Val Phe
 20 25 30

Gly Ile Asn Ala Glu Arg Leu Asn Val Gly Thr Pro Glu His Ala Asp
 35 40 45

Ala Ile Phe Asp Glu Leu Thr Asp Ile Leu Ala Lys Pro Asp Phe Arg
 50 55 60

Pro Arg Ala Leu Ala Glu Gln Phe Asn Leu Glu Val Leu Ala Thr Thr
 65 70 75 80

Asp Asp Pro Leu Asp Asp Leu Ala Asp His Lys Ala Leu Ala Asp Asp
 85 90 95

Pro Thr Phe Ser Pro Arg Val Leu Pro Thr Phe Arg Pro Asp Ala Tyr
 100 105 110

Thr Lys Met Tyr Asn Ala Gly Trp Ala Glu Lys Thr Thr Lys Leu Ile
 115 120 125

Asp Thr Ala Gly Asp Gly Lys Ala Gly Trp Glu Gly Tyr Leu Gln Ala
 130 135 140

Met Arg Asn Arg Arg Gln Tyr Phe Ile Asn His Gly Ala Thr Ser Ala
 145 150 155 160

Asp His Gly Leu His Asp Thr Asp Thr Thr Pro Leu Ser His Lys Asp
 165 170 175

Ala Gln Lys Ile Leu Asp Lys Gly Leu Ala Gly Thr Ala Thr Leu Ala
 180 185 190

Glu Met His Ala Phe Glu Ala Asn Thr Thr Tyr Arg Ser Arg Lys Cys
 195 200 205

Pro Arg Arg Arg Leu Val Met Thr Ile His Gln Val Cys Thr
 210 215 220

<210> 429
 <211> 672
 <212> DNA
 <213> *Corynebacterium glutamicum*

<220>
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 <222> (1)..(672)
 <223> FRXA02872

<400> 429
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 Ala Arg Glu Ala Trp Arg Ile Phe Met Ser His Trp Asp Leu Tyr Ala
 1 5 10 15
 gga acc gca act ggc tac tgg gtg gag cag gaa ttt gag cac gtt ttc 96
 Gly Thr Ala Thr Gly Tyr Trp Val Gln Glu Phe Glu His Val Phe
 20 25 30
 ggc atc aac gcg gag cgc ctg aat gtt ggc acc cca gaa cat gct gac 144
 Gly Ile Asn Ala Glu Arg Leu Asn Val Gly Thr Pro Glu His Ala Asp
 35 40 45
 gcc atc ttt gat gag ctg acc gat att ctt gcc aag cca gat ttc cga 192
 Ala Ile Phe Asp Glu Leu Thr Asp Ile Leu Ala Lys Pro Asp Phe Arg
 50 55 60
 cca cgc gca ctg gct gag cag ttc aac ttg gaa gtt cta gcc acc acc 240
 Pro Arg Ala Leu Ala Glu Gln Phe Asn Leu Glu Val Leu Ala Thr Thr
 65 70 75 80
 gac gat ccg ctc gat gac ctg gca gat cac aag gca ctg gca gat gat 288
 Asp Asp Pro Leu Asp Asp Leu Ala Asp His Lys Ala Leu Ala Asp Asp
 85 90 95
 cca acc ttc tcc cct cgt gtg ctc cct acc ttc cgc cca gac gca tac 336
 Pro Thr Phe Ser Pro Arg Val Leu Pro Thr Phe Arg Pro Asp Ala Tyr
 100 105 110
 acc aag atg tac aac gct ggt tgg gca gaa aaa acc acc aag ctt atc 384
 Thr Lys Met Tyr Asn Ala Gly Trp Ala Glu Lys Thr Thr Lys Leu Ile
 115 120 125
 gat acc gca ggt gac ggc aag gca ggc tgg gag ggt tac ctt cag gca 432
 Asp Thr Ala Gly Asp Gly Lys Ala Gly Trp Glu Gly Tyr Leu Gln Ala
 130 135 140
 atg cgc aac cgc cgc cag tac ttc atc aat cac ggt gca acc tcc gcg 480
 Met Arg Asn Arg Arg Gln Tyr Phe Ile Asn His Gly Ala Thr Ser Ala
 145 150 155 160
 gac cac ggt ctc cac gac acc gac acc acc cca ctg agc cac aaa gat 528
 Asp His Gly Leu His Asp Thr Asp Thr Thr Pro Leu Ser His Lys Asp
 165 170 175
 gcc cag aag atc ttg gac aag ggt ctc gct ggc aca gca acc ttg gct 576
 Ala Gln Lys Ile Leu Asp Lys Gly Leu Ala Gly Thr Ala Thr Leu Ala
 180 185 190
 gaa atg cat gcc ttc gaa gcc aac acc acc tac cgt ttc gcg gaa atg 624

Glu Met His Ala Phe Glu Ala Asn Thr Thr Tyr Arg Phe Ala Glu Met
 195 200 205

tcc caa gaa gac ggc ctg gtc atg acc atc cac cca ggt gtg tac cgc 672
 Ser Gln Glu Asp Gly Leu Val Met Thr Ile His Pro Gly Val Tyr Arg
 210 215 220

<210> 430

<211> 224

<212> PRT

<213> Corynebacterium glutamicum

<400> 430

Ala Arg Glu Ala Trp Arg Ile Phe Met Ser His Trp Asp Leu Tyr Ala
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Gly Thr Ala Thr Gly Tyr Trp Val Glu Gln Glu Phe Glu His Val Phe
 20 25 30

Gly Ile Asn Ala Glu Arg Leu Asn Val Gly Thr Pro Glu His Ala Asp
 35 40 45

Ala Ile Phe Asp Glu Leu Thr Asp Ile Leu Ala Lys Pro Asp Phe Arg
 50 55 60

Pro Arg Ala Leu Ala Glu Gln Phe Asn Leu Glu Val Leu Ala Thr Thr
 65 70 75 80

Asp Asp Pro Leu Asp Asp Leu Ala Asp His Lys Ala Leu Ala Asp Asp
 85 90 95

Pro Thr Phe Ser Pro Arg Val Leu Pro Thr Phe Arg Pro Asp Ala Tyr
 100 105 110

Thr Lys Met Tyr Asn Ala Gly Trp Ala Glu Lys Thr Thr Lys Leu Ile
 115 120 125

Asp Thr Ala Gly Asp Gly Lys Ala Gly Trp Glu Gly Tyr Leu Gln Ala
 130 135 140

Met Arg Asn Arg Arg Gln Tyr Phe Ile Asn His Gly Ala Thr Ser Ala
 145 150 155 160

Asp His Gly Leu His Asp Thr Asp Thr Thr Pro Leu Ser His Lys Asp
 165 170 175

Ala Gln Lys Ile Leu Asp Lys Gly Leu Ala Gly Thr Ala Thr Leu Ala
 180 185 190

Glu Met His Ala Phe Glu Ala Asn Thr Thr Tyr Arg Phe Ala Glu Met
 195 200 205

Ser Gln Glu Asp Gly Leu Val Met Thr Ile His Pro Gly Val Tyr Arg
 210 215 220

<210> 431

<211> 533
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
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 <222> (1)..(510)
 <223> RXN03180

<400> 431
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 Phe Gly Glu Asn Lys Asp Leu Ile Ser Asp Ser Ser Phe Asn Arg Trp
 1 5 10 15
 ctg cgt acg gtt tcc ctc gga tcg acc cag gat gcc gat atg gct gca 96
 Leu Arg Thr Val Ser Leu Gly Ser Thr Gln Asp Ala Asp Met Ala Ala
 20 25 30
 gct tcc aac ttg gca gcc aat tct aaa atg gcc cgc cag aac acc cgc 144
 Ala Ser Asn Leu Ala Ala Asn Ser Lys Met Ala Arg Gln Asn Thr Arg
 35 40 45
 gat atc ctc gac gca gtc tct gat ggt ggc gtc atg ctc ggc cga aac 192
 Asp Ile Leu Asp Ala Val Ser Asp Gly Gly Val Met Leu Gly Arg Asn
 50 55 60
 ggt gcc cta gtg ttg gga cct gtg gtt gga act ctc cac att aaa ttc 240
 Gly Ala Leu Val Leu Gly Pro Val Val Gly Thr Leu His Ile Lys Phe
 65 70 75 80
 att gcg cct ttg aac aag cgt gtg gaa aga gtc atg tac aaa act gga 288
 Ile Ala Pro Leu Asn Lys Arg Val Glu Arg Val Met Tyr Lys Thr Gly
 85 90 95
 ctc tca gaa gct gct gca gct gag caa tgt gct ttg gag gat cgt ctc 336
 Leu Ser Glu Ala Ala Ala Glu Gln Cys Ala Leu Glu Asp Arg Leu
 100 105 110
 cgc gaa gag atg gcc cac gct ttg tat caa tgg aat ccg gga cgc gat 384
 Arg Glu Glu Met Ala His Ala Leu Tyr Gln Trp Asn Pro Gly Arg Asp
 115 120 125
 gaa aac tat gac ctc gtg atc aac acc ggt tcg atg aca tac gaa caa 432
 Glu Asn Tyr Asp Leu Val Ile Asn Thr Gly Ser Met Thr Tyr Glu Gln
 130 135 140
 atc gtt gat cta gtt gtg gaa act tac gcc agg aag tat ccg ctc cac 480
 Ile Val Asp Leu Val Val Glu Thr Tyr Ala Arg Lys Tyr Pro Leu His
 145 150 155 160
 gtg aga atc att ccg aac gga aaa gac caa taaacataca gtccccgtga 530
 Val Arg Ile Ile Pro Asn Gly Lys Asp Gln
 165 170
 tgt 533

<210> 432
 <211> 170
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 432

Phe Gly Glu Asn Lys Asp Leu Ile Ser Asp Ser Ser Phe Asn Arg Trp
 1 5 10 15
 Leu Arg Thr Val Ser Leu Gly Ser Thr Gln Asp Ala Asp Met Ala Ala
 20 25 30
 Ala Ser Asn Leu Ala Ala Asn Ser Lys Met Ala Arg Gln Asn Thr Arg
 35 40 45
 Asp Ile Leu Asp Ala Val Ser Asp Gly Gly Val Met Leu Gly Arg Asn
 50 55 60
 Gly Ala Leu Val Leu Gly Pro Val Val Gly Thr Leu His Ile Lys Phe
 65 70 75 80
 Ile Ala Pro Leu Asn Lys Arg Val Glu Arg Val Met Tyr Lys Thr Gly
 85 90 95
 Leu Ser Glu Ala Ala Ala Glu Gln Cys Ala Leu Glu Asp Arg Leu
 100 105 110
 Arg Glu Glu Met Ala His Ala Leu Tyr Gln Trp Asn Pro Gly Arg Asp
 115 120 125
 Glu Asn Tyr Asp Leu Val Ile Asn Thr Gly Ser Met Thr Tyr Glu Gln
 130 135 140
 Ile Val Asp Leu Val Val Glu Thr Tyr Ala Arg Lys Tyr Pro Leu His
 145 150 155 160
 Val Arg Ile Ile Pro Asn Gly Lys Asp Gln
 165 170

<210> 433

<211> 533

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (1)..(510)

<223> FRXA02873

<400> 433

ttc ggt gag aac aaa gat ctc atc tct gac agc agt ttc aac cgc tgg 48
 Phe Gly Glu Asn Lys Asp Leu Ile Ser Asp Ser Ser Phe Asn Arg Trp
 1 5 10 15
 ctg cgt acg gtt tcc ctc gga tcg acc cag gat gcc gat atg gct gca 96
 Leu Arg Thr Val Ser Leu Gly Ser Thr Gln Asp Ala Asp Met Ala Ala
 20 25 30
 gct tcc aac ttg gca gcc aat tct aaa atg gcc cgc cag aac acc cgc 144
 Ala Ser Asn Leu Ala Ala Asn Ser Lys Met Ala Arg Gln Asn Thr Arg
 35 40 45
 gat atc ctc gac gca gtc tct gat ggt ggc gtc atg ctc ggc cga aac 192
 Asp Ile Leu Asp Ala Val Ser Asp Gly Gly Val Met Leu Gly Arg Asn

50	55	60	
ggt gcc cta gtg ttg gga cct gtg gtt gga act ctc cac att aaa ttc			240
Gly Ala Leu Val Leu Gly Pro Val Val Gly Thr Leu His Ile Lys Phe			
65	70	75	80
att gcg cct ttg aac aag cgt gtg gaa aga gtc atg tac aaa act gga			288
Ile Ala Pro Leu Asn Lys Arg Val Glu Arg Val Met Tyr Lys Thr Gly			
85	90		95
ctc tca gaa gct gct gca gct gag caa tgt gct ttg gag gat cgt ctc			336
Leu Ser Glu Ala Ala Ala Ala Glu Gln Cys Ala Leu Glu Asp Arg Leu			
100	105		110
cgc gaa gag atg gcc cac gct ttg tat caa tgg aat ccg gga cgc gat			384
Arg Glu Glu Met Ala His Ala Leu Tyr Gln Trp Asn Pro Gly Arg Asp			
115	120		125
gaa aac tat gac ctc gtg atc aac acc ggt tcg atg aca tac gaa caa			432
Glu Asn Tyr Asp Leu Val Ile Asn Thr Gly Ser Met Thr Tyr Glu Gln			
130	135		140
atc gtt gat cta gtt gtg gaa act tac gcc agg aag tat ccg ctc cac			480
Ile Val Asp Leu Val Val Glu Thr Tyr Ala Arg Lys Tyr Pro Leu His			
145	150	155	160
gtg aga atc att ccg aac gga aaa gac caa taaacataca gtccccgtga			530
Val Arg Ile Ile Pro Asn Gly Lys Asp Gln			
165	170		
tgt			533

<210> 434

<211> 170

<212> PRT

<213> Corynebacterium glutamicum

<400> 434

Phe Gly Glu Asn Lys Asp Leu Ile Ser Asp Ser Ser Phe Asn Arg Trp
1 5 10 15

Leu Arg Thr Val Ser Leu Gly Ser Thr Gln Asp Ala Asp Met Ala Ala
20 25 30

Ala Ser Asn Leu Ala Ala Asn Ser Lys Met Ala Arg Gln Asn Thr Arg
35 40 45

Asp Ile Leu Asp Ala Val Ser Asp Gly Gly Val Met Leu Gly Arg Asn
50 55 60

Gly Ala Leu Val Leu Gly Pro Val Val Gly Thr Leu His Ile Lys Phe
65 70 75 80

Ile Ala Pro Leu Asn Lys Arg Val Glu Arg Val Met Tyr Lys Thr Gly
85 90 95

Leu Ser Glu Ala Ala Ala Ala Glu Gln Cys Ala Leu Glu Asp Arg Leu
100 105 110

Arg Glu Glu Met Ala His Ala Leu Tyr Gln Trp Asn Pro Gly Arg Asp

115	120	125
Glu Asn Tyr Asp Leu Val Ile Asn Thr Gly Ser Met Thr Tyr Glu Gln		
130	135	140
Ile Val Asp Leu Val Val Glu Thr Tyr Ala Arg Lys Tyr Pro Leu His		
145	150	155
Val Arg Ile Ile Pro Asn Gly Lys Asp Gln		
165	170	

<210> 435
 <211> 798
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(775)
 <223> RXA02292

<400> 435
 tgcaccacgc cagctgcaac cctgcgcggt ggtctgggaa gttggtggag gggatcgtcg 60
 aaaagcgtag gcactaaagt tctcctgcac aatggaggat atg gac aat gac ttt 115
 Met Asp Asn Asp Phe
 1 5
 gaa tct atc gag aaa atg agc agc ggc gat tgg tac gtg gct acc ggc 163
 Glu Ser Ile Glu Lys Met Ser Ser Gly Asp Trp Tyr Val Ala Thr Gly
 10 15 20
 gcg gaa cgt gaa gaa gtg gca caa aaa aca gcg tta ctt ttc cac gaa 211
 Ala Glu Arg Glu Glu Val Ala Gln Lys Thr Ala Leu Leu Phe His Glu
 25 30 35
 tac aac caa att gga cct aca gac ccc gca cga act gcc gaa ata cta 259
 Tyr Asn Gln Ile Gly Pro Thr Asp Pro Ala Arg Thr Ala Glu Ile Leu
 40 45 50
 aga act gta cta aat cct gcc agc gga acc tgc acg atc aaa gcg cca 307
 Arg Thr Val Leu Asn Pro Ala Ser Gly Thr Cys Thr Ile Lys Ala Pro
 55 60 65
 gcc atc att gaa tac ggc ttc aac acc acg atc ggc gag cat gtg ttc 355
 Ala Ile Ile Glu Tyr Gly Phe Asn Thr Thr Ile Gly Glu His Val Phe
 70 75 80 85
 atc aac ttt ggc ctc acc att tta gat atc gca ccg gtt cgc atc ggg 403
 Ile Asn Phe Gly Leu Thr Ile Leu Asp Ile Ala Pro Val Arg Ile Gly
 90 95 100
 gca cgc agc atg ctc ggg cca aac tgt cag ctc ttc acc gca ggt cac 451
 Ala Arg Ser Met Leu Gly Pro Asn Cys Gln Leu Phe Thr Ala Gly His
 105 110 115
 ccg gtc gat gac tgg gaa atg cgc tcc ggt ggg tgg gaa aat ggc gca 499
 Pro Val Asp Asp Trp Glu Met Arg Ser Gly Gly Trp Glu Asn Gly Ala
 120 125 130

ccc att tcc att ggc gag gat acg tgg ctg ggt gga aat gtc acc gtc 547
 Pro Ile Ser Ile Gly Glu Asp Thr Trp Leu Gly Gly Asn Val Thr Val
 135 140 145

 gtt ggt ggc gtg agc att ggc gat agg tgt gtg att ggc gcg ggg ccc 595
 Val Gly Gly Val Ser Ile Gly Asp Arg Cys Val Ile Gly Ala Gly Pro
 150 155 160 165

 gtg gtg acc aag gat att ccg gat gat tct att gct gtg ggc aac cct 643
 Val Val Thr Lys Asp Ile Pro Asp Asp Ser Ile Ala Val Gly Asn Pro
 170 175 180

 gcg cga gta gtg cgg aaa cgt gat gat agc cgg ctc gaa cgt tcg cag 691
 Ala Arg Val Val Arg Lys Arg Asp Asp Ser Arg Leu Glu Arg Ser Gln
 185 190 195

 ctg cca gaa ggt gct tcc gtg gat gcg ttg ggg att ctt cct aca aaa 739
 Leu Pro Glu Gly Ala Ser Val Asp Ala Leu Gly Ile Leu Pro Thr Lys
 200 205 210

 tca cct agg ctg tca gaa aat att gcc gaa aaa tat taaatacgcga 785
 Ser Pro Arg Leu Ser Glu Asn Ile Ala Glu Lys Tyr
 215 220 225

 ggcaactaaga aga 798

<210> 436

<211> 225

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 436

Met Asp Asn Asp Phe Glu Ser Ile Glu Lys Met Ser Ser Gly Asp Trp
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 Tyr Val Ala Thr Gly Ala Glu Arg Glu Glu Val Ala Gln Lys Thr Ala
 20 25 30

 Leu Leu Phe His Glu Tyr Asn Gln Ile Gly Pro Thr Asp Pro Ala Arg
 35 40 45

 Thr Ala Glu Ile Leu Arg Thr Val Leu Asn Pro Ala Ser Gly Thr Cys
 50 55 60

 Thr Ile Lys Ala Pro Ala Ile Ile Glu Tyr Gly Phe Asn Thr Thr Ile
 65 70 75 80

 Gly Glu His Val Phe Ile Asn Phe Gly Leu Thr Ile Leu Asp Ile Ala
 85 90 95

 Pro Val Arg Ile Gly Ala Arg Ser Met Leu Gly Pro Asn Cys Gln Leu
 100 105 110

 Phe Thr Ala Gly His Pro Val Asp Asp Trp Glu Met Arg Ser Gly Gly
 115 120 125

 Trp Glu Asn Gly Ala Pro Ile Ser Ile Gly Glu Asp Thr Trp Leu Gly
 130 135 140

 Gly Asn Val Thr Val Val Gly Gly Val Ser Ile Gly Asp Arg Cys Val

145		150		155		160
Ile Gly Ala Gly	Pro Val Val Thr Lys Asp	Ile Pro Asp Asp Ser Ile				
	165	170			175	
Ala Val Gly Asn	Pro Ala Arg Val Val Arg Lys Arg Asp Asp Ser Arg					
	180	185			190	
Leu Glu Arg Ser	Gln Leu Pro Glu Gly Ala Ser Val Asp Ala Leu Gly					
	195	200			205	
Ile Leu Pro Thr	Lys Ser Pro Arg Leu Ser Glu Asn Ile Ala Glu Lys					
	210	215			220	

Tyr
225

<210> 437
 <211> 891
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(868)
 <223> RXA02666

<400> 437
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tcttgacgat	ctgagcttcg	acgacgaaga	ttagacgccc	atg	tcg	tct	aca	cga	115
				Met	Ser	Ser	Thr	Arg	
				1				5	

atc	ccc	gtc	atc	gca	ctc	ctc	gcg	gcg	gcg	ggg	cgc	gga	acc	cgc	ctc	163
Ile	Pro	Val	Ile	Ala	Leu	Leu	Ala	Ala	Ala	Gly	Arg	Gly	Thr	Arg	Leu	
				10					15					20		

ggc	gga	ccc	atc	ccc	aaa	gca	ttc	gtc	acg	ttg	cgt	gaa	cgc	aca	ctt	211
Gly	Gly	Pro	Ile	Pro	Lys	Ala	Phe	Val	Thr	Leu	Arg	Glu	Arg	Thr	Leu	
			25					30					35			

tta	gag	cgc	tcg	ctc	caa	gcc	atg	ctc	acc	tcc	gaa	agc	gtc	gac	gaa	259
Leu	Glu	Arg	Ser	Leu	Gln	Ala	Met	Leu	Thr	Ser	Glu	Ser	Val	Asp	Glu	
			40				45					50				

atc	atc	atc	ctc	gtc	agc	ccc	gac	atg	gaa	acc	tac	gcc	cgc	gat	ttg	307
Ile	Ile	Ile	Leu	Val	Ser	Pro	Asp	Met	Glu	Thr	Tyr	Ala	Arg	Asp	Leu	
		55				60					65					

ctg	cgc	aaa	cgc	ggc	ctt	ttg	aac	gac	ccc	gaa	ggg	gta	cgc	gta	cgg	355
Leu	Arg	Lys	Arg	Gly	Leu	Leu	Asn	Asp	Pro	Glu	Gly	Val	Arg	Val	Arg	
		70			75					80					85	

ctc	gtg	cac	ggc	ggc	ggg	gag	cgc	gcg	gac	tcg	gtc	tg	gca	ggc	ctt	403
Leu	Val	His	Gly	Gly	Gly	Glu	Arg	Ala	Asp	Ser	Val	Trp	Ala	Gly	Leu	
			90						95					100		

cag	gca	att	tcg	ctt	gac	gac	gcc	acc	ccc	gat	gca	att	gtc	tta	atc	451
Gln	Ala	Ile	Ser	Leu	Asp	Asp	Ala	Thr	Pro	Asp	Ala	Ile	Val	Leu	Ile	

105	110	115	
cac gac agc gcc cga gcg ctc aca cca ccc ggc atg att gcg cgc gtg			499
His Asp Ser Ala Arg Ala Leu Thr Pro Pro Gly Met Ile Ala Arg Val			
120	125	130	
gtg cgc aaa gtc cac gaa ggc gcc acc gca gtc atc cca gta ctg cca			547
Val Arg Lys Val His Glu Gly Ala Thr Ala Val Ile Pro Val Leu Pro			
135	140	145	
gta tcg gac acc atc aaa cga gtg tcc cct gat ggc gga gta gtt gtc			595
Val Ser Asp Thr Ile Lys Arg Val Ser Pro Asp Gly Gly Val Val Val			
150	155	160	165
gac aca ccc aac cgt gca gaa ctt cgc gcc gtc caa acc cca caa ggc			643
Asp Thr Pro Asn Arg Ala Glu Leu Arg Ala Val Gln Thr Pro Gln Gly			
170	175	180	
ttc ctg ctg tcc gaa ctt gtt gca gcg aat gag aaa ttc ttc gcc gac			691
Phe Leu Leu Ser Glu Leu Val Ala Ala Asn Glu Lys Phe Phe Ala Asp			
185	190	195	
ccc aac cca ggc ttc atc cca acc gat gac gcc agc ttg atg gaa tgg			739
Pro Asn Pro Gly Phe Ile Pro Thr Asp Asp Ala Ser Leu Met Glu Trp			
200	205	210	
tac ggc gca gat gta gtc tgc gta caa ggc gac cca atg gcg ttt aaa			787
Tyr Gly Ala Asp Val Val Cys Val Gln Gly Asp Pro Met Ala Phe Lys			
215	220	225	
gta aca acc ccc att gat atg atg ctg gca caa cgc atc acc gac gaa			835
Val Thr Thr Pro Ile Asp Met Met Leu Ala Gln Arg Ile Thr Asp Glu			
230	235	240	245
gcc gaa ccc aca ata ttt gag gta cca ggt gac taacccaatc atccccgcg			888
Ala Glu Pro Thr Ile Phe Glu Val Pro Gly Asp			
250	255		
tag			891
<210> 438			
<211> 256			
<212> PRT			
<213> Corynebacterium glutamicum			
<400> 438			
Met Ser Ser Thr Arg Ile Pro Val Ile Ala Leu Leu Ala Ala Ala Gly			
1	5	10	15
Arg Gly Thr Arg Leu Gly Gly Pro Ile Pro Lys Ala Phe Val Thr Leu			
20	25	30	
Arg Glu Arg Thr Leu Leu Glu Arg Ser Leu Gln Ala Met Leu Thr Ser			
35	40	45	
Glu Ser Val Asp Glu Ile Ile Ile Leu Val Ser Pro Asp Met Glu Thr			
50	55	60	
Tyr Ala Arg Asp Leu Leu Arg Lys Arg Gly Leu Leu Asn Asp Pro Glu			
65	70	75	80

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<210> 439
<211> 1065
<212> DNA
<213> Corynebacterium glutamicum
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<400> 439
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ctt	att	gct	ctg	tcc	gct	tct	gtc	gtt	ttg	gct	ttc	agc	ttg	tct	gct	163
Leu	Ile	Ala	Leu	Ser	Ala	Ser	Val	Val	Leu	Ala	Phe	Ser	Leu	Ser	Ala	
				10					15					20		

629

25				30				35								
ggg	tcg	atc	acc	ttg	gct	ctg	tct	acc	cag	acc	aac	ccg	ttc	ttt	gtg	259
Gly	Ser	Ile	Thr	Leu	Ala	Leu	Ser	Thr	Gln	Thr	Asn	Pro	Phe	Phe	Val	
40				45				50								
cag	ctt	cgt	gat	ggg	gcc	cag	gaa	aag	gct	gat	gaa	ttg	ggc	gtg	acc	307
Gln	Leu	Arg	Asp	Gly	Ala	Gln	Glu	Lys	Ala	Asp	Glu	Leu	Gly	Val	Thr	
55				60				65								
ctc	aat	ggt	cag	gat	gct	tcc	gat	gac	gct	gca	acg	cag	gcc	aac	cag	355
Leu	Asn	Val	Gln	Asp	Ala	Ser	Asp	Asp	Ala	Ala	Thr	Gln	Ala	Asn	Gln	
70				75				80				85				
ctc	aac	aac	gct	gtc	acc	acc	ggg	gct	ggc	gtg	gtg	att	gtc	aac	cca	403
Leu	Asn	Asn	Ala	Val	Thr	Thr	Gly	Ala	Gly	Val	Val	Ile	Val	Asn	Pro	
90				95				100								
act	gat	tct	gat	gct	gtg	gtg	ccg	tcg	gtg	gaa	gct	ctc	aac	cag	gct	451
Thr	Asp	Ser	Asp	Ala	Val	Val	Pro	Ser	Val	Glu	Ala	Leu	Asn	Gln	Ala	
105				110				115								
gac	att	cct	ggt	gtg	gct	gtc	gac	cgt	tcc	tcc	aat	ggg	ggc	gag	gtg	499
Asp	Ile	Pro	Val	Val	Ala	Val	Asp	Arg	Ser	Ser	Asn	Gly	Gly	Glu	Val	
120				125				130								
gcg	tcc	ttc	gtg	gca	tct	gac	aac	ggt	gct	ggc	ggc	gcg	cag	gct	gct	547
Ala	Ser	Phe	Val	Ala	Ser	Asp	Asn	Val	Ala	Gly	Gly	Ala	Gln	Ala	Ala	
135				140				145								
gca	gcc	ctg	gca	gag	gcg	atc	ggg	ggc	gaa	ggg	gaa	atc	ctc	atg	ctg	595
Ala	Ala	Leu	Ala	Glu	Ala	Ile	Gly	Gly	Glu	Gly	Glu	Ile	Leu	Met	Leu	
150				155				160				165				
caa	ggc	att	gcg	gga	tcc	tct	gca	tca	cgt	gat	cgt	gga	cag	gga	ttt	643
Gln	Gly	Ile	Ala	Gly	Ser	Ser	Ala	Ser	Arg	Asp	Arg	Gly	Gln	Gly	Phe	
170				175				180								
gaa	gag	gag	atc	gct	aag	cat	gag	ggc	att	tcc	att	gtg	gct	aag	cag	691
Glu	Glu	Glu	Ile	Ala	Lys	His	Glu	Gly	Ile	Ser	Ile	Val	Ala	Lys	Gln	
185				190				195								
acc	gcc	aac	ttt	gac	cgc	ggg	gag	ggc	ctg	gac	gtg	gca	act	aac	ctg	739
Thr	Ala	Asn	Phe	Asp	Arg	Gly	Glu	Gly	Leu	Asp	Val	Ala	Thr	Asn	Leu	
200				205				210								
ctg	cag	gca	cac	ccc	aat	gtg	aag	gcg	atc	ttc	gcg	gaa	aac	gat	gag	787
Leu	Gln	Ala	His	Pro	Asn	Val	Lys	Ala	Ile	Phe	Ala	Glu	Asn	Asp	Glu	
215				220				225								
atg	gcg	ttg	ggc	gca	atc	gaa	gcc	ctg	ggg	gct	cgt	gct	ggg	gaa	gat	835
Met	Ala	Leu	Gly	Ala	Ile	Glu	Ala	Leu	Gly	Ala	Arg	Ala	Gly	Glu	Asp	
230				235				240				245				
gtc	atc	ggt	gtc	ggg	ttc	gat	ggc	acc	aat	gat	ggg	ctg	gca	gcg	gtt	883
Val	Ile	Val	Val	Gly	Phe	Asp	Gly	Thr	Asn	Asp	Gly	Leu	Ala	Ala	Val	
250				255				260								
gaa	gat	gga	cgc	atg	ttg	gcc	acc	gtt	gct	cag	cag	cca	gaa	gag	ctg	931
Glu	Asp	Gly	Arg	Met	Leu	Ala	Thr	Val	Ala	Gln	Gln	Pro	Glu	Glu	Leu	
265				270				275								

gga gca aag gct gtg gaa gaa gca gct aag ctc ctg cgc ggt gag gac 979
 Gly Ala Lys Ala Val Glu Glu Ala Ala Lys Leu Leu Arg Gly Glu Asp
 280 285 290

gct gaa aca gag gta cca gtt gag gtt gtc act gtg aag ctc gac aac 1027
 Ala Glu Thr Glu Val Pro Val Glu Val Val Thr Val Lys Leu Asp Asn
 295 300 305

gtc gcg gac ttc aag tagtcggcga tgaaaaagtc cgt 1065
 Val Ala Asp Phe Lys
 310

<210> 440
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 <213> Corynebacterium glutamicum

<400> 440
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Phe Ser Leu Ser Ala Cys Asn Arg Glu Ser Ser Gly Thr Ser Ala Asp
 20 25 30

Gly Gly Ser Ala Asp Gly Ser Ile Thr Leu Ala Leu Ser Thr Gln Thr
 35 40 45

Asn Pro Phe Phe Val Gln Leu Arg Asp Gly Ala Gln Glu Lys Ala Asp
 50 55 60

Glu Leu Gly Val Thr Leu Asn Val Gln Asp Ala Ser Asp Asp Ala Ala
 65 70 75 80

Thr Gln Ala Asn Gln Leu Asn Asn Ala Val Thr Thr Gly Ala Gly Val
 85 90 95

Val Ile Val Asn Pro Thr Asp Ser Asp Ala Val Val Pro Ser Val Glu
 100 105 110

Ala Leu Asn Gln Ala Asp Ile Pro Val Val Ala Val Asp Arg Ser Ser
 115 120 125

Asn Gly Gly Glu Val Ala Ser Phe Val Ala Ser Asp Asn Val Ala Gly
 130 135 140

Gly Ala Gln Ala Ala Ala Ala Leu Ala Glu Ala Ile Gly Gly Glu Gly
 145 150 155 160

Glu Ile Leu Met Leu Gln Gly Ile Ala Gly Ser Ser Ala Ser Arg Asp
 165 170 175

Arg Gly Gln Gly Phe Glu Glu Glu Ile Ala Lys His Glu Gly Ile Ser
 180 185 190

Ile Val Ala Lys Gln Thr Ala Asn Phe Asp Arg Gly Glu Gly Leu Asp
 195 200 205

Val Ala Thr Asn Leu Leu Gln Ala His Pro Asn Val Lys Ala Ile Phe
 210 215 220

Ala Glu Asn Asp Glu Met Ala Leu Gly Ala Ile Glu Ala Leu Gly Ala
 225 230 235 240

Arg Ala Gly Glu Asp Val Ile Val Val Gly Phe Asp Gly Thr Asn Asp
 245 250 255

Gly Leu Ala Ala Val Glu Asp Gly Arg Met Leu Ala Thr Val Ala Gln
 260 265 270

Gln Pro Glu Glu Leu Gly Ala Lys Ala Val Glu Glu Ala Ala Lys Leu
 275 280 285

Leu Arg Gly Glu Asp Ala Glu Thr Glu Val Pro Val Glu Val Val Thr
 290 295 300

Val Lys Leu Asp Asn Val Ala Asp Phe Lys
 305 310

<210> 441
 <211> 963
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
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 <222> (101)..(940)
 <223> RXA02440

<400> 441
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 Met Val Ser His Gly
 1 5

gcg ccg ggc gat act ttt tgg gat ttg gtc cga aaa ggt gct gaa gac 163
 Ala Pro Gly Asp Thr Phe Trp Asp Leu Val Arg Lys Gly Ala Glu Asp
 10 15 20

gcc gcc caa aaa gac aac gtt gaa ctc cgc tat tcc tct aat ccg gaa 211
 Ala Ala Gln Lys Asp Asn Val Glu Leu Arg Tyr Ser Ser Asn Pro Glu
 25 30 35

atc cct gaa caa tcc aac ctc gtg caa aat gcc atc gat tca cgc gtc 259
 Ile Pro Glu Gln Ser Asn Leu Val Gln Asn Ala Ile Asp Ser Arg Val
 40 45 50

gac ggc atc gcc atg acc atg cct aat gct caa tca cta gga ccg gtc 307
 Asp Gly Ile Ala Met Thr Met Pro Asn Ala Gln Ser Leu Gly Pro Val
 55 60 65

gct caa aag gcc gtg gat gcg ggc att cct gtg gtt ggt ctc aac gct 355
 Ala Gln Lys Ala Val Asp Ala Gly Ile Pro Val Val Gly Leu Asn Ala
 70 75 80 85

gga atg aac gaa tac caa gat tat gga atg aca gga ttc ttt ggt caa 403
 Gly Met Asn Glu Tyr Gln Asp Tyr Gly Met Thr Gly Phe Phe Gly Gln
 90 95 100

gat gaa tcc gtc gca gga gca tcc gca gga gcg cgc ctt gcc gag gaa 451
Asp Glu Ser Val Ala Gly Ala Ser Ala Gly Ala Arg Leu Ala Glu Glu
105 110 115

aac gca caa aaa gtt ttg tgt gtg atc cat gaa cag gcc aac tcc tcc 499
Asn Ala Gln Lys Val Leu Cys Val Ile His Glu Gln Gly Asn Ser Ser
120 125 130

cag gaa gct cgc tgt ggt gcc gtg tct gaa ggt ttg gcc aaa caa gta 547
Gln Glu Ala Arg Cys Gly Gly Val Ser Glu Gly Leu Gly Lys Gln Val
135 140 145

gaa acc ctg tat gtc aac gcc atg gat ctc acc tca gtg aac tcc acc 595
Glu Thr Leu Tyr Val Asn Gly Met Asp Leu Thr Ser Val Asn Ser Thr
150 155 160 165

ctg cag gca aaa ctt gct caa gac cgc agc att gat tgg gtt gtg gga 643
Leu Gln Ala Lys Leu Ala Gln Asp Arg Ser Ile Asp Trp Val Val Gly
170 175 180

ctc cag gct ggt gta tca atg gct att tct gat gcg gca gac gct gcg 691
Leu Gln Ala Gly Val Ser Met Ala Ile Ser Asp Ala Ala Asp Ala Ala
185 190 195

aac tcag gaa gta aag atc gcc acc ttt gat aca aac gca cag ctc atg 739
Asn Ser Glu Val Lys Ile Ala Thr Phe Asp Thr Asn Ala Gln Leu Met
200 205 210

acc gct att cgt gat gcc aag atc caa ttc gcc att gat cag caa cca 787
Thr Ala Ile Arg Asp Gly Lys Ile Gln Phe Ala Ile Asp Gln Gln Pro
215 220 225

tat ctg cag gcc tac atg gcc gtg gat tcg ctg tgg ttg gcg cac cga 835
Tyr Leu Gln Gly Tyr Met Ala Val Asp Ser Leu Trp Leu Ala His Arg
230 235 240 245

aac gcc acc act gtt ggt gcc gga cga ccc gtg tac aca gga cca gcc 883
Asn Gly Thr Thr Val Gly Gly Gly Arg Pro Val Tyr Thr Gly Pro Ala
250 255 260

att gtg gat gcc acc aac gtt gat gtc att gct gaa gcc gtt ggg gag 931
Ile Val Asp Ala Thr Asn Val Asp Val Ile Ala Glu Ala Val Gly Glu
265 270 275

ggt ctg cga tgacaaaaat caagagtggg gag 963
Gly Leu Arg
280

<210> 442

<211> 280

<212> PRT

<213> Corynebacterium glutamicum

<400> 442

Met Val Ser His Gly Ala Pro Gly Asp Thr Phe Trp Asp Leu Val Arg
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20 25 30

Ser Ser Asn Pro Glu Ile Pro Glu Gln Ser Asn Leu Val Gln Asn Ala
 35 40 45
 Ile Asp Ser Arg Val Asp Gly Ile Ala Met Thr Met Pro Asn Ala Gln
 50 55 60
 Ser Leu Gly Pro Val Ala Gln Lys Ala Val Asp Ala Gly Ile Pro Val
 65 70 75 80
 Val Gly Leu Asn Ala Gly Met Asn Glu Tyr Gln Asp Tyr Gly Met Thr
 85 90 95
 Gly Phe Phe Gly Gln Asp Glu Ser Val Ala Gly Ala Ser Ala Gly Ala
 100 105 110
 Arg Leu Ala Glu Glu Asn Ala Gln Lys Val Leu Cys Val Ile His Glu
 115 120 125
 Gln Gly Asn Ser Ser Gln Glu Ala Arg Cys Gly Gly Val Ser Glu Gly
 130 135 140
 Leu Gly Lys Gln Val Glu Thr Leu Tyr Val Asn Gly Met Asp Leu Thr
 145 150 155 160
 Ser Val Asn Ser Thr Leu Gln Ala Lys Leu Ala Gln Asp Arg Ser Ile
 165 170 175
 Asp Trp Val Val Gly Leu Gln Ala Gly Val Ser Met Ala Ile Ser Asp
 180 185 190
 Ala Ala Asp Ala Ala Asn Ser Glu Val Lys Ile Ala Thr Phe Asp Thr
 195 200 205
 Asn Ala Gln Leu Met Thr Ala Ile Arg Asp Gly Lys Ile Gln Phe Ala
 210 215 220
 Ile Asp Gln Gln Pro Tyr Leu Gln Gly Tyr Met Ala Val Asp Ser Leu
 225 230 235 240
 Trp Leu Ala His Arg Asn Gly Thr Thr Val Gly Gly Gly Arg Pro Val
 245 250 255
 Tyr Thr Gly Pro Ala Ile Val Asp Ala Thr Asn Val Asp Val Ile Ala
 260 265 270
 Glu Ala Val Gly Glu Gly Leu Arg
 275 280

<210> 443

<211> 1482

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1459)

<223> RXN01569

<400> 443

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agaacaacgt cgaagctacc tacgctaagc agggacaata atg gaa tac ggt aaa	115
Met Glu Tyr Gly Lys	
1 5	
caa ctc acc tcc cac acc acc gac atc gaa ggc cta ctg gtt ttc gat	163
Gln Leu Thr Ser His Thr Thr Asp Ile Glu Gly Leu Leu Val Phe Asp	
10 15 20	
ttc ccc gtc cac ggc gac aac cgc ggc tgg ttc aag gaa aat tgg cag	211
Phe Pro Val His Gly Asp Asn Arg Gly Trp Phe Lys Glu Asn Trp Gln	
25 30 35	
cgc acc aag atg acc aac ctg ggg ctg ccc gat ttt ggc ccc gtc caa	259
Arg Thr Lys Met Thr Asn Leu Gly Leu Pro Asp Phe Gly Pro Val Gln	
40 45 50	
aac aac atg agt ttc aac gcc acc gcc ggc acg act cgc ggc atg cac	307
Asn Asn Met Ser Phe Asn Ala Thr Ala Gly Thr Thr Arg Gly Met His	
55 60 65	
gct gag ccg tgg gat aaa ttt gtg tcc gtc gcg gtg ggt tcc gtt ttc	355
Ala Glu Pro Trp Asp Lys Phe Val Ser Val Ala Val Gly Ser Val Phe	
70 75 80 85	
gga gct tgg gtg gat ctg cgc gcg ggc tgc agc acg tac ggt aac gtc	403
Gly Ala Trp Val Asp Leu Arg Ala Gly Ser Ser Thr Tyr Gly Asn Val	
90 95 100	
gta acg caa aaa att acc cct gac gtg gga gtt tac gtc ccg cgt ggt	451
Val Thr Gln Lys Ile Thr Pro Asp Val Gly Val Tyr Val Pro Arg Gly	
105 110 115	
gtg gca aac ggc ttc cag gcg ctc gag gac ggc acg ctg tac acc tac	499
Val Ala Asn Gly Phe Gln Ala Leu Glu Asp Gly Thr Leu Tyr Thr Tyr	
120 125 130	
ctc gtc aac gat cat tgg tcc ccc gac gcg cat tac gcc aac gtc aac	547
Leu Val Asn Asp His Trp Ser Pro Asp Ala His Tyr Ala Asn Val Asn	
135 140 145	
ctc aac atg atc gac tgg ccg ctg ccc atc acc gag atc tcc gaa aaa	595
Leu Asn Met Ile Asp Trp Pro Leu Pro Ile Thr Glu Ile Ser Glu Lys	
150 155 160 165	
gat aaa aaa cat cca gcg ctt atc gac gcc acc ccc ctg ccc gcc cgc	643
Asp Lys Lys His Pro Ala Leu Ile Asp Ala Thr Pro Leu Pro Ala Arg	
170 175 180	
aag gtt ctc gtg gtc ggc gcc ggc gga caa ctg gga acc gcg cta cgc	691
Lys Val Leu Val Val Gly Ala Gly Gly Gln Leu Gly Thr Ala Leu Arg	
185 190 195	
gcg cag ttc cca gac gcg gaa ttt gtc acg cgc caa gaa ctc gat atc	739
Ala Gln Phe Pro Asp Ala Glu Phe Val Thr Arg Gln Glu Leu Asp Ile	
200 205 210	
acc tca gat ctc acc gag gct cgc gcg tgg aaa caa tac tcc acc atc	787
Thr Ser Asp Leu Thr Glu Ala Arg Ala Trp Lys Gln Tyr Ser Thr Ile	
215 220 225	

ata aac gcc gcc gcc tac act gcc gtt gac cag gca gaa cac gac cgc	835
Ile Asn Ala Ala Ala Tyr Thr Ala Val Asp Gln Ala Glu His Asp Arg	
230 235 240 245	
gca gca gcg tgg gac atc aac gca gcg gca gtg gct aac ctc gcg acc	883
Ala Ala Ala Trp Asp Ile Asn Ala Ala Ala Val Ala Asn Leu Ala Thr	
250 255 260	
atc gcg cgc gac aac aac ctc acc ctc gtg cac gtg tcc tca gat tat	931
Ile Ala Arg Asp Asn Asn Leu Thr Leu Val His Val Ser Ser Asp Tyr	
265 270 275	
gtc ttc gac ggt gcg gcc gaa tcc tac gat gaa aac gca ccg ttt tcc	979
Val Phe Asp Gly Ala Ala Glu Ser Tyr Asp Glu Asn Ala Pro Phe Ser	
280 285 290	
cca ctc ggc gtg tac ggc caa tcc aaa gca gcc ggc gac atc gga gac	1027
Pro Leu Gly Val Tyr Gly Gln Ser Lys Ala Ala Gly Asp Ile Gly Asp	
295 300 305	
acc acc gca ccg cgc cac tac att gtg cgc acc agc tgg gtg att ggc	1075
Thr Thr Ala Pro Arg His Tyr Ile Val Arg Thr Ser Trp Val Ile Gly	
310 315 320 325	
gat ggc aat aat ttt gtc cgc acc atg aaa tcc ctc gac gaa cgc ggc	1123
Asp Gly Asn Asn Phe Val Arg Thr Met Lys Ser Leu Asp Glu Arg Gly	
330 335 340	
atc gca cca tca gta gtt gat gat caa atc ggc cgc cta tcc ttc acc	1171
Ile Ala Pro Ser Val Val Asp Asp Gln Ile Gly Arg Leu Ser Phe Thr	
345 350 355	
gaa gac atc gca gcc ggc atc gcg cac ctt ttg gaa gtg ggt gca gca	1219
Glu Asp Ile Ala Ala Gly Ile Ala His Leu Leu Glu Val Gly Ala Ala	
360 365 370	
tat ggc acc tac aac ctc acc aac acc ggc gaa ccc gca agc tgg gcc	1267
Tyr Gly Thr Tyr Asn Leu Thr Asn Thr Gly Glu Pro Ala Ser Trp Ala	
375 380 385	
gat gtt gcc cgc gca gta ttt tcc gac ccc acc aaa gtt acc ggc gtg	1315
Asp Val Ala Arg Ala Val Phe Ser Asp Pro Thr Lys Val Thr Gly Val	
390 395 400 405	
agc acc gcc gag tac ttc gcc aac aaa gac gca gcg ccc cgc cca ctg	1363
Ser Thr Ala Glu Tyr Phe Ala Asn Lys Asp Ala Ala Pro Arg Pro Leu	
410 415 420	
aac tcc gtt ttg gat ctc ggc aaa atc gaa gcc acc gga ttt agc gca	1411
Asn Ser Val Leu Asp Leu Gly Lys Ile Glu Ala Thr Gly Phe Ser Ala	
425 430 435	
ccg acc tgg cag acc cgc ctc aac gac tac ctc aag gaa ctc tca aag	1459
Pro Thr Trp Gln Thr Arg Leu Asn Asp Tyr Leu Lys Glu Leu Ser Lys	
440 445 450	
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<211> 453

<212> PRT

<213> Corynebacterium glutamicum

<400> 444

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Leu Leu Val Phe Asp Phe Pro Val His Gly Asp Asn Arg Gly Trp Phe
      20              25              30

Lys Glu Asn Trp Gln Arg Thr Lys Met Thr Asn Leu Gly Leu Pro Asp
      35              40              45

Phe Gly Pro Val Gln Asn Asn Met Ser Phe Asn Ala Thr Ala Gly Thr
      50              55              60

Thr Arg Gly Met His Ala Glu Pro Trp Asp Lys Phe Val Ser Val Ala
      65              70              75              80

Val Gly Ser Val Phe Gly Ala Trp Val Asp Leu Arg Ala Gly Ser Ser
      85              90              95

Thr Tyr Gly Asn Val Val Thr Gln Lys Ile Thr Pro Asp Val Gly Val
      100              105              110

Tyr Val Pro Arg Gly Val Ala Asn Gly Phe Gln Ala Leu Glu Asp Gly
      115              120              125

Thr Leu Tyr Thr Tyr Leu Val Asn Asp His Trp Ser Pro Asp Ala His
      130              135              140

Tyr Ala Asn Val Asn Leu Asn Met Ile Asp Trp Pro Leu Pro Ile Thr
      145              150              155              160

Glu Ile Ser Glu Lys Asp Lys Lys His Pro Ala Leu Ile Asp Ala Thr
      165              170              175

Pro Leu Pro Ala Arg Lys Val Leu Val Val Gly Ala Gly Gly Gln Leu
      180              185              190

Gly Thr Ala Leu Arg Ala Gln Phe Pro Asp Ala Glu Phe Val Thr Arg
      195              200              205

Gln Glu Leu Asp Ile Thr Ser Asp Leu Thr Glu Ala Arg Ala Trp Lys
      210              215              220

Gln Tyr Ser Thr Ile Ile Asn Ala Ala Ala Tyr Thr Ala Val Asp Gln
      225              230              235              240

Ala Glu His Asp Arg Ala Ala Ala Trp Asp Ile Asn Ala Ala Val
      245              250              255

Ala Asn Leu Ala Thr Ile Ala Arg Asp Asn Asn Leu Thr Leu Val His
      260              265              270

Val Ser Ser Asp Tyr Val Phe Asp Gly Ala Ala Glu Ser Tyr Asp Glu
      275              280              285

Asn Ala Pro Phe Ser Pro Leu Gly Val Tyr Gly Gln Ser Lys Ala Ala
      290              295              300

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Gly Asp Ile Gly Asp Thr Thr Ala Pro Arg His Tyr Ile Val Arg Thr
 305 310 315 320

Ser Trp Val Ile Gly Asp Gly Asn Asn Phe Val Arg Thr Met Lys Ser
 325 330 335

Leu Asp Glu Arg Gly Ile Ala Pro Ser Val Val Asp Asp Gln Ile Gly
 340 345 350

Arg Leu Ser Phe Thr Glu Asp Ile Ala Ala Gly Ile Ala His Leu Leu
 355 360 365

Glu Val Gly Ala Ala Tyr Gly Thr Tyr Asn Leu Thr Asn Thr Gly Glu
 370 375 380

Pro Ala Ser Trp Ala Asp Val Ala Arg Ala Val Phe Ser Asp Pro Thr
 385 390 395 400

Lys Val Thr Gly Val Ser Thr Ala Glu Tyr Phe Ala Asn Lys Asp Ala
 405 410 415

Ala Pro Arg Pro Leu Asn Ser Val Leu Asp Leu Gly Lys Ile Glu Ala
 420 425 430

Thr Gly Phe Ser Ala Pro Thr Trp Gln Thr Arg Leu Asn Asp Tyr Leu
 435 440 445

Lys Glu Leu Ser Lys
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<210> 445
 <211> 449
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (1)..(426)
 <223> FRXA01569

<400> 445
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 Ala Pro Arg His Tyr Ile Val Arg Thr Ser Trp Val Ile Gly Asp Gly
 1 5 10 15

aat aat ttt gtc cgc acc atg aaa tcc ctc gac gaa cgc ggc atc gca 96
 Asn Asn Phe Val Arg Thr Met Lys Ser Leu Asp Glu Arg Gly Ile Ala
 20 25 30

cca tca gta gtt gat gat caa atc ggc cgc cta tcc ttc acc gaa gac 144
 Pro Ser Val Val Asp Asp Gln Ile Gly Arg Leu Ser Phe Thr Glu Asp
 35 40 45

atc gca gcc ggc atc gcg cac ctt ttg gaa gtg ggt gca gca tat ggc 192
 Ile Ala Ala Gly Ile Ala His Leu Leu Glu Val Gly Ala Ala Tyr Gly
 50 55 60

acc tac aac ctc acc aac acc ggc gaa ccc gca agc tgg gcc gat gtt 240
 Thr Tyr Asn Leu Thr Asn Thr Gly Glu Pro Ala Ser Trp Ala Asp Val
 65 70 75 80

gcc cgc gca gta ttt tcc gac ccc acc aaa gtt acc ggc gtg agc acc 288
 Ala Arg Ala Val Phe Ser Asp Pro Thr Lys Val Thr Gly Val Ser Thr
 85 90 95

gcc gag tac ttc gcc aac aaa gac gca gcg ccc cgc cca ctg aac tcc 336
 Ala Glu Tyr Phe Ala Asn Lys Asp Ala Ala Pro Arg Pro Leu Asn Ser
 100 105 110

gtt ttg gat ctc ggc aaa atc gaa gcc acc gga ttt agc gca ccg acc 384
 Val Leu Asp Leu Gly Lys Ile Glu Ala Thr Gly Phe Ser Ala Pro Thr
 115 120 125

tgg cag acc cgc ctc aac gac tac ctc aag gaa ctc tca aag 426
 Trp Gln Thr Arg Leu Asn Asp Tyr Leu Lys Glu Leu Ser Lys
 130 135 140

tgaaaggcat catcctcgca ggt 449

<210> 446

<211> 142

<212> PRT

<213> Corynebacterium glutamicum.

<400> 446

Ala Pro Arg His Tyr Ile Val Arg Thr Ser Trp Val Ile Gly Asp Gly
 1 5 10 15

Asn Asn Phe Val Arg Thr Met Lys Ser Leu Asp Glu Arg Gly Ile Ala
 20 25 30

Pro Ser Val Val Asp Asp Gln Ile Gly Arg Leu Ser Phe Thr Glu Asp
 35 40 45

Ile Ala Ala Gly Ile Ala His Leu Leu Glu Val Gly Ala Ala Tyr Gly
 50 55 60

Thr Tyr Asn Leu Thr Asn Thr Gly Glu Pro Ala Ser Trp Ala Asp Val
 65 70 75 80

Ala Arg Ala Val Phe Ser Asp Pro Thr Lys Val Thr Gly Val Ser Thr
 85 90 95

Ala Glu Tyr Phe Ala Asn Lys Asp Ala Ala Pro Arg Pro Leu Asn Ser
 100 105 110

Val Leu Asp Leu Gly Lys Ile Glu Ala Thr Gly Phe Ser Ala Pro Thr
 115 120 125

Trp Gln Thr Arg Leu Asn Asp Tyr Leu Lys Glu Leu Ser Lys
 130 135 140

<210> 447

<211> 1028

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1021)

<223> FRXA02055

<400> 447

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agaacaacgt cgaagctacc tacgctaagc agggacaata atg gaa tac ggt aaa 115
                                         Met Glu Tyr Gly Lys
                                         1           5

caa ctc acc tcc cac acc acc gac atc gaa ggc cta ctg gtt ttc gat 163
Gln Leu Thr Ser His Thr Thr Asp Ile Glu Gly Leu Leu Val Phe Asp
                10                15                20

ttc ccc gtc cac ggc gac aac cgc ggc tgg ttc aag gaa aat tgg cag 211
Phe Pro Val His Gly Asp Asn Arg Gly Trp Phe Lys Glu Asn Trp Gln
                25                30                35

cgc acc aag atg acc aac ctg ggg ctg ccc gat ttt ggc ccc gtc caa 259
Arg Thr Lys Met Thr Asn Leu Gly Leu Pro Asp Phe Gly Pro Val Gln
                40                45                50

aac aac atg agt ttc aac gcc acc gcc ggc acg act cgc ggc atg cac 307
Asn Asn Met Ser Phe Asn Ala Thr Ala Gly Thr Thr Arg Gly Met His
                55                60                65

gct gag ccg tgg gat aaa ttt gtg tcc gtc gcg gtg ggt tcc gtt ttc 355
Ala Glu Pro Trp Asp Lys Phe Val Ser Val Ala Val Gly Ser Val Phe
                70                75                80                85

gga gct tgg gtg gat ctg cgc gcg ggc tcg agc acg tac ggt aac gtc 403
Gly Ala Trp Val Asp Leu Arg Ala Gly Ser Ser Thr Tyr Gly Asn Val
                90                95                100

gta acg caa aaa att acc cct gac gtg gga gtt tac gtc ccg cgt ggt 451
Val Thr Gln Lys Ile Thr Pro Asp Val Gly Val Tyr Val Pro Arg Gly
                105                110                115

gtg gca aac ggc ttc cag gcg ctc gag gac ggc acg ctg tac acc tac 499
Val Ala Asn Gly Phe Gln Ala Leu Glu Asp Gly Thr Leu Tyr Thr Tyr
                120                125                130

ctc gtc aac gat cat tgg tcc ccc gac gcg cat tac gcc aac gtc aac 547
Leu Val Asn Asp His Trp Ser Pro Asp Ala His Tyr Ala Asn Val Asn
                135                140                145

ctc aac atg atc gac tgg ccg ctg ccc atc acc gag atc tcc gaa aaa 595
Leu Asn Met Ile Asp Trp Pro Leu Pro Ile Thr Glu Ile Ser Glu Lys
                150                155                160                165

gat aaa aaa cat cca gcg ctt atc gac gcc acc ccc ctg ccc gcc cgc 643
Asp Lys Lys His Pro Ala Leu Ile Asp Ala Thr Pro Leu Pro Ala Arg
                170                175                180

aag gtt ctc gtg gtc ggc gcc ggc gga caa ctg gga acc gcg cta cgc 691
Lys Val Leu Val Val Gly Ala Gly Gly Gln Leu Gly Thr Ala Leu Arg
                185                190                195

gcg cag ttc cca gac gcg gaa ttt gtc acg cgc caa gaa ctc gat atc 739
Ala Gln Phe Pro Asp Ala Glu Phe Val Thr Arg Gln Glu Leu Asp Ile
                200                205                210

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acc tca gat ctc acc gag gct cgc gcg tgg aaa caa tac tcc acc atc 787
 Thr Ser Asp Leu Thr Glu Ala Arg Ala Trp Lys Gln Tyr Ser Thr Ile
 215 220 225

ata aac gcc gcc gcc tac act gcc gtt gac cag gca gaa cac gac cgc 835
 Ile Asn Ala Ala Ala Tyr Thr Ala Val Asp Gln Ala Glu His Asp Arg
 230 235 240 245

gca gca gcg tgg gac att aac gca gcg gca gtg gct acc tcg cga cca 883
 Ala Ala Ala Trp Asp Ile Asn Ala Ala Ala Val Ala Thr Ser Arg Pro
 250 255 260

tcg cgc gcg aca aca acc tca ccc tcg tgc acg tgt cct cag att atg 931
 Ser Arg Ala Thr Thr Ser Pro Ser Cys Thr Cys Pro Gln Ile Met
 265 270 275

tct tcg acg gtg cgg gcg aat cct acg atg aaa acg cac cgt ttt ccc 979
 Ser Ser Thr Val Arg Ala Asn Pro Thr Met Lys Thr His Arg Phe Pro
 280 285 290

cac tcg gcg tgt acg gcc aat cca aag cag ccg gcg aca tcg 1021
 His Ser Ala Cys Thr Ala Asn Pro Lys Gln Pro Ala Thr Ser
 295 300 305

taagcac 1028

<210> 448
 <211> 307
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 448
 Met Glu Tyr Gly Lys Gln Leu Thr Ser His Thr Thr Asp Ile Glu Gly
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Leu Leu Val Phe Asp Phe Pro Val His Gly Asp Asn Arg Gly Trp Phe
 20 25 30

Lys Glu Asn Trp Gln Arg Thr Lys Met Thr Asn Leu Gly Leu Pro Asp
 35 40 45

Phe Gly Pro Val Gln Asn Asn Met Ser Phe Asn Ala Thr Ala Gly Thr
 50 55 60

Thr Arg Gly Met His Ala Glu Pro Trp Asp Lys Phe Val Ser Val Ala
 65 70 75 80

Val Gly Ser Val Phe Gly Ala Trp Val Asp Leu Arg Ala Gly Ser Ser
 85 90 95

Thr Tyr Gly Asn Val Val Thr Gln Lys Ile Thr Pro Asp Val Gly Val
 100 105 110

Tyr Val Pro Arg Gly Val Ala Asn Gly Phe Gln Ala Leu Glu Asp Gly
 115 120 125

Thr Leu Tyr Thr Tyr Leu Val Asn Asp His Trp Ser Pro Asp Ala His
 130 135 140

Tyr Ala Asn Val Asn Leu Asn Met Ile Asp Trp Pro Leu Pro Ile Thr
 145 150 155 160
 Glu Ile Ser Glu Lys Asp Lys Lys His Pro Ala Leu Ile Asp Ala Thr
 165 170 175
 Pro Leu Pro Ala Arg Lys Val Leu Val Val Gly Ala Gly Gly Gln Leu
 180 185 190
 Gly Thr Ala Leu Arg Ala Gln Phe Pro Asp Ala Glu Phe Val Thr Arg
 195 200 205
 Gln Glu Leu Asp Ile Thr Ser Asp Leu Thr Glu Ala Arg Ala Trp Lys
 210 215 220
 Gln Tyr Ser Thr Ile Ile Asn Ala Ala Ala Tyr Thr Ala Val Asp Gln
 225 230 235 240
 Ala Glu His Asp Arg Ala Ala Ala Trp Asp Ile Asn Ala Ala Ala Val
 245 250 255
 Ala Thr Ser Arg Pro Ser Arg Ala Thr Thr Thr Ser Pro Ser Cys Thr
 260 265 270
 Cys Pro Gln Ile Met Ser Ser Thr Val Arg Ala Asn Pro Thr Met Lys
 275 280 285
 Thr His Arg Phe Pro His Ser Ala Cys Thr Ala Asn Pro Lys Gln Pro
 290 295 300
 Ala Thr Ser
 305

<210> 449
 <211> 1056
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
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 <222> (101)..(1033)
 <223> RXA00825

<400> 449
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 tagtgcacgc cgattctgag aaacaactaa agtgagccac atg cgc aca gta gtt 115
 Met Arg Thr Val Val
 1 5
 acc ggc ggt gcc ggc ttc atc gga tcc cat ctc gtt gac ctt ttg atc 163
 Thr Gly Gly Ala Gly Phe Ile Gly Ser His Leu Val Asp Leu Leu Ile
 10 15 20
 aag gaa ggc cac gag gtc gtt gtg atc gat aac ctc tcc cgc gga cgc 211
 Lys Glu Gly His Glu Val Val Val Ile Asp Asn Leu Ser Arg Gly Arg
 25 30 35
 ctg gag aat ctc tcc gat gcg gaa gcc acc gga aaa ctc acc ttt gtg 259
 Leu Glu Asn Leu Ser Asp Ala Glu Ala Thr Gly Lys Leu Thr Phe Val

40	45	50	
gaa gcc gat ctt ctc gac gtt gat ttc aac gag ttt cta gga acc cac Glu Ala Asp Leu Leu Asp Val Asp Phe Asn Glu Phe Leu Gly Thr His 55 60 65			307
aag cct gag gtt att ttc cac ctg gca gcg caa atc gat gtg cgc cac Lys Pro Glu Val Ile Phe His Leu Ala Ala Gln Ile Asp Val Arg His 70 75 80 85			355
tct gtt gta gat cct ctt cac gac gcc gaa acc aac att ttg tcc acc Ser Val Val Asp Pro Leu His Asp Ala Glu Thr Asn Ile Leu Ser Thr 90 95 100			403
atc cgc atc gct gac gct gcc cgc cag cac ggt gtt cgc aag gtt gtc Ile Arg Ile Ala Asp Ala Ala Arg Gln His Gly Val Arg Lys Val Val 105 110 115			451
ttt acc tcc tca ggc ggt tcc att tac ggt gag cct tcg gaa ttc cca Phe Thr Ser Ser Gly Gly Ser Ile Tyr Gly Glu Pro Ser Glu Phe Pro 120 125 130			499
gtt gat gaa acc gtg cca gtg gat cca cat tcc cct tat gcg gca tcc Val Asp Glu Thr Val Pro Val Asp Pro His Ser Pro Tyr Ala Ala Ser 135 140 145			547
aag gtg tcc ggt gaa att tac ctg aac acc ttc cgc cac ctg tac ggc Lys Val Ser Gly Glu Ile Tyr Leu Asn Thr Phe Arg His Leu Tyr Gly 150 155 160 165			595
tta gac tgt tct cac atc gca ccg gca aat gtt tac ggc cca cgc caa Leu Asp Cys Ser His Ile Ala Pro Ala Asn Val Tyr Gly Pro Arg Gln 170 175 180			643
gat cca cac ggt gaa gca gga gtt gtg gcc att ttc gcg ctg cga ctt Asp Pro His Gly Glu Ala Gly Val Val Ala Ile Phe Ala Leu Arg Leu 185 190 195			691
ctg gga ggc ctg gac acc aag gta ttc ggc gac ggc gga aac acc cgc Leu Gly Gly Leu Asp Thr Lys Val Phe Gly Asp Gly Gly Asn Thr Arg 200 205 210			739
gac tac gtc tac gtc ggt gac gta gtt cgt gct ttc tac ctg gct tct Asp Tyr Val Tyr Val Gly Asp Val Val Arg Ala Phe Tyr Leu Ala Ser 215 220 225			787
ggg gaa atc ggt ggg gga gag cgc ttc aac att ggc acc tct gtg gaa Gly Glu Ile Gly Gly Gly Glu Arg Phe Asn Ile Gly Thr Ser Val Glu 230 235 240 245			835
acc tct gac cgc cag ctg cac acc ctc gtg gcc act gcg gca ggt tcc Thr Ser Asp Arg Gln Leu His Thr Leu Val Ala Thr Ala Ala Gly Ser 250 255 260			883
aaa gat gat cct gaa tat gca cct gca cgt ctc ggc gat gtg cca cgc Lys Asp Asp Pro Glu Tyr Ala Pro Ala Arg Leu Gly Asp Val Pro Arg 265 270 275			931
agt gca ctc agc ttc ggc aag gcc aaa gag gtg ctt ggt tgg gag cct Ser Ala Leu Ser Phe Gly Lys Ala Lys Glu Val Leu Gly Trp Glu Pro 280 285 290			979

gag gtg aac atc gaa caa ggt gtg gcc aag act gtg gag tac ttc cgc 1027
 Glu Val Asn Ile Glu Gln Gly Val Ala Lys Thr Val Glu Tyr Phe Arg
 295 300 305

act cac taggggaaaa tccaccacaa atc 1056
 Thr His
 310

<210> 450

<211> 311

<212> PRT

<213> Corynebacterium glutamicum

<400> 450

Met Arg Thr Val Val Thr Gly Gly Ala Gly Phe Ile Gly Ser His Leu
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Val Asp Leu Leu Ile Lys Glu Gly His Glu Val Val Val Ile Asp Asn
 20 25 30

Leu Ser Arg Gly Arg Leu Glu Asn Leu Ser Asp Ala Glu Ala Thr Gly
 35 40 45

Lys Leu Thr Phe Val Glu Ala Asp Leu Leu Asp Val Asp Phe Asn Glu
 50 55 60

Phe Leu Gly Thr His Lys Pro Glu Val Ile Phe His Leu Ala Ala Gln
 65 70 75 80

Ile Asp Val Arg His Ser Val Val Asp Pro Leu His Asp Ala Glu Thr
 85 90 95

Asn Ile Leu Ser Thr Ile Arg Ile Ala Asp Ala Ala Arg Gln His Gly
 100 105 110

Val Arg Lys Val Val Phe Thr Ser Ser Gly Gly Ser Ile Tyr Gly Glu
 115 120 125

Pro Ser Glu Phe Pro Val Asp Glu Thr Val Pro Val Asp Pro His Ser
 130 135 140

Pro Tyr Ala Ala Ser Lys Val Ser Gly Glu Ile Tyr Leu Asn Thr Phe
 145 150 155 160

Arg His Leu Tyr Gly Leu Asp Cys Ser His Ile Ala Pro Ala Asn Val
 165 170 175

Tyr Gly Pro Arg Gln Asp Pro His Gly Glu Ala Gly Val Val Ala Ile
 180 185 190

Phe Ala Leu Arg Leu Leu Gly Gly Leu Asp Thr Lys Val Phe Gly Asp
 195 200 205

Gly Gly Asn Thr Arg Asp Tyr Val Tyr Val Gly Asp Val Val Arg Ala
 210 215 220

Phe Tyr Leu Ala Ser Gly Glu Ile Gly Gly Gly Glu Arg Phe Asn Ile
 225 230 235 240

Gly Thr Ser Val Glu Thr Ser Asp Arg Gln Leu His Thr Leu Val Ala
 245 250 255
 Thr Ala Ala Gly Ser Lys Asp Asp Pro Glu Tyr Ala Pro Ala Arg Leu
 260 265 270
 Gly Asp Val Pro Arg Ser Ala Leu Ser Phe Gly Lys Ala Lys Glu Val
 275 280 285
 Leu Gly Trp Glu Pro Glu Val Asn Ile Glu Gln Gly Val Ala Lys Thr
 290 295 300
 Val Glu Tyr Phe Arg Thr His
 305 310

<210> 451
 <211> 1140
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
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 <222> (101)..(1117)
 <223> RXA02054

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 taactctgcc agctcgccccg gacgaactaa ggtagacggc atg act tct ttg ctt 115
 Met Thr Ser Leu Leu
 1 5
 gtg acc gga ggt gcc gga ttt atc ggc gcc aac ttc gtc cgc caa acc 163
 Val Thr Gly Gly Ala Gly Phe Ile Gly Ala Asn Phe Val Arg Gln Thr
 10 15 20
 gta gag cag cac cct gaa tac acc cac atc acg gtg ctg gat aaa ctc 211
 Val Glu Gln His Pro Glu Tyr Thr His Ile Thr Val Leu Asp Lys Leu
 25 30 35
 acc tac gca gga aac gcc gac aat ctc aaa ggc ctc ccc gac agc aaa 259
 Thr Tyr Ala Gly Asn Ala Asp Asn Leu Lys Gly Leu Pro Asp Ser Lys
 40 45 50
 gta acc ctc atc gaa ggc gat atc tgc gat gct gaa tta gtc gac tcc 307
 Val Thr Leu Ile Glu Gly Asp Ile Cys Asp Ala Glu Leu Val Asp Ser
 55 60 65
 ctg gtc aaa gac cac gac atc aca gtc cac ttc gca gca gaa tcc cac 355
 Leu Val Lys Asp His Asp Ile Thr Val His Phe Ala Ala Glu Ser His
 70 75 80 85
 aac gac aac tcc ctc aac gac ccc tcc ccg ttt gtt cac act aac ctc 403
 Asn Asp Asn Ser Leu Asn Asp Pro Ser Pro Phe Val His Thr Asn Leu
 90 95 100
 atc ggc acc ttt gtc ctg cta gaa gca gtc cgc aag cac aac aaa cgc 451
 Ile Gly Thr Phe Val Leu Leu Glu Ala Val Arg Lys His Asn Lys Arg
 105 110 115

ttc cac cac atc tcc acc gat gaa gtc ttc ggc gat cta gag ctg gat	499
Phe His His Ile Ser Thr Asp Glu Val Phe Gly Asp Leu Glu Leu Asp	
120 125 130	
gat cca aac cgc ttc act gaa acc acc gcc tac aag cca tcg tct cca	547
Asp Pro Asn Arg Phe Thr Glu Thr Thr Ala Tyr Lys Pro Ser Ser Pro	
135 140 145	
tat tct gca acc aag gca ggg tct gat cac ttg gta cac gca tgg atc	595
Tyr Ser Ala Thr Lys Ala Gly Ser Asp His Leu Val His Ala Trp Ile	
150 155 160 165	
cgc tcc ttc gga atc cag gca acc atg tct aac tgc tcc aac aat tac	643
Arg Ser Phe Gly Ile Gln Ala Thr Met Ser Asn Cys Ser Asn Asn Tyr	
170 175 180	
ggt ccc tac cag cac att gaa aag ttc atc ccc cgc cag atc acc aat	691
Gly Pro Tyr Gln His Ile Glu Lys Phe Ile Pro Arg Gln Ile Thr Asn	
185 190 195	
att ctg gcc ggc ctg aca cca aaa ctt tat gga acc ggc gag cag gtc	739
Ile Leu Ala Gly Leu Thr Pro Lys Leu Tyr Gly Thr Gly Glu Gln Val	
200 205 210	
cgc gac tgg atc cac gtc gat gat cac aat gac gcc gtc cac ctg atc	787
Arg Asp Trp Ile His Val Asp Asp His Asn Asp Ala Val His Leu Ile	
215 220 225	
ctg agt aag ggc aag atc ggc gaa acc tac atc atc ggc gcc gac aac	835
Leu Ser Lys Gly Lys Ile Gly Glu Thr Tyr Ile Ile Gly Ala Asp Asn	
230 235 240 245	
gat cat gtg aat aac aag cag gtc atc gag ctt att tgt gaa ctc atg	883
Asp His Val Asn Asn Lys Gln Val Ile Glu Leu Ile Cys Glu Leu Met	
250 255 260	
ggc ctc gac aaa aac gca tac gag cac gtc gca gac cgc ccc ggc cac	931
Gly Leu Asp Lys Asn Ala Tyr Glu His Val Ala Asp Arg Pro Gly His	
265 270 275	
gat atg cgt tac gcc atg gat tcc acc aag ctg cgc acc gag ctc ggc	979
Asp Met Arg Tyr Ala Met Asp Ser Thr Lys Leu Arg Thr Glu Leu Gly	
280 285 290	
tgg gca cct aaa tac acc gac gtt gat tcc ggc atg cgc aaa ggc cta	1027
Trp Ala Pro Lys Tyr Thr Asp Val Asp Ser Gly Met Arg Lys Gly Leu	
295 300 305	
gag cag acc atc gat tgg tac cgc gaa aac gag gcc tgg tgg cgc cct	1075
Glu Gln Thr Ile Asp Trp Tyr Arg Glu Asn Glu Ala Trp Trp Arg Pro	
310 315 320 325	
gcc aag aac aac gtc gaa gct acc tac gct aag cag gga caa	1117
Ala Lys Asn Asn Val Glu Ala Thr Tyr Ala Lys Gln Gly Gln	
330 335	
taatggaata cggtaaacaa ctc	1140

<210> 452

<211> 339

<212> PRT

<213> Corynebacterium glutamicum

<400> 452

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Met Thr Ser Leu Leu Val Thr Gly Gly Ala Gly Phe Ile Gly Ala Asn
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Phe Val Arg Gln Thr Val Glu Gln His Pro Glu Tyr Thr His Ile Thr
      20           25           30

Val Leu Asp Lys Leu Thr Tyr Ala Gly Asn Ala Asp Asn Leu Lys Gly
      35           40           45

Leu Pro Asp Ser Lys Val Thr Leu Ile Glu Gly Asp Ile Cys Asp Ala
      50           55           60

Glu Leu Val Asp Ser Leu Val Lys Asp His Asp Ile Thr Val His Phe
      65           70           75           80

Ala Ala Glu Ser His Asn Asp Asn Ser Leu Asn Asp Pro Ser Pro Phe
      85           90           95

Val His Thr Asn Leu Ile Gly Thr Phe Val Leu Leu Glu Ala Val Arg
      100          105          110

Lys His Asn Lys Arg Phe His His Ile Ser Thr Asp Glu Val Phe Gly
      115          120          125

Asp Leu Glu Leu Asp Asp Pro Asn Arg Phe Thr Glu Thr Thr Ala Tyr
      130          135          140

Lys Pro Ser Ser Pro Tyr Ser Ala Thr Lys Ala Gly Ser Asp His Leu
      145          150          155          160

Val His Ala Trp Ile Arg Ser Phe Gly Ile Gln Ala Thr Met Ser Asn
      165          170          175

Cys Ser Asn Asn Tyr Gly Pro Tyr Gln His Ile Glu Lys Phe Ile Pro
      180          185          190

Arg Gln Ile Thr Asn Ile Leu Ala Gly Leu Thr Pro Lys Leu Tyr Gly
      195          200          205

Thr Gly Glu Gln Val Arg Asp Trp Ile His Val Asp Asp His Asn Asp
      210          215          220

Ala Val His Leu Ile Leu Ser Lys Gly Lys Ile Gly Glu Thr Tyr Ile
      225          230          235          240

Ile Gly Ala Asp Asn Asp His Val Asn Asn Lys Gln Val Ile Glu Leu
      245          250          255

Ile Cys Glu Leu Met Gly Leu Asp Lys Asn Ala Tyr Glu His Val Ala
      260          265          270

Asp Arg Pro Gly His Asp Met Arg Tyr Ala Met Asp Ser Thr Lys Leu
      275          280          285

Arg Thr Glu Leu Gly Trp Ala Pro Lys Tyr Thr Asp Val Asp Ser Gly
      290          295          300

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Met Arg Lys Gly Leu Glu Gln Thr Ile Asp Trp Tyr Arg Glu Asn Glu
305 310 315 320

Ala Trp Trp Arg Pro Ala Lys Asn Asn Val Glu Ala Thr Tyr Ala Lys
325 330 335

Gln Gly Gln

<210> 453

<211> 909

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(886)

<223> RXN00427

<400> 453

gcgggtcattg tgaccacaaa tcgtgtggaa ttgctgcggc attccctcga ggttggttgcc 60

aatcaaacct atccggtgaa acacattgtg gtggtggata atg ggg cgg atc cta 115
Met Gly Arg Ile Leu
1 5

gta ttc tat agt gtc act tta gag gtg gcg gga gac cgt ccc gtt tac 163
Val Phe Tyr Ser Val Thr Leu Glu Val Ala Gly Asp Arg Pro Val Tyr
10 15 20

acg cct tcg cgc acc aat ttg ggc gac ggt ggc ggt ttt gct ttt ggt 211
Thr Pro Ser Arg Thr Asn Leu Gly Asp Gly Gly Gly Phe Ala Phe Gly
25 30 35

ttt ttg acg gcg ttg gcg ctg ggg gcg aac gcg gtg tgg tgc aca gac 259
Phe Leu Thr Ala Leu Ala Leu Gly Ala Asn Ala Val Trp Cys Thr Asp
40 45 50

gat gac ggc cgg ccg gag ggg cca ggg gtg ttg aag acg ctt atc gac 307
Asp Asp Gly Arg Pro Glu Gly Pro Gly Val Leu Lys Thr Leu Ile Asp
55 60 65

gcc gct tct cgg cat aat ctg gag gag gtt tct ccg gtg gta tgc aat 355
Ala Ala Ser Arg His Asn Leu Glu Glu Val Ser Pro Val Val Cys Asn
70 75 80 85

gct gat gat ccg gag cgg ttg gca ttt ccg ctg cgt cgg ggc ttg gag 403
Ala Asp Asp Pro Glu Arg Leu Ala Phe Pro Leu Arg Arg Gly Leu Glu
90 95 100

tgg cgt cgg atg cgc agt gag ttg att gat cca gcc aac ccg gag gat 451
Trp Arg Arg Met Arg Ser Glu Leu Ile Asp Pro Ala Asn Pro Glu Asp
105 110 115

gat ttg ctg ccg ggc atc gcc tcc ttg ttc aat ggt gcc ctg atc agc 499
Asp Leu Leu Pro Gly Ile Ala Ser Leu Phe Asn Gly Ala Leu Ile Ser
120 125 130

gct tat gca atg gag cgc att ggc gtg ccg gac tat cga ctg ttt att 547
Ala Tyr Ala Met Glu Arg Ile Gly Val Pro Asp Tyr Arg Leu Phe Ile

135	140	145	
cgc ggc gat gag gtg gag tat cac cgc cgt ttg gtg cgt tcc ggt ttg			595
Arg Gly Asp Glu Val Glu Tyr His Arg Arg Leu Val Arg Ser Gly Leu			
150	155	160	165
ccg ttt ggt acg tgt ttg acc acg gcg tat ttg cac ccg gat ggt tct			643
Pro Phe Gly Thr Cys Leu Thr Thr Ala Tyr Leu His Pro Asp Gly Ser			
	170	175	180
gat gag ttc aag ccg att ctg ggt ggg cgg atg cat acg cag tat ccg			691
Asp Glu Phe Lys Pro Ile Leu Gly Gly Arg Met His Thr Gln Tyr Pro			
	185	190	195
gat aat gat ttc aag agg ttt ttc acc tac cgc aac cgt ggc tac ctg			739
Asp Asn Asp Phe Lys Arg Phe Phe Thr Tyr Arg Asn Arg Gly Tyr Leu			
	200	205	210
atg agc cag ccg gga atg cgc aag ctt ctc cct cag gaa tat gcg cgc			787
Met Ser Gln Pro Gly Met Arg Lys Leu Leu Pro Gln Glu Tyr Ala Arg			
	215	220	225
ttt gcg tgg ttc ttc ctg gtt cag aaa cgg gat gtg aag gga ttc cgg			835
Phe Ala Trp Phe Phe Leu Val Gln Lys Arg Asp Val Lys Gly Phe Arg			
	230	235	240
gag tgg ctg cgc ctg cac aaa ctg ggc cgc gac gag aaa ttc aat agg			883
Glu Trp Leu Arg Leu His Lys Leu Gly Arg Asp Glu Lys Phe Asn Arg			
	250	255	260
ccc tagatcagtt ttagtagttc ctc			909
Pro			

<210> 454

<211> 262

<212> PRT

<213> Corynebacterium glutamicum

<400> 454

Met Gly Arg Ile Leu Val Phe Tyr Ser Val Thr Leu Glu Val Ala Gly			
1	5	10	15
Asp Arg Pro Val Tyr Thr Pro Ser Arg Thr Asn Leu Gly Asp Gly Gly			
	20	25	30
Gly Phe Ala Phe Gly Phe Leu Thr Ala Leu Ala Leu Gly Ala Asn Ala			
	35	40	45
Val Trp Cys Thr Asp Asp Asp Gly Arg Pro Glu Gly Pro Gly Val Leu			
	50	55	60
Lys Thr Leu Ile Asp Ala Ala Ser Arg His Asn Leu Glu Glu Val Ser			
	65	70	75
Pro Val Val Cys Asn Ala Asp Asp Pro Glu Arg Leu Ala Phe Pro Leu			
	85	90	95
Arg Arg Gly Leu Glu Trp Arg Arg Met Arg Ser Glu Leu Ile Asp Pro			
	100	105	110

Ala Asn Pro Glu Asp Asp Leu Leu Pro Gly Ile Ala Ser Leu Phe Asn
 115 120 125

Gly Ala Leu Ile Ser Ala Tyr Ala Met Glu Arg Ile Gly Val Pro Asp
 130 135 140

Tyr Arg Leu Phe Ile Arg Gly Asp Glu Val Glu Tyr His Arg Arg Leu
 145 150 155 160

Val Arg Ser Gly Leu Pro Phe Gly Thr Cys Leu Thr Thr Ala Tyr Leu
 165 170 175

His Pro Asp Gly Ser Asp Glu Phe Lys Pro Ile Leu Gly Gly Arg Met
 180 185 190

His Thr Gln Tyr Pro Asp Asn Asp Phe Lys Arg Phe Phe Thr Tyr Arg
 195 200 205

Asn Arg Gly Tyr Leu Met Ser Gln Pro Gly Met Arg Lys Leu Leu Pro
 210 215 220

Gln Glu Tyr Ala Arg Phe Ala Trp Phe Phe Leu Val Gln Lys Arg Asp
 225 230 235 240

Val Lys Gly Phe Arg Glu Trp Leu Arg Leu His Lys Leu Gly Arg Asp
 245 250 255

Glu Lys Phe Asn Arg Pro
 260

<210> 455
 <211> 555
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(532)
 <223> FRXA00427

<400> 455
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 gcgcagtgag ttgattgac cagccaaccc ggaggatgat ttg ctg ccg ggc atc 115
 Leu Leu Pro Gly Ile
 1 5

gcc tcc ttg ttc aat ggt gcc ctg atc agc gct tat gca atg gag cgc 163
 Ala Ser Leu Phe Asn Gly Ala Leu Ile Ser Ala Tyr Ala Met Glu Arg
 10 15 20

att ggc gtg ccg gac tat cga ctg ttt att cgc ggc gat gag gtg gag 211
 Ile Gly Val Pro Asp Tyr Arg Leu Phe Ile Arg Gly Asp Glu Val Glu
 25 30 35

tat cac cgc cgt ttg gtg cgt tcc ggt ttg ccg ttt ggt acg tgt ttg 259
 Tyr His Arg Arg Leu Val Arg Ser Gly Leu Pro Phe Gly Thr Cys Leu
 40 45 50

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acc acg gcg tat ttg cac ccg gat ggt tct gat gag ttc aag ccg att 307
Thr Thr Ala Tyr Leu His Pro Asp Gly Ser Asp Glu Phe Lys Pro Ile
    55                      60                      65

ctg ggt ggg cgg atg cat acg cag tat ccg gat aat gat ttc aag agg 355
Leu Gly Gly Arg Met His Thr Gln Tyr Pro Asp Asn Asp Phe Lys Arg
    70                      75                      80                      85

ttt ttc acc tac cgc aac cgt ggc tac ctg atg agc cag ccg gga atg 403
Phe Phe Thr Tyr Arg Asn Arg Gly Tyr Leu Met Ser Gln Pro Gly Met
    90                      95                      100

cgc aag ctt ctc cct cag gaa tat gcg cgc ttt gcg tgg ttc ttc ctg 451
Arg Lys Leu Leu Pro Gln Glu Tyr Ala Arg Phe Ala Trp Phe Phe Leu
    105                      110                      115

gtt cag aaa cgg gat gtg aag gga ttc cgg gag tgg ctg cgc ctg cac 499
Val Gln Lys Arg Asp Val Lys Gly Phe Arg Glu Trp Leu Arg Leu His
    120                      125                      130

aaa ctg ggc cgc gac gag aaa ttc aat agg ccc tagatcagtt ttagtagttc 552
Lys Leu Gly Arg Asp Glu Lys Phe Asn Arg Pro
    135                      140

ctc 555

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<210> 456
<211> 144
<212> PRT
<213> Corynebacterium glutamicum

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<400> 456
Leu Leu Pro Gly Ile Ala Ser Leu Phe Asn Gly Ala Leu Ile Ser Ala
  1                      5                      10                      15

Tyr Ala Met Glu Arg Ile Gly Val Pro Asp Tyr Arg Leu Phe Ile Arg
    20                      25                      30

Gly Asp Glu Val Glu Tyr His Arg Arg Leu Val Arg Ser Gly Leu Pro
    35                      40                      45

Phe Gly Thr Cys Leu Thr Thr Ala Tyr Leu His Pro Asp Gly Ser Asp
    50                      55                      60

Glu Phe Lys Pro Ile Leu Gly Gly Arg Met His Thr Gln Tyr Pro Asp
    65                      70                      75                      80

Asn Asp Phe Lys Arg Phe Phe Thr Tyr Arg Asn Arg Gly Tyr Leu Met
    85                      90                      95

Ser Gln Pro Gly Met Arg Lys Leu Leu Pro Gln Glu Tyr Ala Arg Phe
    100                      105                      110

Ala Trp Phe Phe Leu Val Gln Lys Arg Asp Val Lys Gly Phe Arg Glu
    115                      120                      125

Trp Leu Arg Leu His Lys Leu Gly Arg Asp Glu Lys Phe Asn Arg Pro
    130                      135                      140

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<210> 457
<211> 507
<212> DNA
<213> Corynebacterium glutamicum
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<220>  
<221> CDS  
<222> (101) .. (484)  
<223> RXA00327
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<400> 457																
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ctaggggggcc	aggcgcgga	tgattgggtt	tgtcacgccg	atg	att	cag	gcg	gcg	115							
				Met	Ile	Gln	Ala	Ala								
					1			5								
ttg	tgg	atc	gtg	ctc	ttt	tta	ttc	gct	gat	cgc	ctg	tcc	aat	ccg	ctg	163
Leu	Trp	Ile	Val	Leu	Phe	Leu	Phe	Ala	Asp	Arg	Leu	Ser	Asn	Pro	Leu	
			10					15						20		
gtt	ttt	gtc	agc	gcc	atc	atg	ttc	gcg	att	tcc	ttt	agc	tcc	ccc	gtg	211
Val	Phe	Val	Ser	Ala	Ile	Met	Phe	Ala	Ile	Ser	Phe	Ser	Ser	Pro	Val	
			25					30					35			
gcg	aac	ttc	ggt	ttc	gat	acg	atc	tgc	gaa	aaa	ctc	gac	cgc	cgc	gtc	259
Ala	Asn	Phe	Gly	Phe	Asp	Thr	Ile	Cys	Glu	Lys	Leu	Asp	Arg	Arg	Val	
		40					45					50				
atg	gtc	gcc	ggc	acc	ggc	atg	gcc	aac	atg	agc	gcc	tac	att	tgc	gcg	307
Met	Val	Ala	Gly	Thr	Gly	Met	Ala	Asn	Met	Ser	Ala	Tyr	Ile	Cys	Ala	
		55				60					65					
atg	ctg	gcc	aca	caa	atc	atc	gga	ttt	tta	ctc	gac	tgg	aac	gcc	gac	355
Met	Leu	Ala	Thr	Gln	Ile	Ile	Gly	Phe	Leu	Leu	Asp	Trp	Asn	Ala	Asp	
					75					80					85	
ggc	cac	gcc	tac	acc	tgg	tcg	aat	ttc	cag	gtg	gcg	tgg	ctt	ggt	ctg	403
Gly	His	Ala	Tyr	Thr	Trp	Ser	Asn	Phe	Gln	Val	Ala	Trp	Leu	Gly	Leu	
				90					95					100		
ggc	gcg	gtg	tgg	ctg	gca	ggc	atg	atc	ggg	ctt	gca	gtc	tgc	ctc	ctg	451
Gly	Ala	Val	Trp	Leu	Ala	Gly	Met	Ile	Gly	Leu	Ala	Val	Cys	Leu	Leu	
			105					110					115			
ctg	cag	cgt	cga	aaa	aat	att	gct	ttt	cga	cgc	taaaaccgga	ccgtaaccgc	504			
Leu	Gln	Arg	Arg	Lys	Asn	Ile	Ala	Phe	Arg	Arg						
		120					125									
taq															507	

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<210> 458
<211> 128
<212> PRT
<213> Corynebacterium glutamicum
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<400> 458

Met Ile Gln Ala Ala Leu Trp Ile Val Leu Phe Leu Phe Ala Asp Arg
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 Leu Ser Asn Pro Leu Val Phe Val Ser Ala Ile Met Phe Ala Ile Ser
 20 25 30
 Phe Ser Ser Pro Val Ala Asn Phe Gly Phe Asp Thr Ile Cys Glu Lys
 35 40 45
 Leu Asp Arg Arg Val Met Val Ala Gly Thr Gly Met Ala Asn Met Ser
 50 55 60
 Ala Tyr Ile Cys Ala Met Leu Ala Thr Gln Ile Ile Gly Phe Leu Leu
 65 70 75 80
 Asp Trp Asn Ala Asp Gly His Ala Tyr Thr Trp Ser Asn Phe Gln Val
 85 90 95
 Ala Trp Leu Gly Leu Gly Ala Val Trp Leu Ala Gly Met Ile Gly Leu
 100 105 110
 Ala Val Cys Leu Leu Leu Gln Arg Arg Lys Asn Ile Ala Phe Arg Arg
 115 120 125

<210> 459
 <211> 615
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(592)
 <223> RXA00328

<400> 459
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 attaggtcta ccaaggactt ttaaagatcg ggtaaaacct gtg ggc gtt gaa agg 115
 Val Gly Val Glu Arg
 1 5
 ggc aag gtc tct gcc aag gca cta gtt gtc tgg ttg acg gca atg tgc 163
 Gly Lys Val Ser Ala Lys Ala Leu Val Val Trp Leu Thr Ala Met Cys
 10 15 20
 gtg tac atc gtg gcc att gct ggt cga aca tca ttt ggt gtc gcc gga 211
 Val Tyr Ile Val Ala Ile Ala Gly Arg Thr Ser Phe Gly Val Ala Gly
 25 30 35
 gtg cat gcg atc gat cgc ttt gat atc gac gcc tcc cgg ttg gcc gtg 259
 Val His Ala Ile Asp Arg Phe Asp Ile Asp Ala Ser Arg Leu Ala Val
 40 45 50
 ttc act tct gtt cag gtt gga gtc tat gtt ctc gcg cag att ccc atg 307
 Phe Thr Ser Val Gln Val Gly Val Tyr Val Leu Ala Gln Ile Pro Met
 55 60 65

ggc atg ctg gtg gac agg ttc gac gcc cgg aaa ctc ttg ctg gct ggc 355
 Gly Met Leu Val Asp Arg Phe Asp Ala Arg Lys Leu Leu Leu Ala Gly
 70 75 80 85

 gct tta att ttg gca gct ggc cag ctc att ttg ggt ttc act gat tct 403
 Ala Leu Ile Leu Ala Ala Gly Gln Leu Ile Leu Gly Phe Thr Asp Ser
 90 95 100

 tat atg atc gcc att ttt gcc cga gtg ctc atc agt gtt ggc gat tct 451
 Tyr Met Ile Ala Ile Phe Ala Arg Val Leu Ile Ser Val Gly Asp Ser
 105 110 115

 tct gca ttt ttg tcc gtg atg cga ctg ttg ccc aac tgg ttc ccg atg 499
 Ser Ala Phe Leu Ser Val Met Arg Leu Leu Pro Asn Trp Phe Pro Met
 120 125 130

 tct tgg aca cct gtg ttg cag cag ctc acg ggc gct ttt ggc ttt gtg 547
 Ser Trp Thr Pro Val Leu Gln Gln Leu Thr Gly Ala Phe Gly Phe Val
 135 140 145

 ggg cag ttt tct ccg cgg tgc cgt ttt tgc aca tac tca aca cct 592
 Gly Gln Phe Ser Pro Arg Cys Arg Phe Cys Thr Tyr Ser Thr Pro
 150 155 160

 taggggtggac aattcctttc gca 615

<210> 460

<211> 164

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 460

Val Gly Val Glu Arg Gly Lys Val Ser Ala Lys Ala Leu Val Val Trp
 1 5 10 15

 Leu Thr Ala Met Cys Val Tyr Ile Val Ala Ile Ala Gly Arg Thr Ser
 20 25 30

 Phe Gly Val Ala Gly Val His Ala Ile Asp Arg Phe Asp Ile Asp Ala
 35 40 45

 Ser Arg Leu Ala Val Phe Thr Ser Val Gln Val Gly Val Tyr Val Leu
 50 55 60

 Ala Gln Ile Pro Met Gly Met Leu Val Asp Arg Phe Asp Ala Arg Lys
 65 70 75 80

 Leu Leu Leu Ala Gly Ala Leu Ile Leu Ala Ala Gly Gln Leu Ile Leu
 85 90 95

 Gly Phe Thr Asp Ser Tyr Met Ile Ala Ile Phe Ala Arg Val Leu Ile
 100 105 110

 Ser Val Gly Asp Ser Ser Ala Phe Leu Ser Val Met Arg Leu Leu Pro
 115 120 125

 Asn Trp Phe Pro Met Ser Trp Thr Pro Val Leu Gln Gln Leu Thr Gly
 130 135 140

 Ala Phe Gly Phe Val Gly Gln Phe Ser Pro Arg Cys Arg Phe Cys Thr

145

150

155

160

Tyr Ser Thr Pro

<210> 461

<211> 1347

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1324)

<223> RXA00329

<400> 461

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ccgcgccttc atagtttggg cagcagcctg tcttgtgtat atg gca gcc att acc 115
 Met Ala Ala Ile Thr
 1 5

agc cgc acc agc ttt ggt gtg gct gga gtg gag gcc att gat cgt ttt 163
 Ser Arg Thr Ser Phe Gly Val Ala Gly Val Glu Ala Ile Asp Arg Phe
 10 15 20

cag gta gac gcc aca cgc att gca gta ttc act tct gtt cag gtt ggt 211
 Gln Val Asp Ala Thr Arg Ile Ala Val Phe Thr Ser Val Gln Val Gly
 25 30 35

gtg tac gcg ttt gct cag att ccg atg ggc att ttg atc gat aag ttt 259
 Val Tyr Ala Phe Ala Gln Ile Pro Met Gly Ile Leu Ile Asp Lys Phe
 40 45 50

ggt cct cgg aag ctc ctt gcc att ggt gct ttg gtg atg ggt atc ggc 307
 Gly Pro Arg Lys Leu Leu Ala Ile Gly Ala Leu Val Met Gly Ile Gly
 55 60 65

cag ctc att ttg ggc ttt acg gat agc tat tcc atc gcg att att gcc 355
 Gln Leu Ile Leu Gly Phe Thr Asp Ser Tyr Ser Ile Ala Ile Ile Ala
 70 75 80 85

cgc gtg ttt atc ggc gcc ggc gat gca tcg atc ttc ctt tcg gtt atg 403
 Arg Val Phe Ile Gly Ala Gly Asp Ala Ser Ile Phe Leu Ser Val Met
 90 95 100

cgc atc ctg ccg ttt tgg ttc cca ctg aag cac acc cct att ttc acg 451
 Arg Ile Leu Pro Phe Trp Phe Pro Leu Lys His Thr Pro Ile Phe Thr
 105 110 115

cag tta act acc tgc ctt ggc cag ttg ggc cag ttc ttt tct gcg gtg 499
 Gln Leu Thr Thr Cys Leu Gly Gln Leu Gly Gln Phe Phe Ser Ala Val
 120 125 130

cct ttc atg gcg ttg ttg ggt ggc cag ggt tgg cct gtg gcg ttt gtc 547
 Pro Phe Met Ala Leu Leu Gly Ala Gln Gly Trp Pro Val Ala Phe Val
 135 140 145

agc ctt ggt tcc gtg gtg gca ctc att gcg atc gca gcg ctg gtg gcc 595
 Ser Leu Gly Ser Val Val Ala Leu Ile Ala Ile Ala Ala Leu Val Ala

150	155	160	165	
gtt cgg gat act cca gat cct cag cca aaa cct gtc gaa tca gct cag 643				
Val Arg Asp Thr Pro Asp Pro Gln Pro Lys Pro Val Glu Ser Ala Gln	170	175	180	
gaa gca gat aaa cca agc ctg cgc gcg agt ttg aag ttg att gtc cgc 691				
Glu Ala Asp Lys Pro Ser Leu Arg Ala Ser Leu Lys Leu Ile Val Arg	185	190	195	
aat ccg att acg tgg cag ggt ttc ttc att cac tac gta ttg atg gtg 739				
Asn Pro Ile Thr Trp Gln Gly Phe Phe Ile His Tyr Val Leu Met Val	200	205	210	
tgg cag acc gtg ttc tcc atg atg tgg ggc gtc ccg ctg atg act ttg 787				
Trp Gln Thr Val Phe Ser Met Met Trp Gly Val Pro Leu Met Thr Leu	215	220	225	
ggc atg gga ctg tct gca acg acg gct ggt ttg gtg ttg agc atc aac 835				
Gly Met Gly Leu Ser Ala Thr Thr Ala Gly Leu Val Leu Ser Ile Asn	230	235	240	245
acg ctg tgc atg gtg gta tcg gcg cca atc atc gga ata att tcc gca 883				
Thr Leu Cys Met Val Val Ser Ala Pro Ile Ile Gly Ile Ile Ser Ala	250	255	260	
cgc ctt ggg tat cgc cgt gac gtg gtc gcc att gcg ctg tcg ttt gtt 931				
Arg Leu Gly Tyr Arg Arg Asp Val Val Ala Ile Ala Leu Ser Phe Val	265	270	275	
caa tcc gca gta tgg ctg gtg ttc ttg gcc tcc gat gca cct cgt ggt 979				
Gln Ser Ala Val Trp Leu Val Phe Leu Ala Ser Asp Ala Pro Arg Gly	280	285	290	
ttg atg gct atc atc ttg gtc aac atc gtc atg ggt ctg act act gcg 1027				
Leu Met Ala Ile Ile Leu Val Asn Ile Val Met Gly Leu Thr Thr Ala	295	300	305	
gct tct ggt tat ggc ttt gac acc att cgt gag cgc cta gat cgc aag 1075				
Ala Ser Gly Tyr Gly Phe Asp Thr Ile Arg Glu Arg Leu Asp Arg Lys	310	315	320	325
att ttg gct gcg ggc acg gga ctg gca aac atg ggt gga ttc ttg tca 1123				
Ile Leu Ala Ala Gly Thr Gly Leu Ala Asn Met Gly Gly Phe Leu Ser	330	335	340	
tcg atg gtt gca gcg cag gtt atg ggg ttc ctt ctt gat cac agc gcg 1171				
Ser Met Val Ala Ala Gln Val Met Gly Phe Leu Leu Asp His Ser Ala	345	350	355	
cat ggt agc acc tat act tgg gtg gac ttc cgt ttt ggt ttc ctt gcg 1219				
His Gly Ser Thr Tyr Thr Trp Val Asp Phe Arg Phe Gly Phe Leu Ala	360	365	370	
att ctt gtc aca tgg gcc gtc gga gtc acg gga ttt gtt gta gcc cga 1267				
Ile Leu Val Thr Trp Ala Val Gly Val Thr Gly Phe Val Val Ala Arg	375	380	385	
ctc aag ggt gga ccg ggc cgc aga tta ctc gcc cag att agg tct acc 1315				
Leu Lys Gly Gly Pro Gly Arg Arg Leu Leu Ala Gln Ile Arg Ser Thr	390	395	400	405

aag gac ttt taaagatcgg gtaaaacctg tgg
Lys Asp Phe

1347

<210> 462

<211> 408

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 462

Met Ala Ala Ile Thr Ser Arg Thr Ser Phe Gly Val Ala Gly Val Glu
1 5 10 15

Ala Ile Asp Arg Phe Gln Val Asp Ala Thr Arg Ile Ala Val Phe Thr
20 25 30

Ser Val Gln Val Gly Val Tyr Ala Phe Ala Gln Ile Pro Met Gly Ile
35 40 45

Leu Ile Asp Lys Phe Gly Pro Arg Lys Leu Leu Ala Ile Gly Ala Leu
50 55 60

Val Met Gly Ile Gly Gln Leu Ile Leu Gly Phe Thr Asp Ser Tyr Ser
65 70 75 80

Ile Ala Ile Ile Ala Arg Val Phe Ile Gly Ala Gly Asp Ala Ser Ile
85 90 95

Phe Leu Ser Val Met Arg Ile Leu Pro Phe Trp Phe Pro Leu Lys His
100 105 110

Thr Pro Ile Phe Thr Gln Leu Thr Thr Cys Leu Gly Gln Leu Gly Gln
115 120 125

Phe Phe Ser Ala Val Pro Phe Met Ala Leu Leu Gly Ala Gln Gly Trp
130 135 140

Pro Val Ala Phe Val Ser Leu Gly Ser Val Val Ala Leu Ile Ala Ile
145 150 155 160

Ala Ala Leu Val Ala Val Arg Asp Thr Pro Asp Pro Gln Pro Lys Pro
165 170 175

Val Glu Ser Ala Gln Glu Ala Asp Lys Pro Ser Leu Arg Ala Ser Leu
180 185 190

Lys Leu Ile Val Arg Asn Pro Ile Thr Trp Gln Gly Phe Phe Ile His
195 200 205

Tyr Val Leu Met Val Trp Gln Thr Val Phe Ser Met Met Trp Gly Val
210 215 220

Pro Leu Met Thr Leu Gly Met Gly Leu Ser Ala Thr Thr Ala Gly Leu
225 230 235 240

Val Leu Ser Ile Asn Thr Leu Cys Met Val Val Ser Ala Pro Ile Ile
245 250 255

Gly Ile Ile Ser Ala Arg Leu Gly Tyr Arg Arg Asp Val Val Ala Ile

260					265					270					
Ala	Leu	Ser	Phe	Val	Gln	Ser	Ala	Val	Trp	Leu	Val	Phe	Leu	Ala	Ser
	275						280					285			
Asp	Ala	Pro	Arg	Gly	Leu	Met	Ala	Ile	Ile	Leu	Val	Asn	Ile	Val	Met
	290					295					300				
Gly	Leu	Thr	Thr	Ala	Ala	Ser	Gly	Tyr	Gly	Phe	Asp	Thr	Ile	Arg	Glu
305					310					315					320
Arg	Leu	Asp	Arg	Lys	Ile	Leu	Ala	Ala	Gly	Thr	Gly	Leu	Ala	Asn	Met
				325					330					335	
Gly	Gly	Phe	Leu	Ser	Ser	Met	Val	Ala	Ala	Gln	Val	Met	Gly	Phe	Leu
			340					345					350		
Leu	Asp	His	Ser	Ala	His	Gly	Ser	Thr	Tyr	Thr	Trp	Val	Asp	Phe	Arg
	355						360					365			
Phe	Gly	Phe	Leu	Ala	Ile	Leu	Val	Thr	Trp	Ala	Val	Gly	Val	Thr	Gly
	370					375					380				
Phe	Val	Val	Ala	Arg	Leu	Lys	Gly	Gly	Pro	Gly	Arg	Arg	Leu	Leu	Ala
385					390					395					400
Gln	Ile	Arg	Ser	Thr	Lys	Asp	Phe								
				405											

<210> 463

<211> 2265

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(2242)

<223> RXN01554

<400> 463

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				Leu	Lys	Lys	His	Val	
				1				5	

acc	tca	gcc	gtt	acc	gcc	gtg	gtg	acg	gct	ttt	tca	acg	gct	gcg	ctt	163
Thr	Ser	Ala	Val	Thr	Ala	Val	Val	Thr	Ala	Phe	Ser	Thr	Ala	Ala	Leu	
			10					15						20		

ggt	tta	agt	att	gcc	gtt	tct	cct	gct	ggt	gcc	caa	gtg	gct	aat	cca	211
Gly	Leu	Ser	Ile	Ala	Val	Ser	Pro	Ala	Val	Ala	Gln	Val	Ala	Asn	Pro	
		25					30					35				

gct	cca	gat	ctt	tct	gcg	ccg	tat	aca	tgg	gtg	gaa	gag	ttt	gat	tcc	259
Ala	Pro	Asp	Leu	Ser	Ala	Pro	Tyr	Thr	Trp	Val	Glu	Glu	Phe	Asp	Ser	
		40					45					50				

gag	gat	gct	ctc	aaa	ggg	tgg	aac	att	ttc	cgc	cag	cca	gat	tat	ggc	307
Glu	Asp	Ala	Leu	Lys	Gly	Trp	Asn	Ile	Phe	Arg	Gln	Pro	Asp	Tyr	Gly	

55	60	65	
agc gac aaa gtt ctc tat acc gaa gat gct tta agt atc gaa gat ggc Ser Asp Lys Val Leu Tyr Thr Glu Asp Ala Leu Ser Ile Glu Asp Gly 70 75 80 85			355
aag ctc acc atc acc act cag cgc cac tgc gtt gac gaa gac ttc gcg Lys Leu Thr Ile Thr Thr Gln Arg His Cys Val Asp Glu Asp Phe Ala 90 95 100			403
atc agt gat cct gtc aac cgc gga aag ctc aat gac agc acc gcg caa Ile Ser Asp Pro Val Asn Arg Gly Lys Leu Asn Asp Ser Thr Ala Gln 105 110 115			451
gtt gaa cct tgt gct cca ggt cag ttt gaa aag ttc acc agt gcg cgc Val Glu Pro Cys Ala Pro Gly Gln Phe Glu Lys Phe Thr Ser Ala Arg 120 125 130			499
atc gtc act ccg aaa att gct cgt gga gag ttc gac ctt tct gtc act Ile Val Thr Pro Lys Ile Ala Arg Gly Glu Phe Asp Leu Ser Val Thr 135 140 145			547
gca act ctt aac acc ggt ggc gtc gaa ggt gtc cga agt gcc att tgg Ala Thr Leu Asn Thr Gly Gly Val Glu Gly Val Arg Ser Ala Ile Trp 150 155 160 165			595
atg caa aac ggt gaa cag gcg tgt tcc tca gca acc aac aat ggc ctc Met Gln Asn Gly Glu Gln Ala Cys Ser Ser Ala Thr Asn Asn Gly Leu 170 175 180			643
tac gga gaa cta gac ctg gta gag cac ttt tct tac gat ctt cgc tcg Tyr Gly Glu Leu Asp Leu Val Glu His Phe Ser Tyr Asp Leu Arg Ser 185 190 195			691
cca tgg tct cca tca aac acc cac ttg ggt tgt gat cct gaa agt gtc Pro Trp Ser Pro Ser Asn Thr His Leu Gly Cys Asp Pro Glu Ser Val 200 205 210			739
aac ggc acc aac cgt gca cct cgt gaa ctt aaa cta gat gag tca ctc Asn Gly Thr Asn Arg Ala Pro Arg Glu Leu Lys Leu Asp Glu Ser Leu 215 220 225			787
gat ggc gtg gag cac acc tgg act gtg agc acc acc cgc gac ggc gtt Asp Gly Val Glu His Thr Trp Thr Val Ser Thr Thr Arg Asp Gly Val 230 235 240 245			835
gag tac ttc att gat gat gag gcg att aac cgc cag tca tgg cgc aac Glu Tyr Phe Ile Asp Asp Glu Ala Ile Asn Arg Gln Ser Trp Arg Asn 250 255 260			883
gat gtc act ttg ggg cat gcc gaa att gat gat ttc ggg atc tcc gcg Asp Val Thr Leu Gly His Ala Glu Ile Asp Asp Phe Gly Ile Ser Ala 265 270 275			931
cag acg ttt gat gag atc gtc gac cgc gaa tgg act ctc act ctt aat Gln Thr Phe Asp Glu Ile Val Asp Arg Glu Trp Thr Leu Thr Leu Asn 280 285 290			979
caa aag gta gaa agc gcc gac tgg gca aaa cca cgt tcc tct gag gaa Gln Lys Val Glu Ser Ala Asp Trp Ala Lys Pro Arg Ser Ser Glu Glu 295 300 305			1027

gat ttc cca gtc cgg tcc atg gtg att gac cgc atc gag gtc acc gga	1075
Asp Phe Pro Val Arg Ser Met Val Ile Asp Arg Ile Glu Val Thr Gly	
310 315 320 325	
tct ccc gca gta tct gaa gac acc ccc atg cca gat acc acc cag ctt	1123
Ser Pro Ala Val Ser Glu Asp Thr Pro Met Pro Asp Thr Thr Gln Leu	
330 335 340	
ttg acc caa gac act ctg gaa tac ctc ggt cgc atg cca gtg ctg gaa	1171
Leu Thr Gln Asp Thr Leu Glu Tyr Leu Gly Arg Met Pro Val Leu Glu	
345 350 355	
cgc tac gag cca gca agt gct gat ttt gcc gat ggc cgc agg cct tcc	1219
Arg Tyr Glu Pro Ala Ser Ala Asp Phe Ala Asp Gly Arg Arg Pro Ser	
360 365 370	
tgg aac tac ttc aat ttg aag gaa tcg tgg cag aat cca gaa ctc gag	1267
Trp Asn Tyr Phe Asn Leu Lys Glu Ser Trp Gln Asn Pro Glu Leu Glu	
375 380 385	
caa cgc cca gaa gct gtc gaa ttc gtt gat gga cgc atg gat atc gtg	1315
Gln Arg Pro Glu Ala Val Glu Phe Val Asp Gly Arg Met Asp Ile Val	
390 395 400 405	
acc cgt cgc cac tgt ctg gcc acc act gat gac atc gcc act ccg gaa	1363
Thr Arg Arg His Cys Leu Ala Thr Thr Asp Asp Ile Ala Thr Pro Glu	
410 415 420	
aac gca cag gag gaa ccg tgc gcg ccg ggt gag gtg aca cgc tac agc	1411
Asn Ala Gln Glu Glu Pro Cys Ala Pro Gly Glu Val Thr Arg Tyr Ser	
425 430 435	
tca gcg cgt gtc cac ctt cca gag atc ccc gcc ggc aac ttc cgg ctc	1459
Ser Ala Arg Val His Leu Pro Glu Ile Pro Ala Gly Asn Phe Arg Leu	
440 445 450	
acc gtg cgc gca cgg gcg cag tcc gaa gag ctt gtc gac ggc gtc cgc	1507
Thr Val Arg Ala Arg Ala Gln Ser Glu Glu Leu Val Asp Gly Val Arg	
455 460 465	
ccc gct atc tgg atg cag aac aat acc aac ttc tgt gct gac aac gat	1555
Pro Ala Ile Trp Met Gln Asn Asn Thr Asn Phe Cys Ala Asp Asn Asp	
470 475 480 485	
gga cgc cct tat ggt gaa ctg gat att act gag ttc tac agc tct cgt	1603
Gly Arg Pro Tyr Gly Glu Leu Asp Ile Thr Glu Phe Tyr Ser Ser Arg	
490 495 500	
gtg aac acc cag tac tcg gca gta cac ctt gga tgt gct ggc aac cgc	1651
Val Asn Thr Gln Tyr Ser Ala Val His Leu Gly Cys Ala Gly Asn Arg	
505 510 515	
cca gag atg aag ctt cgc caa atg gaa atg gaa gag tcc atg ttt ggg	1699
Pro Glu Met Lys Leu Arg Gln Met Glu Met Glu Glu Ser Met Phe Gly	
520 525 530	
gat tgg cat gac tgg ggc gtc gaa gtc ttc gac ggc cag atc gta ttc	1747
Asp Trp His Asp Trp Gly Val Glu Val Phe Asp Gly Gln Ile Val Phe	
535 540 545	

acc att gac ggc aag gca gta act tcc tct ggc aaa gat gtc ttt ggc 1795
 Thr Ile Asp Gly Lys Ala Val Thr Ser Ser Gly Lys Asp Val Phe Gly
 550 555 560 565

aac tct gtt acc cca gcc gct gca cct ctt cgc ccc gcg cac ttc aag 1843
 Asn Ser Val Thr Pro Ala Ala Ala Pro Leu Arg Pro Ala His Phe Lys
 570 575 580

ttg tcg gaa gag gaa tac cgt gaa gtc atc ggg cag cct tgg cac ctt 1891
 Leu Ser Glu Glu Glu Tyr Arg Glu Val Ile Gly Gln Pro Trp His Leu
 585 590 595

att ttg aac acc atg gtg gag cag tct ggc aaa gac agc tgg att aca 1939
 Ile Leu Asn Thr Met Val Glu Gln Ser Gly Lys Asp Ser Trp Ile Thr
 600 605 610

gcg gtc gac aat aac gag gcg ttc cca gaa cac cgc ttc caa att gac 1987
 Ala Val Asp Asn Asn Glu Ala Phe Pro Glu His Arg Phe Gln Ile Asp
 615 620 625

cat gtg gca gta gat atc gag tct gac tct gtg gac aat gta tgg cct 2035
 His Val Ala Val Asp Ile Glu Ser Asp Ser Val Asp Asn Val Trp Pro
 630 635 640 645

gac gct gcg aat gaa atc cca gac aat gtt ggt att gaa gac tct gat 2083
 Asp Ala Ala Asn Glu Ile Pro Asp Asn Val Gly Ile Glu Asp Ser Asp
 650 655 660

gat ggc agc gac ctg gag gtt ggt tcg acc gga agc tct aca gct gag 2131
 Asp Gly Ser Asp Leu Glu Val Gly Ser Thr Gly Ser Ser Thr Ala Glu
 665 670 675

acc gtg agc tgg atc tcg ttg ttc acc gcg ttg agc tcg ctg gtc ttc 2179
 Thr Val Ser Trp Ile Ser Leu Phe Thr Ala Leu Ser Ser Leu Val Phe
 680 685 690

aca ctg gct ctc aat caa gaa gca ttg cag aat ttg att aat cag ttc 2227
 Thr Leu Ala Leu Asn Gln Glu Ala Leu Gln Asn Leu Ile Asn Gln Phe
 695 700 705

atg aga cag ttc aag taatccttgt gggcgctttg tct 2265
 Met Arg Gln Phe Lys
 710

<210> 464

<211> 714

<212> PRT

<213> Corynebacterium glutamicum

<400> 464

Leu Lys Lys His Val Thr Ser Ala Val Thr Ala Val Val Thr Ala Phe
 1 5 10 15

Ser Thr Ala Ala Leu Gly Leu Ser Ile Ala Val Ser Pro Ala Val Ala
 20 25 30

Gln Val Ala Asn Pro Ala Pro Asp Leu Ser Ala Pro Tyr Thr Trp Val
 35 40 45

Glu Glu Phe Asp Ser Glu Asp Ala Leu Lys Gly Trp Asn Ile Phe Arg

50					55					60					
Gln	Pro	Asp	Tyr	Gly	Ser	Asp	Lys	Val	Leu	Tyr	Thr	Glu	Asp	Ala	Leu
65					70					75					80
Ser	Ile	Glu	Asp	Gly	Lys	Leu	Thr	Ile	Thr	Thr	Gln	Arg	His	Cys	Val
				85					90					95	
Asp	Glu	Asp	Phe	Ala	Ile	Ser	Asp	Pro	Val	Asn	Arg	Gly	Lys	Leu	Asn
			100					105					110		
Asp	Ser	Thr	Ala	Gln	Val	Glu	Pro	Cys	Ala	Pro	Gly	Gln	Phe	Glu	Lys
			115				120					125			
Phe	Thr	Ser	Ala	Arg	Ile	Val	Thr	Pro	Lys	Ile	Ala	Arg	Gly	Glu	Phe
	130					135					140				
Asp	Leu	Ser	Val	Thr	Ala	Thr	Leu	Asn	Thr	Gly	Gly	Val	Glu	Gly	Val
145					150					155					160
Arg	Ser	Ala	Ile	Trp	Met	Gln	Asn	Gly	Glu	Gln	Ala	Cys	Ser	Ser	Ala
			165						170					175	
Thr	Asn	Asn	Gly	Leu	Tyr	Gly	Glu	Leu	Asp	Leu	Val	Glu	His	Phe	Ser
			180					185					190		
Tyr	Asp	Leu	Arg	Ser	Pro	Trp	Ser	Pro	Ser	Asn	Thr	His	Leu	Gly	Cys
		195					200					205			
Asp	Pro	Glu	Ser	Val	Asn	Gly	Thr	Asn	Arg	Ala	Pro	Arg	Glu	Leu	Lys
	210					215					220				
Leu	Asp	Glu	Ser	Leu	Asp	Gly	Val	Glu	His	Thr	Trp	Thr	Val	Ser	Thr
225					230					235					240
Thr	Arg	Asp	Gly	Val	Glu	Tyr	Phe	Ile	Asp	Asp	Glu	Ala	Ile	Asn	Arg
			245						250					255	
Gln	Ser	Trp	Arg	Asn	Asp	Val	Thr	Leu	Gly	His	Ala	Glu	Ile	Asp	Asp
			260					265					270		
Phe	Gly	Ile	Ser	Ala	Gln	Thr	Phe	Asp	Glu	Ile	Val	Asp	Arg	Glu	Trp
	275						280					285			
Thr	Leu	Thr	Leu	Asn	Gln	Lys	Val	Glu	Ser	Ala	Asp	Trp	Ala	Lys	Pro
	290					295					300				
Arg	Ser	Ser	Glu	Glu	Asp	Phe	Pro	Val	Arg	Ser	Met	Val	Ile	Asp	Arg
305					310					315					320
Ile	Glu	Val	Thr	Gly	Ser	Pro	Ala	Val	Ser	Glu	Asp	Thr	Pro	Met	Pro
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Asp	Thr	Thr	Gln	Leu	Leu	Thr	Gln	Asp	Thr	Leu	Glu	Tyr	Leu	Gly	Arg
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Met	Pro	Val	Leu	Glu	Arg	Tyr	Glu	Pro	Ala	Ser	Ala	Asp	Phe	Ala	Asp
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	370					375					380				

Asn Pro Glu Leu Glu Gln Arg Pro Glu Ala Val Glu Phe Val Asp Gly
 385 390 395 400
 Arg Met Asp Ile Val Thr Arg Arg His Cys Leu Ala Thr Thr Asp Asp
 405 410 415
 Ile Ala Thr Pro Glu Asn Ala Gln Glu Glu Pro Cys Ala Pro Gly Glu
 420 425 430
 Val Thr Arg Tyr Ser Ser Ala Arg Val His Leu Pro Glu Ile Pro Ala
 435 440 445
 Gly Asn Phe Arg Leu Thr Val Arg Ala Arg Ala Gln Ser Glu Glu Leu
 450 455 460
 Val Asp Gly Val Arg Pro Ala Ile Trp Met Gln Asn Asn Thr Asn Phe
 465 470 475 480
 Cys Ala Asp Asn Asp Gly Arg Pro Tyr Gly Glu Leu Asp Ile Thr Glu
 485 490 495
 Phe Tyr Ser Ser Arg Val Asn Thr Gln Tyr Ser Ala Val His Leu Gly
 500 505 510
 Cys Ala Gly Asn Arg Pro Glu Met Lys Leu Arg Gln Met Glu Met Glu
 515 520 525
 Glu Ser Met Phe Gly Asp Trp His Asp Trp Gly Val Glu Val Phe Asp
 530 535 540
 Gly Gln Ile Val Phe Thr Ile Asp Gly Lys Ala Val Thr Ser Ser Gly
 545 550 555 560
 Lys Asp Val Phe Gly Asn Ser Val Thr Pro Ala Ala Ala Pro Leu Arg
 565 570 575
 Pro Ala His Phe Lys Leu Ser Glu Glu Glu Tyr Arg Glu Val Ile Gly
 580 585 590
 Gln Pro Trp His Leu Ile Leu Asn Thr Met Val Glu Gln Ser Gly Lys
 595 600 605
 Asp Ser Trp Ile Thr Ala Val Asp Asn Asn Glu Ala Phe Pro Glu His
 610 615 620
 Arg Phe Gln Ile Asp His Val Ala Val Asp Ile Glu Ser Asp Ser Val
 625 630 635 640
 Asp Asn Val Trp Pro Asp Ala Ala Asn Glu Ile Pro Asp Asn Val Gly
 645 650 655
 Ile Glu Asp Ser Asp Asp Gly Ser Asp Leu Glu Val Gly Ser Thr Gly
 660 665 670
 Ser Ser Thr Ala Glu Thr Val Ser Trp Ile Ser Leu Phe Thr Ala Leu
 675 680 685
 Ser Ser Leu Val Phe Thr Leu Ala Leu Asn Gln Glu Ala Leu Gln Asn
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Leu Ile Asn Gln Phe Met Arg Gln Phe Lys
705 710

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<223> RXN03015

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Leu Gly Val Gly Thr
1 5
cct cag cag aag ggt act tat gcg gcg gat ctg acg tat gtt cgt cag 163
Pro Gln Gln Lys Gly Thr Tyr Ala Ala Asp Leu Thr Tyr Val Arg Gln
10 15 20
gtt gtt gag gat ttg gtg ccg ctg ctt gag ggc gag cac att att ttc 211
Val Val Glu Asp Leu Val Pro Leu Leu Glu Gly Glu His Ile Ile Phe
25 30 35
ggc aag tct acg gtt ccg gtt ggt act gct gag cag ttg cag gag ctt 259
Gly Lys Ser Thr Val Pro Val Gly Thr Ala Glu Gln Leu Gln Glu Leu
40 45 50
gct gat tct ctg gtc aag cct ggt tcg cac gtg gag atc gcg tgg aat 307
Ala Asp Ser Leu Val Lys Pro Gly Ser His Val Glu Ile Ala Trp Asn
55 60 65
ccg gag ttc ttg cgt gag ggc tac gcg gtc aaa gac acc atc act ccg 355
Pro Glu Phe Leu Arg Glu Gly Tyr Ala Val Lys Asp Thr Ile Thr Pro
70 75 80 85
gac cgc atc gtg gtg ggt gtg cgt gaa taagaca 389
Asp Arg Ile Val Val Gly Val Arg Glu
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20 25 30
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35 40 45

Gln Leu Gln Glu Leu Ala Asp Ser Leu Val Lys Pro Gly Ser His Val
 50 55 60

Glu Ile Ala Trp Asn Pro Glu Phe Leu Arg Glu Gly Tyr Ala Val Lys
 65 70 75 80

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<210> 467

<211> 801

<212> DNA

<213> Corynebacterium glutamicum

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 Leu Asp Ala Ala Gly
 1 5

att tca ctt tca gcc gtt gga tcc gac ttc ggc aag atc aac atc acc 163
 Ile Ser Leu Ser Ala Val Gly Ser Asp Phe Gly Lys Ile Asn Ile Thr
 10 15 20

gat cct ttt gaa gat cac ttg gag cgc gca cgc cac ggt gtt gag gtc 211
 Asp Pro Phe Glu Asp His Leu Glu Arg Ala Arg His Gly Val Glu Val
 25 30 35

gct aag ctc ttc ggc gcg aaa tac atc cgc atg ttc tcc ttc ttt att 259
 Ala Lys Leu Phe Gly Ala Lys Tyr Ile Arg Met Phe Ser Phe Phe Ile
 40 45 50

gca gaa ggc gac aac cct gaa agc ttc cgc aaa gaa gta ctc tcc cgc 307
 Ala Glu Gly Asp Asn Pro Glu Ser Phe Arg Lys Glu Val Leu Ser Arg
 55 60 65

acc cac gca atg gtc gaa ctc gca gaa gcc ggc ggc atc acc ctc ctc 355
 Thr His Ala Met Val Glu Leu Ala Glu Ala Gly Gly Ile Thr Leu Leu
 70 75 80 85

cac gaa aat gaa aag gga atc tat ggc gac tcc ccg cag cgc gtg aag 403
 His Glu Asn Glu Lys Gly Ile Tyr Gly Asp Ser Pro Gln Arg Val Lys
 90 95 100

gat tta atc acc agc atc gac tcc cct aac tac cgc gca atc tac gac 451
 Asp Leu Ile Thr Ser Ile Asp Ser Pro Asn Tyr Arg Ala Ile Tyr Asp
 105 110 115

gca gct aac tac gtg caa acc gga ttc aag cct ttt gat gag gca tgg 499
 Ala Ala Asn Tyr Val Gln Thr Gly Phe Lys Pro Phe Asp Glu Ala Trp
 120 125 130

ccg atc gtt aag gac tac gtc gac tac gtc cac atc aag gac gcg acc 547
 Pro Ile Val Lys Asp Tyr Val Asp Tyr Val His Ile Lys Asp Ala Thr

135 140 145
 att cca gat gca gag cac ccc atc gga atc atc aag cca gca gga caa 595
 Ile Pro Asp Ala Glu His Pro Ile Gly Ile Ile Lys Pro Ala Gly Gln
 150 155 160 165
 ggc gac ggc caa tac cca gag ctc ctt gcc gcg cta aac gcc gac ggt 643
 Gly Asp Gly Gln Tyr Pro Glu Leu Leu Ala Ala Leu Asn Ala Asp Gly
 170 175 180
 tac aac gga ttc gtc tcc atc gag cct cac ctg ggt gac ttc gat gaa 691
 Tyr Asn Gly Phe Val Ser Ile Glu Pro His Leu Gly Asp Phe Asp Glu
 185 190 195
 ttc ggc gga ctc tgc gga cct gac ctg tgg acc agc gca tgc gac gct 739
 Phe Gly Gly Leu Cys Gly Pro Asp Leu Trp Thr Ser Ala Cys Asp Ala
 200 205 210
 ctc gca gga atc ctg aac aac atc aac gcc gag tac aac taaggacaac 788
 Leu Ala Gly Ile Leu Asn Asn Ile Asn Ala Glu Tyr Asn
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 <211> 226
 <212> PRT
 <213> Corynebacterium glutamicum

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 His Gly Val Glu Val Ala Lys Leu Phe Gly Ala Lys Tyr Ile Arg Met
 35 40 45
 Phe Ser Phe Phe Ile Ala Glu Gly Asp Asn Pro Glu Ser Phe Arg Lys
 50 55 60
 Glu Val Leu Ser Arg Thr His Ala Met Val Glu Leu Ala Glu Ala Gly
 65 70 75 80
 Gly Ile Thr Leu Leu His Glu Asn Glu Lys Gly Ile Tyr Gly Asp Ser
 85 90 95
 Pro Gln Arg Val Lys Asp Leu Ile Thr Ser Ile Asp Ser Pro Asn Tyr
 100 105 110
 Arg Ala Ile Tyr Asp Ala Ala Asn Tyr Val Gln Thr Gly Phe Lys Pro
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 145 150 155 160

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cca ggg gta acc ttg gtg tct tcc gag tca gaa gca gat ctt gca atc															259
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ggt caa gag gga gga cca aag ggc aag ctg cca ttg act gtt cct gct 547
 Gly Gln Glu Gly Gly Pro Lys Gly Lys Leu Pro Leu Thr Val Pro Ala
 135 140 145

tcc atg cag gcg att gct gat tcc cct cgc gat atc cca ggc aag ttc 595
 Ser Met Gln Ala Ile Ala Asp Ser Pro Arg Asp Ile Pro Gly Lys Phe
 150 155 160 165

ctc gat gag tct tac acc tac gtg gac tcc gca ggg atg gcc tac aag 643
 Leu Asp Glu Ser Tyr Thr Tyr Val Asp Ser Ala Gly Met Ala Tyr Lys
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<210> 470
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 <212> PRT
 <213> Corynebacterium glutamicum

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Ile Arg Ala Glu Leu Pro Gly Val Thr Leu Val Ser Ser Glu Ser Glu
 35 40 45

Ala Asp Leu Ala Ile Val Trp Ala Arg Pro Glu Ile Ala Leu Phe Glu
 50 55 60

Asp Asp Leu Glu Gly Val Ser Leu Ser Val Asp Pro Arg Ala Asn Gly
 65 70 75 80

Val Asp Val Glu Arg Val Gln Ala Val Glu Ala Ala Val Pro Thr Ile
 85 90 95

Leu Ala Val Asn Phe Thr Asn Pro Trp Val Leu Ser Glu Ile Glu Pro
 100 105 110

Gly Ala Ala Ala Val Val Gly Thr Phe Glu Ile Lys Pro Glu Phe Leu
 115 120 125

Leu Lys Ala Leu Thr Gly Gln Glu Gly Gly Pro Lys Gly Lys Leu Pro
 130 135 140

Leu Thr Val Pro Ala Ser Met Gln Ala Ile Ala Asp Ser Pro Arg Asp
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 165 170 175

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185

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<211> 1062
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<213> Corynebacterium glutamicum
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<223> RXN00401
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cca caa gat ctc gca gac cac ctc aag gat gga ctg ctc tct ttc ccg															163
Pro	Gln	Asp	Leu	Ala	Asp	His	Leu	Lys	Asp	Gly	Leu	Leu	Ser	Phe	Pro
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gcc acc gct ttc caa gat gac ctc gaa gta gat gaa gct gct tat gtc															211
Ala	Thr	Ala	Phe	Gln	Asp	Asp	Leu	Glu	Val	Asp	Glu	Ala	Ala	Tyr	Val
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Glu	His	Ile	Glu	Trp	Gln	Ser	Ser	Tyr	Pro	Val	Ala	Gly	Leu	Phe	Ala
		40					45					50			
gct ggc ggt act ggc gaa gga ttc agc ctt acc gtt gag gaa aac cac															307
Ala	Gly	Gly	Thr	Gly	Glu	Gly	Phe	Ser	Leu	Thr	Val	Glu	Glu	Asn	His
	55					60					65				
cgt gtc act caa ctt gca gtt cag gcg tcc agc ccg gaa gtt ccc gtg															355
Arg	Val	Thr	Gln	Leu	Ala	Val	Gln	Ala	Ser	Ser	Pro	Glu	Val	Pro	Val
	70				75					80					85
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				90					95					100	
ggc gca gag gca gca ggc gct gaa ggt gtc ctc ctg ctt cct ccc tac															451
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Cys	Glu	Ser	Thr	Ser	Leu	Gly	Val	Ile	Val	Tyr	Asn	Arg	Ala	Asn	Ala
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Ile	Tyr	Ser	Pro	Glu	Val	Ile	Ala	Arg	Leu	Ser	Glu	Arg	Tyr	Pro	Asn
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Phe Ile Gly Phe Lys Asp Gly Thr Gly Asn Ile Glu His Leu Ala Lys
 170 175 180
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 Ile Thr Thr Leu Cys Gly Asp Arg Leu Phe Tyr Leu Gly Gly Leu Pro
 185 190 195
 acc gct gag acc ttt gca cta cca ctg ctt cag atg ggc atg agc acc 739
 Thr Ala Glu Thr Phe Ala Leu Pro Leu Leu Gln Met Gly Met Ser Thr
 200 205 210
 tac tcc tct gca atg ttc aac ttc att cca gat ttc gca ctg agc ttc 787
 Tyr Ser Ser Ala Met Phe Asn Phe Ile Pro Asp Phe Ala Leu Ser Phe
 215 220 225
 tac gcc gat gtt cgt gcg cag gac agc gca gca gta aag cag aag ctg 835
 Tyr Ala Asp Val Arg Ala Gln Asp Ser Ala Ala Val Lys Gln Lys Leu
 230 235 240 245
 agc gat ttt gtg ctc ccc tac ttg gat atc cgc gat cgc gca caa ggc 883
 Ser Asp Phe Val Leu Pro Tyr Leu Asp Ile Arg Asp Arg Ala Gln Gly
 250 255 260
 tac ggt gtc tcc att ggt aag ggc gga ctc aag gct gtt ggc cgc aac 931
 Tyr Gly Val Ser Ile Gly Lys Gly Gly Leu Lys Ala Val Gly Arg Asn
 265 270 275
 gct ggc ggc gtt cgc cca cca ctg cgt aac ctt tcc gag caa gat atc 979
 Ala Gly Gly Val Arg Pro Pro Leu Arg Asn Leu Ser Glu Gln Asp Ile
 280 285 290
 gcg gac ctg tgc gat ttg ctt gcc acc tct ggc gca ggt tcc tac cgc 1027
 Ala Asp Leu Ser Asp Leu Leu Ala Thr Ser Gly Ala Gly Ser Tyr Arg
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 Leu Gln Leu Arg
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<210> 472

<211> 313

<212> PRT

<213> *Corynebacterium glutamicum*

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 Ala Gly Leu Phe Ala Ala Gly Gly Thr Gly Glu Gly Phe Ser Leu Thr
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<212> DNA
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Val	Ala	Gly	Tyr	Arg	Asn	Ile	Asp	Thr	Ala	Leu	Ala	Tyr	Gly	Asn	Glu	
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cgc	ggc	gtt	ggc	gaa	ggc	att	cgc	acc	gct	gga	gtg	ccc	cgc	gag	gag	259
Arg	Gly	Val	Gly	Glu	Gly	Ile	Arg	Thr	Ala	Gly	Val	Pro	Arg	Glu	Glu	
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Leu	Phe	Ile	Ser	Thr	Lys	Leu	Ala	Ala	Glu	Ile	Lys	Asp	Tyr	Asp	Gly	
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Ala	Val	Ala	Ala	Ile	Asp	Glu	Ser	Leu	Ala	Lys	Ile	Gly	Leu	Asp	Tyr	
	70				75					80				85		
gtc	gat	ctg	atg	ctc	att	cac	tcc	cca	caa	cca	tgg	agt	gat	ttc	cgt	403
Val	Asp	Leu	Met	Leu	Ile	His	Ser	Pro	Gln	Pro	Trp	Ser	Asp	Phe	Arg	
				90					95					100		
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Gly	Gly	Asp	Tyr	Ser	Glu	Gly	Asn	Arg	Glu	Ala	Trp	Arg	Ala	Leu	Glu	
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gat	gcc	tac	aaa	gcc	gga	aag	att	cga	tcc	att	ggt	gtc	tcg	aac	ttc	499
Asp	Ala	Tyr	Lys	Ala	Gly	Lys	Ile	Arg	Ser	Ile	Gly	Val	Ser	Asn	Phe	
		120					125					130				
ctg	gag	gcc	gat	ctg	gag	aat	atc	tta	gac	tcc	gcg	acg	gtt	gct	cct	547
Leu	Glu	Ala	Asp	Leu	Glu	Asn	Ile	Leu	Asp	Ser	Ala	Thr	Val	Ala	Pro	
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His	Val	Asn	Gln	Leu	Leu	Val	His	Val	Gly	Asn	Thr	Pro	Ser	Glu	Leu	
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Ile	Ser	Phe	Cys	Asp	Ser	Lys	Gly	Ile	Leu	Val	Glu	Ala	Tyr	Ser	Pro	
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atc	gcc	cac	gga	gag	atg	ctg	aag	aac	cag	cag	gtc	aag	gcg	att	gct	691
Ile	Ala	His	Gly	Glu	Met	Leu	Lys	Asn	Gln	Gln	Val	Lys	Ala	Ile	Ala	
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Asp	Lys	Tyr	Asn	Val	Ser	Ile	Pro	Gln	Leu	Cys	Ile	Arg	Tyr	Thr	Ile	
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Gln	Leu	Gly	Thr	Val	Ser	Leu	Pro	Lys	Thr	Ala	Asn	Pro	Asp	His	Met	
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Ser	Ser	Asn	Ala	Gln	Ile	Asp	Phe	Glu	Ile	Ser	Glu	Glu	Asp	Met	Ala	
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<213> Corynebacterium glutamicum

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Ala Tyr Gly Asn Glu Arg Gly Val Gly Glu Gly Ile Arg Thr Ala Gly
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Val Pro Arg Glu Glu Leu Phe Ile Ser Thr Lys Leu Ala Ala Glu Ile
 50 55 60

Lys Asp Tyr Asp Gly Ala Val Ala Ala Ile Asp Glu Ser Leu Ala Lys
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Ile Gly Leu Asp Tyr Val Asp Leu Met Leu Ile His Ser Pro Gln Pro
 85 90 95

Trp Ser Asp Phe Arg Gly Gly Asp Tyr Ser Glu Gly Asn Arg Glu Ala
 100 105 110

Trp Arg Ala Leu Glu Asp Ala Tyr Lys Ala Gly Lys Ile Arg Ser Ile
 115 120 125

Gly Val Ser Asn Phe Leu Glu Ala Asp Leu Glu Asn Ile Leu Asp Ser
 130 135 140

Ala Thr Val Ala Pro His Val Asn Gln Leu Leu Val His Val Gly Asn
 145 150 155 160

Thr Pro Ser Glu Leu Ile Ser Phe Cys Asp Ser Lys Gly Ile Leu Val
 165 170 175

Glu Ala Tyr Ser Pro Ile Ala His Gly Glu Met Leu Lys Asn Gln Gln
 180 185 190

Val Lys Ala Ile Ala Asp Lys Tyr Asn Val Ser Ile Pro Gln Leu Cys
 195 200 205

Ile Arg Tyr Thr Ile Gln Leu Gly Thr Val Ser Leu Pro Lys Thr Ala
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Asn Pro Asp His Met Ser Ser Asn Ala Gln Ile Asp Phe Glu Ile Ser
 225 230 235 240

Glu Glu Asp Met Ala Ala Leu Gln Glu Val Thr Ala Arg Asp Tyr Gly
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Glu His Ser Gly Phe Pro Val Tyr Ser Gly Lys
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 Met Arg Gln Val Gly
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 ggt aat ggg ggc cat caa cta gac tcg atc aac gtg tca gat gta gtt 163
 Gly Asn Gly Gly His Gln Leu Asp Ser Ile Asn Val Ser Asp Val Val
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 gag tcg aag aaa cta aag ggt tct gcg caa gaa ccc ccg cag gtt gcc 211
 Glu Ser Lys Lys Leu Lys Gly Ser Ala Gln Glu Pro Pro Gln Val Ala
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 ccg ggc tgg ctg aag aaa ctg gct atc tca tca ggt ctg ctt ggc ctg 259
 Pro Gly Trp Leu Lys Lys Leu Ala Ile Ser Ser Gly Leu Leu Gly Leu
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 Leu Met Phe Val Leu Leu Pro Phe Leu Pro Val Asn Gln Val Gln Ser
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 tcg ctg tca tgg cca caa aat ggt gag ctt tcc agc gtt aac gcc ccg 355
 Ser Leu Ser Trp Pro Gln Asn Gly Glu Leu Ser Ser Val Asn Ala Pro
 70 75 80 85
 ctg att tcc tac gca ccg cag tcg atg gat gcg tcc atc cct gtg tcc 403
 Leu Ile Ser Tyr Ala Pro Gln Ser Met Asp Ala Ser Ile Pro Val Ser
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 Ala Leu Asp Ser Leu Asn Asp Asn Gln Ser Leu Val Met Gly Thr Leu
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 Pro Leu Asp Ser Thr Asp Ala Thr Asn Arg Gly Leu Phe Val Arg Thr
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 atc gac ggt aac ctt gac gtg att gtt cgc ggt gag gtg ctg ttg gat 547
 Ile Asp Gly Asn Leu Asp Val Ile Val Arg Gly Glu Val Leu Leu Asp
 135 140 145
 ctt tca cca aca gag gtg aac cgt ctg cca gat gat gcg atc cta gag 595

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Ile	Ser	Ser	Thr	Glu	Glu	Thr	Thr	Ser	Ala	Glu	Ile	Thr	Gly	Thr	Ala	
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ttc	agc	ggc	gag	acc	gaa	ggc	gat	gag	cgg	cct	cag	gtc	acc	ggc	gtt	691
Phe	Ser	Gly	Glu	Thr	Glu	Gly	Asp	Glu	Arg	Pro	Gln	Val	Thr	Gly	Val	
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tac	acc	gag	ctt	gtc	gac	gac	ccc	tcc	acc	gca	tcg	gcc	ctg	gcc	tca	739
Tyr	Thr	Glu	Leu	Val	Asp	Asp	Pro	Ser	Thr	Ala	Ser	Ala	Leu	Ala	Ser	
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gcg	ggc	tta	aac	gtt	gat	att	gag	atc	aac	tcc	cgc	ttc	act	tca	tcc	787
Ala	Gly	Leu	Asn	Val	Asp	Ile	Glu	Ile	Asn	Ser	Arg	Phe	Thr	Ser	Ser	
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ccc	agc	ctt	cta	aag	tac	gca	gcc	atc	ttc	att	ggc	ctt	gcg	tct	gtg	835
Pro	Ser	Leu	Leu	Lys	Tyr	Ala	Ala	Ile	Phe	Ile	Gly	Leu	Ala	Ser	Val	
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ttg	gtc	tcc	ctg	tgg	aca	ctg	cac	cgc	atg	gat	att	ttg	gat	ggc	cga	883
Leu	Val	Ser	Leu	Trp	Thr	Leu	His	Arg	Met	Asp	Ile	Leu	Asp	Gly	Arg	
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aaa	gca	cac	cgc	ttc	ctg	cct	gcc	aac	tgg	tac	aag	ctg	aag	cca	ctt	931
Lys	Ala	His	Arg	Phe	Leu	Pro	Ala	Asn	Trp	Tyr	Lys	Leu	Lys	Pro	Leu	
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gat	ggc	gtt	gtc	gta	gcg	att	ttg	gtg	ttc	tgg	cac	ttc	ctt	ggc	gcc	979
Asp	Gly	Val	Val	Val	Ala	Ile	Leu	Val	Phe	Trp	His	Phe	Leu	Gly	Ala	
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aac	acc	tct	gac	gac	ggc	ttc	atc	atg	acc	atg	gcc	cgc	gtg	tcc	cag	1027
Asn	Thr	Ser	Asp	Asp	Gly	Phe	Ile	Met	Thr	Met	Ala	Arg	Val	Ser	Gln	
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Ser	Pro	Phe	Gly	Ala	Pro	Tyr	Tyr	Asp	Leu	Leu	Ala	Leu	Met	Ala	Tyr	
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Ile	Ser	Thr	Ser	Ser	Ile	Trp	Leu	Arg	Leu	Pro	Ala	Leu	Leu	Ala	Gly	
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ctg	atc	atg	tgg	ttc	gtg	atc	acc	aga	gag	gtc	atg	cca	cgg	ttt	ggc	1219
Leu	Ile	Met	Trp	Phe	Val	Ile	Thr	Arg	Glu	Val	Met	Pro	Arg	Phe	Gly	
		360					365					370				
tca	ttg	gtt	aac	ggc	cgc	cgc	gtt	gcg	cac	tgg	tct	gca	gcc	atg	gtg	1267
Ser	Leu	Val	Asn	Gly	Arg	Arg	Val	Ala	His	Trp	Ser	Ala	Ala	Met	Val	
		375				380					385					
ttc	ctg	gcg	ttc	tgg	ctt	cca	tac	aac	aac	ggc	act	cgc	cca	gag	cca	1315
Phe	Leu	Ala	Phe	Trp	Leu	Pro	Tyr	Asn	Asn	Gly	Thr	Arg	Pro	Glu	Pro	

390	395	400	405
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acc att tcc ctg gca tca ggc ccc acc ggt cta atg gca gtt gct gcg Thr Ile Ser Leu Ala Ser Gly Pro Thr Gly Leu Met Ala Val Ala Ala 440 445 450	1459		
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Phe Leu Leu Ala Leu Ala Leu Ala Gly Val Asn Gly Phe Trp Tyr Thr	
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Ser Ser Tyr Ala Val Pro Trp Trp Asp Lys Thr Ile Gln Ile Lys Gly	
665 670 675	
atc gaa gca tcc acc gta gtg ctc gtg atc gcc gtg atc gtg ctg atc	2179
Ile Glu Ala Ser Thr Val Val Leu Val Ile Ala Val Ile Val Leu Ile	
680 685 690	
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Ile Gly Val Ile Gln Ser Phe Val His Asp Val Lys Thr Ala Gln Ala	
695 700 705	
gaa acc aat cac tcc atg ggc gaa ctc gtg gcg gaa gat gaa gca aag	2275
Glu Thr Asn His Ser Met Gly Glu Leu Val Ala Glu Asp Glu Ala Lys	
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Arg Glu Arg Ala Ser Arg Phe Thr Gly Leu Ala Ala Ser Pro Ile Ala	
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Gly Val Ser Ala Leu Val Val Leu Ile Thr Cys Ala Ser Met Gly Lys	
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Gly Phe Val Asp Gln Tyr Pro Ala Tyr Ser Val Gly Leu Gly Asn Leu	
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cgc tcc ctg acc ggc aac aca tgt ggc ctt gcc tcc gac gcc atg ctg	2467
Arg Ser Leu Thr Gly Asn Thr Cys Gly Leu Ala Ser Asp Ala Met Leu	
775 780 785	
gaa acc aac tcc aac gat tcc ttc ctc act cca gtg aac tcc aca ctt	2515
Glu Thr Asn Ser Asn Asp Ser Phe Leu Thr Pro Val Asn Ser Thr Leu	
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ggc gag tcc ctg gaa tcc gaa gat att cgc ggc ttt agt gct gcc ggc	2563
Gly Glu Ser Leu Glu Ser Glu Asp Ile Arg Gly Phe Ser Ala Ala Gly	
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Ile Pro Pro Ser Ile Ser Gln Asp Gln Ala Asp Leu Ser Ala Val Gly	
825 830 835	
gcc att gcc aac act gac gac tcc acc gaa acc ggc gga tcc gac gaa	2659
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Ser Ser Gly Gln Ser Thr Gly Asn Thr Gly Gly Val Arg Gly Ser Glu	
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Gly Ile Asn Gly Ser Asn Ala Arg Leu Pro Phe Asn Leu Asp Tyr Thr	
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Asn Ile Thr Thr Asp Trp Tyr Glu Ile Pro Glu Ala Thr Glu Glu Ala	
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Pro Ile Ile Val Val Ser Ala Ala Gly Arg Ile Glu His Tyr Asp Ile	
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Asn Gly Val Arg Gln Ser Gly Gln Ser Val Met Leu Glu Tyr Gly Arg	
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Leu Arg Asp Asn Gly Asp Val Glu Asp Leu Gly Glu Ala Met Met Tyr	
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Gln Leu Pro Glu Glu Ala Asp Val Val Arg Ile Val Ala Thr Asp Val	
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1080 1085 1090	
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Ser Tyr Leu Arg Asn Asp Trp Gly Arg Asp Trp Gly Ser Ile Glu Arg	
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<213> *Corynebacterium glutamicum*

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Gly Leu Leu Gly Leu Leu Met Phe Val Leu Leu Pro Phe Leu Pro Val
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Asn Gln Val Gln Ser Ser Leu Ser Trp Pro Gln Asn Gly Glu Leu Ser
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Ser Val Asn Ala Pro Leu Ile Ser Tyr Ala Pro Gln Ser Met Asp Ala
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Ser Ile Pro Val Ser Ala Leu Asp Ser Leu Asn Asp Asn Gln Ser Leu
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Val Met Gly Thr Leu Pro Leu Asp Ser Thr Asp Ala Thr Asn Arg Gly
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Leu Phe Val Arg Thr Ile Asp Gly Asn Leu Asp Val Ile Val Arg Gly
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Glu Val Leu Leu Asp Leu Ser Pro Thr Glu Val Asn Arg Leu Pro Asp
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Asp Ala Ile Leu Glu Ile Ser Ser Thr Glu Glu Thr Thr Ser Ala Glu
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Ile Thr Gly Thr Ala Phe Ser Gly Glu Thr Glu Gly Asp Glu Arg Pro
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Gln Val Thr Gly Val Tyr Thr Glu Leu Val Asp Asp Pro Ser Thr Ala
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Ser Ala Leu Ala Ser Ala Gly Leu Asn Val Asp Ile Glu Ile Asn Ser
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Arg Phe Thr Ser Ser Pro Ser Leu Leu Lys Tyr Ala Ala Ile Phe Ile
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 Thr Trp Tyr His Glu Tyr Val Arg Tyr Gln Thr Val Met Glu Gln Thr
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 Cys Leu Ala Ile Val Val Ile Ala Ile Leu Arg Tyr Gly Arg Ile Pro
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Gly Ala Ala Lys Gly Pro Ser Leu Arg Leu Met Met Val Ile Phe Gly
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 Gly Val Tyr Ala Gly Leu Ala Gly Ala Leu Ala Gly Leu Ala Ala Val
 610 615 620
 Gly Leu Ser Tyr Val Ala Val Lys Ser Pro Arg Met Arg Thr Ile Ser
 625 630 635 640
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 645 650 655
 Gly Phe Trp Tyr Thr Ser Ser Tyr Ala Val Pro Trp Trp Asp Lys Thr
 660 665 670
 Ile Gln Ile Lys Gly Ile Glu Ala Ser Thr Val Val Leu Val Ile Ala
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 Val Ile Val Leu Ile Ile Gly Val Ile Gln Ser Phe Val His Asp Val
 690 695 700
 Lys Thr Ala Gln Ala Glu Thr Asn His Ser Met Gly Glu Leu Val Ala
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 Ala Ser Pro Ile Ala Gly Val Ser Ala Leu Val Val Leu Ile Thr Cys
 740 745 750
 Ala Ser Met Gly Lys Gly Phe Val Asp Gln Tyr Pro Ala Tyr Ser Val
 755 760 765
 Gly Leu Gly Asn Leu Arg Ser Leu Thr Gly Asn Thr Cys Gly Leu Ala
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 Ser Asp Ala Met Leu Glu Thr Asn Ser Asn Asp Ser Phe Leu Thr Pro
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 Val Asn Ser Thr Leu Gly Glu Ser Leu Glu Ser Glu Asp Ile Arg Gly
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 Phe Ser Ala Ala Gly Ile Pro Pro Ser Ile Ser Gln Asp Gln Ala Asp
 820 825 830
 Leu Ser Ala Val Gly Ala Ile Ala Asn Thr Asp Asp Ser Thr Glu Thr
 835 840 845
 Gly Gly Ser Asp Glu Ser Ser Gly Gln Ser Thr Gly Asn Thr Gly Gly
 850 855 860
 Val Arg Gly Ser Glu Gly Ile Asn Gly Ser Asn Ala Arg Leu Pro Phe
 865 870 875 880
 Asn Leu Asp Tyr Thr Gln Val Pro Val Val Gly Ser Trp Ser Ala Gly
 885 890 895
 Thr Gln Asn Pro Ala Asn Ile Thr Thr Asp Trp Tyr Glu Ile Pro Glu

900	905	910
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Glu His Tyr Asp Ile Asn Gly Val Arg Gln Ser Gly Gln Ser Val Met 930 935 940		
Leu Glu Tyr Gly Arg Leu Arg Asp Asn Gly Asp Val Glu Asp Leu Gly 945 950 955 960		
Glu Ala Met Met Tyr Asp Ile Gly Pro Glu Pro Ser Trp Arg Asn Leu 965 970 975		
Arg Tyr Pro Leu Asp Gln Leu Pro Glu Glu Ala Asp Val Val Arg Ile 980 985 990		
Val Ala Thr Asp Val Asn Leu Asp Glu Asp Gln Trp Val Ala Leu Thr 995 1000 1005		
Pro Pro Arg Val Pro Asn Leu Asp Ser Leu Asn Asn Val Ile Gly Ser 1010 1015 1020		
Glu Thr Pro Gly Leu Leu Asp Trp Ala Val Gly Leu Gln Phe Pro Cys 1025 1030 1035 1040		
Gln Arg Thr Phe Asp His Tyr Ala Gly Val Thr Glu Ile Pro Glu Tyr 1045 1050 1055		
Arg Ile Ser Pro Asp His Gly Gly Lys Ser Thr Leu Ser Pro Phe Gln 1060 1065 1070		
Asp Trp Ala Gly Gly Gly Ser Met Gly Thr Ala Glu Ala Val Asn Asn 1075 1080 1085		
Ala Tyr Glu Ile Pro Ser Tyr Leu Arg Asn Asp Trp Gly Arg Asp Trp 1090 1095 1100		
Gly Ser Ile Glu Arg Tyr Ser Leu Arg Thr Asn Ser Asn Gly Asp Ala 1105 1110 1115 1120		
Pro Lys Val Ala Asp Ile Asn Leu Glu Thr Ile Gln Arg Ser Gly Leu 1125 1130 1135		
Trp Asn Pro Gly His Met Lys Val Asp Glu 1140 1145		

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 <223> RXN01175

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	Val Ser Trp Thr Val	
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gat atc cct aaa gaa gtt ctc cct gat ttg cca cca ttg cca gaa ggc	163	
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atg cag cag cag ttc gag gac acc att tcc cgt gac gct aag cag caa	211	
Met Gln Gln Gln Phe Glu Asp Thr Ile Ser Arg Asp Ala Lys Gln Gln		
25 30 35		
cct acg tgg gat cgt gca cag gca gaa aac gtg cgc aag atc ctt gag	259	
Pro Thr Trp Asp Arg Ala Gln Ala Glu Asn Val Arg Lys Ile Leu Glu		
40 45 50		
tcg gtt cct cca atc gtt gtt gcc cct gag gta ctt gag ctg aag cag	307	
Ser Val Pro Pro Ile Val Val Ala Pro Glu Val Leu Glu Leu Lys Gln		
55 60 65		
aag ctt gct gat gtt gcc aac ggt aag gcc ttc ctc ttg cag ggt ggt	355	
Lys Leu Ala Asp Val Ala Asn Gly Lys Ala Phe Leu Leu Gln Gly Gly		
70 75 80 85		
gac tgt gcg gaa act ttc gag tca aac act gag ccg cac att cgc gcc	403	
Asp Cys Ala Glu Thr Phe Glu Ser Asn Thr Glu Pro His Ile Arg Ala		
90 95 100		
aac gta aag act ctg ctg cag atg gca gtt gtt ttg acc tac ggt gca	451	
Asn Val Lys Thr Leu Leu Gln Met Ala Val Val Leu Thr Tyr Gly Ala		
105 110 115		
tcc act cct gtg atc aag atg gct cgt att gct ggt cag tac gca aag	499	
Ser Thr Pro Val Ile Lys Met Ala Arg Ile Ala Gly Gln Tyr Ala Lys		
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Pro Arg Ser Ser Asp Leu Asp Gly Asn Gly Leu Pro Asn Tyr Arg Gly		
135 140 145		
gat atc gtc aac ggt gtg gag gca acc cca gag gct cgt cgc cac gat	595	
Asp Ile Val Asn Gly Val Glu Ala Thr Pro Glu Ala Arg Arg His Asp		
150 155 160 165		
cct gcc cgc atg atc cgt gct tac gct aac gct tct gct gcg atg aac	643	
Pro Ala Arg Met Ile Arg Ala Tyr Ala Asn Ala Ser Ala Ala Met Asn		
170 175 180		
ttg gtg cgc gcg ctc acc agc tct ggc acc gct gat ctt tac cgt ctc	691	
Leu Val Arg Ala Leu Thr Ser Ser Gly Thr Ala Asp Leu Tyr Arg Leu		
185 190 195		
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Ser Glu Trp Asn Arg Glu Phe Val Ala Asn Ser Pro Ala Gly Ala Arg		
200 205 210		
tac gag gct ctt gct cgt gag atc gac tcc ggt ctg cgc ttc atg gaa	787	
Tyr Glu Ala Leu Ala Arg Glu Ile Asp Ser Gly Leu Arg Phe Met Glu		
215 220 225		
gca tgt ggc gtg tcc gat gag tcc ctg cgt gct gca gat atc tac tgc	835	

Ala Cys Gly Val Ser Asp Glu Ser Leu Arg Ala Ala Asp Ile Tyr Cys 230 235 240 245	
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gca acc gat gag gaa ggc aac gag gaa ctt tac gat ctt tca gct cac Ala Thr Asp Glu Glu Gly Asn Glu Glu Leu Tyr Asp Leu Ser Ala His 265 270 275	931
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ggt atc acc cct gaa gag gct gtt gca tac gct gac aag ctc gat ccg Gly Ile Thr Pro Glu Glu Ala Val Ala Tyr Ala Asp Lys Leu Asp Pro 310 315 320 325	1075
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acc gca tcc aat ggc tac aag acc cgt cac ttc gac aag gtt atc gat Thr Ala Ser Asn Gly Tyr Lys Thr Arg His Phe Asp Lys Val Ile Asp 375 380 385	1267
gag gtc cag ggc ttc ttc gag gtc cac cgc gca ttg ggc acc cac cca Glu Val Gln Gly Phe Phe Glu Val His Arg Ala Leu Gly Thr His Pro 390 395 400 405	1315
ggc gga atc cac att gag ttc act ggt gaa gat gtc acc gag tgc ctc Gly Gly Ile His Ile Glu Phe Thr Gly Glu Asp Val Thr Glu Cys Leu 410 415 420	1363
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<210> 478

<211> 462

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 478

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Asp Ala Lys Gln Gln Pro Thr Trp Asp Arg Ala Gln Ala Glu Asn Val
      35           40           45

Arg Lys Ile Leu Glu Ser Val Pro Pro Ile Val Val Ala Pro Glu Val
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Leu Glu Leu Lys Gln Lys Leu Ala Asp Val Ala Asn Gly Lys Ala Phe
 65           70           75           80

Leu Leu Gln Gly Gly Asp Cys Ala Glu Thr Phe Glu Ser Asn Thr Glu
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Pro His Ile Arg Ala Asn Val Lys Thr Leu Leu Gln Met Ala Val Val
      100           105           110

Leu Thr Tyr Gly Ala Ser Thr Pro Val Ile Lys Met Ala Arg Ile Ala
      115           120           125

Gly Gln Tyr Ala Lys Pro Arg Ser Ser Asp Leu Asp Gly Asn Gly Leu
      130           135           140

Pro Asn Tyr Arg Gly Asp Ile Val Asn Gly Val Glu Ala Thr Pro Glu
      145           150           155           160

Ala Arg Arg His Asp Pro Ala Arg Met Ile Arg Ala Tyr Ala Asn Ala
          165           170           175

Ser Ala Ala Met Asn Leu Val Arg Ala Leu Thr Ser Ser Gly Thr Ala
          180           185           190

Asp Leu Tyr Arg Leu Ser Glu Trp Asn Arg Glu Phe Val Ala Asn Ser
      195           200           205

Pro Ala Gly Ala Arg Tyr Glu Ala Leu Ala Arg Glu Ile Asp Ser Gly
      210           215           220

Leu Arg Phe Met Glu Ala Cys Gly Val Ser Asp Glu Ser Leu Arg Ala
      225           230           235           240

Ala Asp Ile Tyr Cys Ser His Glu Ala Leu Leu Val Asp Tyr Glu Arg
          245           250           255

Ser Met Leu Arg Leu Ala Thr Asp Glu Glu Gly Asn Glu Glu Leu Tyr
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Asp Leu Ser Ala His Gln Leu Trp Ile Gly Glu Arg Thr Arg Gly Met
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Asp Asp Phe His Val Asn Phe Ala Ser Met Ile Ser Asn Pro Ile Gly
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 Ile Lys Ile Gly Pro Gly Ile Thr Pro Glu Glu Ala Val Ala Tyr Ala
 305 310 315 320
 Asp Lys Leu Asp Pro Asn Phe Glu Pro Gly Arg Leu Thr Ile Val Ala
 325 330 335
 Arg Met Gly His Asp Lys Val Arg Ser Val Leu Pro Gly Val Ile Gln
 340 345 350
 Ala Val Glu Ala Ser Gly His Lys Val Ile Trp Gln Ser Asp Pro Met
 355 360 365
 His Gly Asn Thr Phe Thr Ala Ser Asn Gly Tyr Lys Thr Arg His Phe
 370 375 380
 Asp Lys Val Ile Asp Glu Val Gln Gly Phe Phe Glu Val His Arg Ala
 385 390 395 400
 Leu Gly Thr His Pro Gly Gly Ile His Ile Glu Phe Thr Gly Glu Asp
 405 410 415
 Val Thr Glu Cys Leu Gly Gly Ala Glu Asp Ile Thr Asp Val Asp Leu
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 435 440 445
 Ser Leu Glu Leu Ala Phe Leu Val Ala Glu Met Leu Arg Asn
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 <212> DNA
 <213> Corynebacterium glutamicum

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 <223> RXN01376

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 Val Thr Tyr Ser Pro
 1 5
 ggt aaa tac ttg gcg tcg ttc ctg gat tct ttg cct ggt gcg act tca 163
 Gly Lys Tyr Leu Ala Ser Phe Leu Asp Ser Leu Pro Gly Ala Thr Ser
 10 15 20
 cga gac acc cac gtt gtg atg gca gac aat ggt tct gtg gac ggt gtt 211
 Arg Asp Thr His Val Val Met Ala Asp Asn Gly Ser Val Asp Gly Val
 25 30 35
 cct gag cag gca gca gcc tca cgc agc aac gtg gag ttc ctc tca act 259
 Pro Glu Gln Ala Ala Ala Ser Arg Ser Asn Val Glu Phe Leu Ser Thr

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gtc tca aac cct gat gtt gtt ttt gac gaa gac tct att gat caa ttg Val Ser Asn Pro Asp Val Val Phe Asp Glu Asp Ser Ile Asp Gln Leu 90 95 100			403
ctt gaa tgt gcg aaa cgt cac cct gaa gca gga gcg gtt ggc ccg ttg Leu Glu Cys Ala Lys Arg His Pro Glu Ala Gly Ala Val Gly Pro Leu 105 110 115			451
atc cgt gag gcg gac ggt tcg gcg tat ccg tcg gct cgg gcg gta ccc Ile Arg Glu Ala Asp Gly Ser Ala Tyr Pro Ser Ala Arg Ala Val Pro 120 125 130			499
act ttg gcg aat ggc att ggt cac gct ttg ttg ggt gct gtg tgg aaa Thr Leu Ala Asn Gly Ile Gly His Ala Leu Leu Gly Ala Val Trp Lys 135 140 145			547
tcc aat ccg tgg tcg gcg gct tac cgt gac gat gaa gat atg gac act Ser Asn Pro Trp Ser Ala Ala Tyr Arg Asp Asp Glu Asp Met Asp Thr 150 155 160 165			595
gag cgc act gct ggc tgg ctg tcg gga tcg tgc ctg tta tta agg tgg Glu Arg Thr Ala Gly Trp Leu Ser Gly Ser Cys Leu Leu Leu Arg Trp 170 175 180			643
gat gcg ttt gat cga gtt ggt ggt ttt gat gag cgc tac ttc atg tac Asp Ala Phe Asp Arg Val Gly Gly Phe Asp Glu Arg Tyr Phe Met Tyr 185 190 195			691
atg gaa gac gtt gac ctg gga gat ccg ctg gtt cgc gcc ggt ttc acc Met Glu Asp Val Asp Leu Gly Asp Arg Leu Val Arg Ala Gly Phe Thr 200 205 210			739
aac gtc ttt tgc cca agt gcg cag atc atc cac gcg aaa ggt cat gtt Asn Val Phe Cys Pro Ser Ala Gln Ile Ile His Ala Lys Gly His Val 215 220 225			787
gcg ggt aaa aac cca gag aac atg ttg ccc gca cac cac gag agc gcg Ala Gly Lys Asn Pro Glu Asn Met Leu Pro Ala His His Glu Ser Ala 230 235 240 245			835
tat cgc ttc cag gct gat cgc ctc gcg aag ccg tgg caa gcc cca att Tyr Arg Phe Gln Ala Asp Arg Leu Ala Lys Pro Trp Gln Ala Pro Ile 250 255 260			883
ccg ttg gct ctg cga att ggt ttg aaa tta cga gcc gga gtc gcg gtt Arg Leu Ala Leu Arg Ile Gly Leu Lys Leu Arg Ala Gly Val Ala Val 265 270 275			931
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gac

984

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<211> 287

<212> PRT

<213> Corynebacterium glutamicum

<400> 480

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Ser Val Asp Gly Val Pro Glu Gln Ala Ala Ala Ser Arg Ser Asn Val
 35 40 45

Glu Phe Leu Ser Thr Gly Gly Asn Leu Gly Tyr Gly Thr Ala Ile Asn
 50 55 60

Ile Ala Ala Arg Ser Leu Arg Ala Arg Arg Glu Ala Gly Glu Ile Asp
 65 70 75 80

Gly Glu Phe Phe Leu Val Ser Asn Pro Asp Val Val Phe Asp Glu Asp
 85 90 95

Ser Ile Asp Gln Leu Leu Glu Cys Ala Lys Arg His Pro Glu Ala Gly
 100 105 110

Ala Val Gly Pro Leu Ile Arg Glu Ala Asp Gly Ser Ala Tyr Pro Ser
 115 120 125

Ala Arg Ala Val Pro Thr Leu Ala Asn Gly Ile Gly His Ala Leu Leu
 130 135 140

Gly Ala Val Trp Lys Ser Asn Pro Trp Ser Ala Ala Tyr Arg Asp Asp
 145 150 155 160

Glu Asp Met Asp Thr Glu Arg Thr Ala Gly Trp Leu Ser Gly Ser Cys
 165 170 175

Leu Leu Leu Arg Trp Asp Ala Phe Asp Arg Val Gly Gly Phe Asp Glu
 180 185 190

Arg Tyr Phe Met Tyr Met Glu Asp Val Asp Leu Gly Asp Arg Leu Val
 195 200 205

Arg Ala Gly Phe Thr Asn Val Phe Cys Pro Ser Ala Gln Ile Ile His
 210 215 220

Ala Lys Gly His Val Ala Gly Lys Asn Pro Glu Asn Met Leu Pro Ala
 225 230 235 240

His His Glu Ser Ala Tyr Arg Phe Gln Ala Asp Arg Leu Ala Lys Pro
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Trp Gln Ala Pro Ile Arg Leu Ala Leu Arg Ile Gly Leu Lys Leu Arg
 260 265 270

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 275 280 285

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 <211> 1002
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
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 <222> (101)..(979)
 <223> RXN01631

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 Met Lys Pro Gln Leu
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 att gca tct tgc tgg acc agc gcg gga gac gcc gca ccc gat cgt gac 163
 Ile Ala Ser Cys Trp Thr Ser Ala Gly Asp Ala Ala Pro Asp Arg Asp
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 Asp Leu Ser Ser Pro Val Ala Ile Asp Glu Arg Ile Ala Leu Val Ala
 25 30 35
 gaa acc ggt tgg gca ggc att ggg ctt gtt cac gcc gat ctc atc aaa 259
 Glu Thr Gly Trp Ala Gly Ile Gly Leu Val His Ala Asp Leu Ile Lys
 40 45 50
 gca cgc gac acc att ggc tac gag gaa ttg cgc cga cgc atc cac gct 307
 Ala Arg Asp Thr Ile Gly Tyr Glu Glu Leu Arg Arg Arg Ile His Ala
 55 60 65
 gca gga att gaa atc att gag gtg gag ttc ctc aat ggt tgg tgg gcg 355
 Ala Gly Ile Glu Ile Ile Glu Val Glu Phe Leu Asn Gly Trp Trp Ala
 70 75 80 85
 act ggt gcg gaa cgc caa gag tcc gat gcc gtt cgt gcg gat ctg ttt 403
 Thr Gly Ala Glu Arg Gln Glu Ser Asp Ala Val Arg Ala Asp Leu Phe
 90 95 100
 gct gcg gcg caa gct ctt ggt tcc cca cac att aag gtc gga gca gga 451
 Ala Ala Ala Gln Ala Leu Gly Ser Pro His Ile Lys Val Gly Ala Gly
 105 110 115
 gag ggc acc aat ggt gtg gtt ccc att gct cac atg gcc agt gcg ttt 499
 Glu Gly Thr Asn Gly Val Val Pro Ile Ala His Met Ala Ser Ala Phe
 120 125 130
 act gat ctc gct gcg gaa gct gaa gct cat ggc gtc aag ctc gcg ttg 547
 Thr Asp Leu Ala Ala Glu Ala Glu Ala His Gly Val Lys Leu Ala Leu
 135 140 145
 gaa gca act ccg ttt tct cac ctg aag acc atc tac gac gcg ctg gaa 595
 Glu Ala Thr Pro Phe Ser His Leu Lys Thr Ile Tyr Asp Ala Leu Glu
 150 155 160 165

gtt gtc agc cat tcc gat agc cca tcg gct gga ctc atg gtt gat atc 643
 Val Val Ser His Ser Asp Ser Pro Ser Ala Gly Leu Met Val Asp Ile
 170 175 180

tgg cac acc gcg aaa atc gga atc ccc aac gat gaa ctg tgg cgc aac 691
 Trp His Thr Ala Lys Ile Gly Ile Pro Asn Asp Glu Leu Trp Arg Asn
 185 190 195

att cca ctg tcc aag gtc aac gca gtg gag gtt gat gat ggt ttc att 739
 Ile Pro Leu Ser Lys Val Asn Ala Val Glu Val Asp Asp Gly Phe Ile
 200 205 210

gac acc cca att gat ctt ttc gat gac tcc acc aac cgt cgc gcg tac 787
 Asp Thr Pro Ile Asp Leu Phe Asp Asp Ser Thr Asn Arg Arg Ala Tyr
 215 220 225

tgc ggt gaa ggc gaa ttt gat ccc gca agc ttc atc cgt ggc gcc atc 835
 Cys Gly Glu Gly Glu Phe Asp Pro Ala Ser Phe Ile Arg Gly Ala Ile
 230 235 240 245

gac gcc ggt tgg acg ggc gca tat ggt gtg gaa att att tcc gca gag 883
 Asp Ala Gly Trp Thr Gly Ala Tyr Gly Val Glu Ile Ile Ser Ala Glu
 250 255 260

cac cga agc ctc ccg gtg aaa gaa ggg ctg caa cgt gct ttc gac acc 931
 His Arg Ser Leu Pro Val Lys Glu Gly Leu Gln Arg Ala Phe Asp Thr
 265 270 275

acc atc gca gcg ttt gaa caa gct gct cgt ctc gcc ccc tcc act aac 979
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 <213> Corynebacterium glutamicum

<400> 482
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 35 40 45
 Ala Asp Leu Ile Lys Ala Arg Asp Thr Ile Gly Tyr Glu Glu Leu Arg
 50 55 60
 Arg Arg Ile His Ala Ala Gly Ile Glu Ile Ile Glu Val Glu Phe Leu
 65 70 75 80
 Asn Gly Trp Trp Ala Thr Gly Ala Glu Arg Gln Glu Ser Asp Ala Val
 85 90 95
 Arg Ala Asp Leu Phe Ala Ala Ala Gln Ala Leu Gly Ser Pro His Ile
 100 105 110

Lys Val Gly Ala Gly Glu Gly Thr Asn Gly Val Val Pro Ile Ala His
 115 120 125
 Met Ala Ser Ala Phe Thr Asp Leu Ala Ala Glu Ala Glu Ala His Gly
 130 135 140
 Val Lys Leu Ala Leu Glu Ala Thr Pro Phe Ser His Leu Lys Thr Ile
 145 150 155 160
 Tyr Asp Ala Leu Glu Val Val Ser His Ser Asp Ser Pro Ser Ala Gly
 165 170 175
 Leu Met Val Asp Ile Trp His Thr Ala Lys Ile Gly Ile Pro Asn Asp
 180 185 190
 Glu Leu Trp Arg Asn Ile Pro Leu Ser Lys Val Asn Ala Val Glu Val
 195 200 205
 Asp Asp Gly Phe Ile Asp Thr Pro Ile Asp Leu Phe Asp Asp Ser Thr
 210 215 220
 Asn Arg Arg Ala Tyr Cys Gly Glu Gly Glu Phe Asp Pro Ala Ser Phe
 225 230 235 240
 Ile Arg Gly Ala Ile Asp Ala Gly Trp Thr Gly Ala Tyr Gly Val Glu
 245 250 255
 Ile Ile Ser Ala Glu His Arg Ser Leu Pro Val Lys Glu Gly Leu Gln
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 Ala Pro Ser Thr Asn
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<220>
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 <222> (101)..(967)
 <223> RXN01593

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 Met Tyr Val Thr Asn
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 aat gcc tcc cgt gct ccg gag gtg gtg gct gcg caa ctc cgt gag att 163
 Asn Ala Ser Arg Ala Pro Glu Val Val Ala Ala Gln Leu Arg Glu Ile
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 Gly Leu Ala Asp Thr Thr Ala Asp Asn Val Met Thr Ser Ala Gln Ala

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Ala Cys Lys Met Ala Ala Glu Lys Ile Pro Ala Gly Ser Lys Val Tyr			
40	45	50	
gtt ttg ggt tca gaa tcc ttc cgc gag cta gct act gaa gct ggt ttt			307
Val Leu Gly Ser Glu Ser Phe Arg Glu Leu Ala Thr Glu Ala Gly Phe			
55	60	65	
gtg gtg gtt gat tcg gct gat gat aaa cct gtg gct gtg ctt cac ggc			355
Val Val Val Asp Ser Ala Asp Asp Lys Pro Val Ala Val Leu His Gly			
70	75	80	85
cac aac cct gag acc ggt tgg gct cag ttg agc gag gct gcg ctg tca			403
His Asn Pro Glu Thr Gly Trp Ala Gln Leu Ser Glu Ala Ala Leu Ser			
90	95	100	
att aat gct ggc gcg cag tat ttt gca tca aat ttg gat tcc acc ctt			451
Ile Asn Ala Gly Ala Gln Tyr Phe Ala Ser Asn Leu Asp Ser Thr Leu			
105	110	115	
ccc atg gaa cgc ggt cgt cac att ggc aac ggt tcc atg gtg gct gcc			499
Pro Met Glu Arg Gly Arg His Ile Gly Asn Gly Ser Met Val Ala Ala			
120	125	130	
gtg gtc aac gcg act ggc gta aag cct ctt tcc gca ggt aag cca ggc			547
Val Val Asn Ala Thr Gly Val Lys Pro Leu Ser Ala Gly Lys Pro Gly			
135	140	145	
ccc gcg atg ttc tat gcg ggg gct gaa act ctt aat tct tca aag cct			595
Pro Ala Met Phe Tyr Ala Gly Ala Glu Thr Leu Asn Ser Ser Lys Pro			
150	155	160	165
ttg gct gtc ggc gat cgt ctc gat acc gat atc gcc ggc gga aac gct			643
Leu Ala Val Gly Asp Arg Leu Asp Thr Asp Ile Ala Gly Gly Asn Ala			
170	175	180	
gca ggc atg gac aca ttc cag gtc ctg acc ggc gtc agc ggc tac tac			691
Ala Gly Met Asp Thr Phe Gln Val Leu Thr Gly Val Ser Gly Tyr Tyr			
185	190	195	
gat ttg gtg cgc gcc att ccc aga gca gcg ccc cac cta tat cgc cac			739
Asp Leu Val Arg Ala Ile Pro Arg Ala Ala Pro His Leu Tyr Arg His			
200	205	210	
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Leu Asp Ala Gly Ser Leu Gln Arg Ser Gly Arg Ala Gln Ala Arg Cys			
215	220	225	
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Pro Gly Arg Phe Phe Ser Ala Tyr Arg Arg Arg His Pro Gly His Phe			
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cgg cgg cga tgc cgg cgc aac tcc ggt tgc agc act ccg cac tgc gtt			883
Arg Arg Arg Cys Arg Arg Asn Ser Gly Cys Ser Thr Pro His Cys Val			
250	255	260	
gga tgt ggc ctg ggc ggc cac aga gca gtc acc gag gta cgc gct gat			931
Gly Cys Gly Leu Gly Gly His Arg Ala Val Thr Glu Val Arg Ala Asp			
265	270	275	

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<210> 484

<211> 289

<212> PRT

<213> Corynebacterium glutamicum

<400> 484

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 Gln Leu Arg Glu Ile Gly Leu Ala Asp Thr Thr Ala Asp Asn Val Met
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 Thr Ser Ala Gln Ala Ala Cys Lys Met Ala Ala Glu Lys Ile Pro Ala
 35 40 45
 Gly Ser Lys Val Tyr Val Leu Gly Ser Glu Ser Phe Arg Glu Leu Ala
 50 55 60
 Thr Glu Ala Gly Phe Val Val Val Asp Ser Ala Asp Asp Lys Pro Val
 65 70 75 80
 Ala Val Leu His Gly His Asn Pro Glu Thr Gly Trp Ala Gln Leu Ser
 85 90 95
 Glu Ala Ala Leu Ser Ile Asn Ala Gly Ala Gln Tyr Phe Ala Ser Asn
 100 105 110
 Leu Asp Ser Thr Leu Pro Met Glu Arg Gly Arg His Ile Gly Asn Gly
 115 120 125
 Ser Met Val Ala Ala Val Val Asn Ala Thr Gly Val Lys Pro Leu Ser
 130 135 140
 Ala Gly Lys Pro Gly Pro Ala Met Phe Tyr Ala Gly Ala Glu Thr Leu
 145 150 155 160
 Asn Ser Ser Lys Pro Leu Ala Val Gly Asp Arg Leu Asp Thr Asp Ile
 165 170 175
 Ala Gly Gly Asn Ala Ala Gly Met Asp Thr Phe Gln Val Leu Thr Gly
 180 185 190
 Val Ser Gly Tyr Tyr Asp Leu Val Arg Ala Ile Pro Arg Ala Ala Pro
 195 200 205
 His Leu Tyr Arg His Leu Asp Ala Gly Ser Leu Gln Arg Ser Gly Arg
 210 215 220
 Ala Gln Ala Arg Cys Pro Gly Arg Phe Phe Ser Ala Tyr Arg Arg Arg
 225 230 235 240
 His Pro Gly His Phe Arg Arg Arg Cys Arg Arg Asn Ser Gly Cys Ser
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Thr Pro His Cys Val Gly Cys Gly Leu Gly Gly His Arg Ala Val Thr
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Glu Val Arg Ala Asp Ser Glu Val Ala Ala Thr Ala Leu Gln Ser Trp
275 280 285

Trp

<210> 485

<211> 1173

<212> DNA

<213> Corynebacterium glutamicum

<220>

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<222> (101)..(1150)

<223> RXN00337

<400> 485

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                                         Met Leu Leu Thr Tyr
                                         1 5

gcg ttt gtg gat gtg gag gga ggc gtc gaa aag cat tct tta agc act 163
Ala Phe Val Asp Val Glu Gly Gly Val Glu Lys His Ser Leu Ser Thr
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gcg gac att gca gct cgc gca cac gcc cat atg aaa tcc cat gat gtt 211
Ala Asp Ile Ala Ala Arg Ala His Ala His Met Lys Ser His Asp Val
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ttg ggg cgg cag act acg ccg cct cag ccg gag ggc ggc gtt gct gcc 259
Leu Gly Arg Gln Thr Thr Pro Pro Gln Pro Glu Gly Gly Val Ala Ala
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cgg ttg ggc ggg att gcg tgg aca atg atc cat aag caa atg ctt tcg 307
Arg Leu Gly Gly Ile Ala Trp Thr Met Ile His Lys Gln Met Leu Ser
                        55 60 65

cgt gac aca aaa ggc ctg gat atc acc gtg ttg agc acc att cct gag 355
Arg Asp Thr Lys Gly Leu Asp Ile Thr Val Leu Ser Thr Ile Pro Glu
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Gly Val Gly Leu Gly Glu Asn Ser Ala Met Asp Val Ala Leu Ala Leu
                        90 95 100

gcg ctg tat cgg gaa aat att gag gaa gcc ccc acg aag gcg cgc att 451
Ala Leu Tyr Arg Glu Asn Ile Glu Glu Ala Pro Thr Lys Ala Arg Ile
                        105 110 115

gcg gag att tgt tcg cag tcc gca ttc atg ttc agt gag act tca gtg 499
Ala Glu Ile Cys Ser Gln Ser Ala Phe Met Phe Ser Glu Thr Ser Val
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ttg cgt gcg cgg cac acc gtg gcg ttg cgg ggt gaa act gga cag att 547

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Ser	Val	Val	Asp	Tyr	Ala	Asp	Gly	Ser	Val	Thr	Gln	Ala	Pro	His	Pro	
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gtg	agt	cgt	tcc	gct	ggt	ttg	tcg	gca	ttt	ggt	ggt	gct	gcg	caa	act	643
Val	Ser	Arg	Ser	Ala	Gly	Leu	Ser	Ala	Phe	Val	Val	Ala	Ala	Gln	Thr	
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gaa	act	gat	ccg	agc	att	tac	cgc	gag	atc	tat	gct	cga	cat	gcg	ttt	691
Glu	Thr	Asp	Pro	Ser	Ile	Tyr	Arg	Glu	Ile	Tyr	Ala	Arg	His	Ala	Phe	
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Ile	Asp	Glu	Ala	Ala	Arg	Ala	Phe	Ser	Val	Glu	Ser	Leu	Arg	Leu	Leu	
		200					205					210				
ccc	gac	gct	tcc	act	cgt	gtt	gtg	gat	tgg	ttg	cag	gcc	gtg	att	gag	787
Pro	Asp	Ala	Ser	Thr	Arg	Val	Val	Asp	Trp	Leu	Gln	Ala	Val	Ile	Glu	
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gtg	act	ggt	cga	gag	gat	ctg	ccc	tcg	att	gaa	caa	gcc	cag	cgc	tgg	835
Val	Thr	Gly	Arg	Glu	Asp	Leu	Pro	Ser	Ile	Glu	Gln	Ala	Gln	Arg	Trp	
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Leu	Asn	Leu	Trp	Glu	Asn	Glu	Thr	Arg	Arg	Ala	Gln	Arg	Thr	Ala	Asn	
				250					255					260		
gcc	ctg	cgt	tcg	aga	agg	ctg	agt	gag	ttt	tct	gag	ctg	ctg	atg	gaa	931
Ala	Leu	Arg	Ser	Arg	Arg	Leu	Ser	Glu	Phe	Ser	Glu	Leu	Leu	Met	Glu	
			265					270					275			
tcc	caa	gat	gat	ttg	agc	gac	acc	ttc	gat	ttc	ccc	cct	gct	gat	ttg	979
Ser	Gln	Asp	Asp	Leu	Ser	Asp	Thr	Phe	Asp	Phe	Pro	Pro	Ala	Asp	Leu	
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gcg	ctt	gct	cgt	ttg	tgc	gtc	gag	cgg	ggt	gcc	aca	gct	gct	cgg	tcc	1027
Ala	Leu	Ala	Arg	Leu	Cys	Val	Glu	Arg	Gly	Ala	Thr	Ala	Ala	Arg	Ser	
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acg	tca	gcg	cgc	ggt	gtg	att	gcg	ttg	gtt	gat	gcc	cat	cat	gcg	cac	1075
Thr	Ser	Ala	Arg	Gly	Val	Ile	Ala	Leu	Val	Asp	Ala	His	His	Ala	His	
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aat	ttt	gct	gcg	gat	ctc	agc	gag	gat	ggc	ttg	ttg	gtg	gtt	cct	ctc	1123
Asn	Phe	Ala	Ala	Asp	Leu	Ser	Glu	Asp	Gly	Leu	Leu	Val	Val	Pro	Leu	
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ggg	cac	ggg	gac	gtc	gcg	gaa	cag	ggc	tagc	cgcct	actta	accag				1170
Gly	His	Gly	Asp	Val	Ala	Glu	Gln	Gly								
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cct																1173

<210> 486
 <211> 350
 <212> PRT

<213> Corynebacterium glutamicum

<400> 486

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 Lys Ser His Asp Val Leu Gly Arg Gln Thr Thr Pro Pro Gln Pro Glu
 35 40 45
 Gly Gly Val Ala Ala Arg Leu Gly Gly Ile Ala Trp Thr Met Ile His
 50 55 60
 Lys Gln Met Leu Ser Arg Asp Thr Lys Gly Leu Asp Ile Thr Val Leu
 65 70 75 80
 Ser Thr Ile Pro Glu Gly Val Gly Leu Gly Glu Asn Ser Ala Met Asp
 85 90 95
 Val Ala Leu Ala Leu Ala Leu Tyr Arg Glu Asn Ile Glu Glu Ala Pro
 100 105 110
 Thr Lys Ala Arg Ile Ala Glu Ile Cys Ser Gln Ser Ala Phe Met Phe
 115 120 125
 Ser Glu Thr Ser Val Leu Arg Ala Arg His Thr Val Ala Leu Arg Gly
 130 135 140
 Glu Thr Gly Gln Ile Ser Val Val Asp Tyr Ala Asp Gly Ser Val Thr
 145 150 155 160
 Gln Ala Pro His Pro Val Ser Arg Ser Ala Gly Leu Ser Ala Phe Val
 165 170 175
 Val Ala Ala Gln Thr Glu Thr Asp Pro Ser Ile Tyr Arg Glu Ile Tyr
 180 185 190
 Ala Arg His Ala Phe Ile Asp Glu Ala Ala Arg Ala Phe Ser Val Glu
 195 200 205
 Ser Leu Arg Leu Leu Pro Asp Ala Ser Thr Arg Val Val Asp Trp Leu
 210 215 220
 Gln Ala Val Ile Glu Val Thr Gly Arg Glu Asp Leu Pro Ser Ile Glu
 225 230 235 240
 Gln Ala Gln Arg Trp Leu Asn Leu Trp Glu Asn Glu Thr Arg Arg Ala
 245 250 255
 Gln Arg Thr Ala Asn Ala Leu Arg Ser Arg Arg Leu Ser Glu Phe Ser
 260 265 270
 Glu Leu Leu Met Glu Ser Gln Asp Asp Leu Ser Asp Thr Phe Asp Phe
 275 280 285
 Pro Pro Ala Asp Leu Ala Leu Ala Arg Leu Cys Val Glu Arg Gly Ala
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 Thr Ala Ala Arg Ser Thr Ser Ala Arg Gly Val Ile Ala Leu Val Asp

305					310					315					320
Ala	His	His	Ala	His	Asn	Phe	Ala	Ala	Asp	Leu	Ser	Glu	Asp	Gly	Leu
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Leu	Val	Val	Pro	Leu	Gly	His	Gly	Asp	Val	Ala	Glu	Gln	Gly		
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<211> 1248
<212> DNA
<213> Corynebacterium glutamicum
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<222> (101)..(1225)  
<223> BXS00584
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				Met	His	Ser	Pro	Glu								
									1				5			
agg	caa	gaa	aaa	atg	agt	tct	cca	gtc	tca	ctc	gaa	aac	gcg	gcg	tca	163
Arg	Gln	Glu	Lys	Met	Ser	Ser	Pro	Val	Ser	Leu	Glu	Asn	Ala	Ala	Ser	
				10					15					20		
acc	agc	aac	aag	cgc	gtc	gtg	gct	ttc	cac	gag	ctg	cct	agc	cct	aca	211
Thr	Ser	Asn	Lys	Arg	Val	Val	Ala	Phe	His	Glu	Leu	Pro	Ser	Pro	Thr	
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Asp	Leu	Ile	Ala	Ala	Asn	Pro	Leu	Thr	Pro	Lys	Gln	Ala	Ser	Lys	Val	
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Glu	Gln	Asp	Arg	Gln	Asp	Ile	Ala	Asp	Ile	Phe	Ala	Gly	Asp	Asp	Asp	
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cgc	ctc	gtt	gtc	gtt	gtg	gga	cct	tgc	tca	gtt	cac	gat	cct	gaa	gca	355
Arg	Leu	Val	Val	Val	Val	Gly	Pro	Cys	Ser	Val	His	Asp	Pro	Glu	Ala	
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gcc	atc	gat	tac	gca	aac	cgc	ctg	gct	ccg	ctg	gca	aag	cgc	ctt	gat	403
Ala	Ile	Asp	Tyr	Ala	Asn	Arg	Leu	Ala	Pro	Leu	Ala	Lys	Arg	Leu	Asp	
				90					95					100		
cag	gac	ctc	aag	att	gtc	atg	cgc	gtg	tac	ttc	gag	aag	cct	cgc	acc	451
Gln	Asp	Leu	Lys	Ile	Val	Met	Arg	Val	Tyr	Phe	Glu	Lys	Pro	Arg	Thr	
			105					110					115			
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Ile	Val	Gly	Trp	Lys	Gly	Leu	Ile	Asn	Asp	Pro	His	Leu	Asn	Glu	Thr	
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Tyr	Asp	Ile	Pro	Glu	Gly	Leu	Arg	Ile	Ala	Arg	Lys	Val	Leu	Ile	Asp	
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Ser	Pro	Gln	Tyr	Tyr	Ala	Asp	Thr	Val	Ala	Trp	Gly	Ala	Ile	Gly	Ala	
				170					175						180	
cgt	acc	acc	gaa	tct	cag	gtg	cac	cgc	cag	ctg	gct	tct	ggg	atg	tct	691
Arg	Thr	Thr	Glu	Ser	Gln	Val	His	Arg	Gln	Leu	Ala	Ser	Gly	Met	Ser	
			185					190					195			
atg	cca	att	ggg	ttc	aag	aac	gga	act	gac	gga	aac	atc	cag	gtt	gca	739
Met	Pro	Ile	Gly	Phe	Lys	Asn	Gly	Thr	Asp	Gly	Asn	Ile	Gln	Val	Ala	
		200					205					210				
gtc	gac	gcg	gta	cag	gct	gcc	cag	aac	cca	cac	ttc	ttc	ttc	gga	acc	787
Val	Asp	Ala	Val	Gln	Ala	Ala	Gln	Asn	Pro	His	Phe	Phe	Phe	Gly	Thr	
	215					220					225					
tcc	gac	gac	ggc	gcg	ctg	agc	gtc	gtg	gag	acc	gca	ggc	aac	agc	aac	835
Ser	Asp	Asp	Gly	Ala	Leu	Ser	Val	Val	Glu	Thr	Ala	Gly	Asn	Ser	Asn	
230					235					240					245	
tcc	cac	atc	att	ttg	cgc	ggc	ggg	acc	tcc	ggc	ccg	aac	cat	gat	gca	883
Ser	His	Ile	Ile	Leu	Arg	Gly	Gly	Thr	Ser	Gly	Pro	Asn	His	Asp	Ala	
				250					255					260		
gct	tcg	gtg	gag	gcc	gtc	gtc	gag	aag	ctt	ggg	gaa	aac	gct	cgt	ctc	931
Ala	Ser	Val	Glu	Ala	Val	Val	Glu	Lys	Leu	Gly	Glu	Asn	Ala	Arg	Leu	
		265						270					275			
atg	atc	gat	gct	tcc	cat	gct	aac	tcc	ggc	aag	gat	cat	atc	cga	cag	979
Met	Ile	Asp	Ala	Ser	His	Ala	Asn	Ser	Gly	Lys	Asp	His	Ile	Arg	Gln	
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gtt	gag	gtt	gtt	cgt	gaa	atc	gca	gag	cag	att	tct	ggc	ggg	tct	gaa	1027
Val	Glu	Val	Val	Arg	Glu	Ile	Ala	Glu	Gln	Ile	Ser	Gly	Gly	Ser	Glu	
	295					300					305					
gct	gtg	gct	gga	atc	atg	att	gag	tcc	ttc	ctc	gtt	ggg	ggc	gca	cag	1075
Ala	Val	Ala	Gly	Ile	Met	Ile	Glu	Ser	Phe	Leu	Val	Gly	Gly	Ala	Gln	
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Asn	Leu	Asp	Pro	Ala	Lys	Leu	Arg	Ile	Asn	Gly	Gly	Glu	Gly	Leu	Val	
				330					335					340		
tac	gga	cag	tct	gtg	acc	gat	aag	tgc	atc	gat	att	gac	acc	acc	atc	1171
Tyr	Gly	Gln	Ser	Val	Thr	Asp	Lys	Cys	Ile	Asp	Ile	Asp	Thr	Thr	Ile	
			345					350					355			
gat	ttg	ctc	gct	gag	ctg	gcc	gca	gca	gta	agg	gaa	cgc	cga	gca	gca	1219
Asp	Leu	Leu	Ala	Glu	Leu	Ala	Ala	Ala	Val	Arg	Glu	Arg	Arg	Ala	Ala	
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gcc	aag	taattaaggg	cgctagactg	tta												1248
Ala	Lys															
	375															

<210> 488
 <211> 375
 <212> PRT
 <213> *Corynebacterium glutamicum*

<400> 488

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Leu Pro Ser Pro Thr Asp Leu Ile Ala Ala Asn Pro Leu Thr Pro Lys
      35              40              45

Gln Ala Ser Lys Val Glu Gln Asp Arg Gln Asp Ile Ala Asp Ile Phe
      50              55              60

Ala Gly Asp Asp Asp Arg Leu Val Val Val Val Gly Pro Cys Ser Val
      65              70              75              80

His Asp Pro Glu Ala Ala Ile Asp Tyr Ala Asn Arg Leu Ala Pro Leu
      85              90              95

Ala Lys Arg Leu Asp Gln Asp Leu Lys Ile Val Met Arg Val Tyr Phe
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Glu Lys Pro Arg Thr Ile Val Gly Trp Lys Gly Leu Ile Asn Asp Pro
      115             120             125

His Leu Asn Glu Thr Tyr Asp Ile Pro Glu Gly Leu Arg Ile Ala Arg
      130             135             140

Lys Val Leu Ile Asp Val Val Asn Leu Asp Leu Pro Val Gly Cys Glu
      145             150             155             160

Phe Leu Glu Pro Asn Ser Pro Gln Tyr Tyr Ala Asp Thr Val Ala Trp
      165             170             175

Gly Ala Ile Gly Ala Arg Thr Thr Glu Ser Gln Val His Arg Gln Leu
      180             185             190

Ala Ser Gly Met Ser Met Pro Ile Gly Phe Lys Asn Gly Thr Asp Gly
      195             200             205

Asn Ile Gln Val Ala Val Asp Ala Val Gln Ala Ala Gln Asn Pro His
      210             215             220

Phe Phe Phe Gly Thr Ser Asp Asp Gly Ala Leu Ser Val Val Glu Thr
      225             230             235             240

Ala Gly Asn Ser Asn Ser His Ile Ile Leu Arg Gly Gly Thr Ser Gly
      245             250             255

Pro Asn His Asp Ala Ala Ser Val Glu Ala Val Val Glu Lys Leu Gly
      260             265             270

Glu Asn Ala Arg Leu Met Ile Asp Ala Ser His Ala Asn Ser Gly Lys
      275             280             285

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Asp His Ile Arg Gln Val Glu Val Val Arg Glu Ile Ala Glu Gln Ile
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 Ser Gly Gly Ser Glu Ala Val Ala Gly Ile Met Ile Glu Ser Phe Leu
 305 310 315 320
 Val Gly Gly Ala Gln Asn Leu Asp Pro Ala Lys Leu Arg Ile Asn Gly
 325 330 335
 Gly Glu Gly Leu Val Tyr Gly Gln Ser Val Thr Asp Lys Cys Ile Asp
 340 345 350
 Ile Asp Thr Thr Ile Asp Leu Leu Ala Glu Leu Ala Ala Val Arg
 355 360 365
 Glu Arg Arg Ala Ala Ala Lys
 370 375

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 <212> DNA
 <213> Corynebacterium glutamicum

<220>
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 <223> RXS02574

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 Leu Ala Arg Ala Gln
 1 5
 atc cct gaa cag caa cgc gac caa gtc gcg tcg ctg atg atg gtt gga 163
 Ile Pro Glu Gln Gln Arg Asp Gln Val Ala Ser Leu Met Met Val Gly
 10 15 20
 gtt gcg aat tat gat cag gca ttg gat gcg ctc aat cag ggg gtg ggt 211
 Val Ala Asn Tyr Asp Gln Ala Leu Asp Ala Leu Asn Gln Gly Val Gly
 25 30 35
 ggc atc ttt att ggt tcc tgg aca gat gaa aat ctg ctc acg gaa cct 259
 Gly Ile Phe Ile Gly Ser Trp Thr Asp Glu Asn Leu Leu Thr Glu Pro
 40 45 50
 ggc cgt aat att gag gcg ctc cgc gaa gcc gtc ggc agg gat ttc tcc 307
 Gly Arg Asn Ile Glu Ala Leu Arg Glu Ala Val Gly Arg Asp Phe Ser
 55 60 65
 gtc agc atc gac ttc gaa ggc ggc cgc gtc cag cgt gcc acc aat att 355
 Val Ser Ile Asp Phe Glu Gly Gly Arg Val Gln Arg Ala Thr Asn Ile
 70 75 80 85
 ctt ggt gat ttc ccc tca ccg cgc gtg atg gcg caa acc atg acg ccg 403
 Leu Gly Asp Phe Pro Ser Pro Arg Val Met Ala Gln Thr Met Thr Pro
 90 95 100
 gaa caa gta gaa gat ctc gca gaa atc cta ggc act ggt tta gct gca 451

Glu Gln Val Glu Asp Leu Ala Glu Ile Leu Gly Thr Gly Leu Ala Ala	
105 110 115	
cat ggt gtg aca gtt aac ttt gca cct gtt gta gat gta gat gct tgg	499
His Gly Val Thr Val Asn Phe Ala Pro Val Val Asp Val Asp Ala Trp	
120 125 130	
ggt ctc ccc gtc gtt ggc gat cgt tcc ttt tcc aac gac cca gcc gta	547
Gly Leu Pro Val Val Gly Asp Arg Ser Phe Ser Asn Asp Pro Ala Val	
135 140 145	
gca gct act tat gcc aca gct ttt gca aag ggc tta agc aaa gta gga	595
Ala Ala Thr Tyr Ala Thr Ala Phe Ala Lys Gly Leu Ser Lys Val Gly	
150 155 160 165	
att acc cca gta ttc aaa cat ttc cca ggt cac ggt cgt gca agt ggc	643
Ile Thr Pro Val Phe Lys His Phe Pro Gly His Gly Arg Ala Ser Gly	
170 175 180	
gat tcg cac acc caa gat gtg gtg acc ccc gca ctt gat gag ctt aaa	691
Asp Ser His Thr Gln Asp Val Val Thr Pro Ala Leu Asp Glu Leu Lys	
185 190 195	
act tac gac ctc atc cct tat ggt caa gca ctt tct gaa act gac gga	739
Thr Tyr Asp Leu Ile Pro Tyr Gly Gln Ala Leu Ser Glu Thr Asp Gly	
200 205 210	
gcc gtc atg gtg ggc cac atg att gtt cca ggt ctt ggc acc gac gga	787
Ala Val Met Val Gly His Met Ile Val Pro Gly Leu Gly Thr Asp Gly	
215 220 225	
ggt cca tcc tct atc gac ccc gcc acc tat caa ctg ctc cgc agt ggc	835
Val Pro Ser Ser Ile Asp Pro Ala Thr Tyr Gln Leu Leu Arg Ser Gly	
230 235 240 245	
gat tac cca ggt ggc gtg cct ttc gat ggc gtg atc tac acc gac gat	883
Asp Tyr Pro Gly Gly Val Pro Phe Asp Gly Val Ile Tyr Thr Asp Asp	
250 255 260	
ctc tct gga atg agt gcc att tcc gcc acc cat tca ccc gca gaa gca	931
Leu Ser Gly Met Ser Ala Ile Ser Ala Thr His Ser Pro Ala Glu Ala	
265 270 275	
gtg ctt gcc tcc ctc aaa gca ggc gca gac caa gca cta tgg atc gac	979
Val Leu Ala Ser Leu Lys Ala Gly Ala Asp Gln Ala Leu Trp Ile Asp	
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Tyr Gly Ser Leu Gly Ser Ala Ile Asp Arg Val Asp Ala Ala Val Ser	
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agc ggt gaa tac cct caa gaa caa atg ctg gca tct gcg tta aga gtc	1075
Ser Gly Glu Tyr Pro Gln Glu Gln Met Leu Ala Ser Ala Leu Arg Val	
310 315 320 325	
caa ttg ctc tac atc aca cgt ctc gaa caa aag tgaagttacc agtccgtaac	1128
Gln Leu Leu Tyr Ile Thr Arg Leu Glu Gln Lys	
330 335	
ccc	1131

<210> 490
 <211> 336
 <212> PRT
 <213> *Corynebacterium glutamicum*

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 35 40 45
 Leu Leu Thr Glu Pro Gly Arg Asn Ile Glu Ala Leu Arg Glu Ala Val
 50 55 60
 Gly Arg Asp Phe Ser Val Ser Ile Asp Phe Glu Gly Gly Arg Val Gln
 65 70 75 80
 Arg Ala Thr Asn Ile Leu Gly Asp Phe Pro Ser Pro Arg Val Met Ala
 85 90 95
 Gln Thr Met Thr Pro Glu Gln Val Glu Asp Leu Ala Glu Ile Leu Gly
 100 105 110
 Thr Gly Leu Ala Ala His Gly Val Thr Val Asn Phe Ala Pro Val Val
 115 120 125
 Asp Val Asp Ala Trp Gly Leu Pro Val Val Gly Asp Arg Ser Phe Ser
 130 135 140
 Asn Asp Pro Ala Val Ala Ala Thr Tyr Ala Thr Ala Phe Ala Lys Gly
 145 150 155 160
 Leu Ser Lys Val Gly Ile Thr Pro Val Phe Lys His Phe Pro Gly His
 165 170 175
 Gly Arg Ala Ser Gly Asp Ser His Thr Gln Asp Val Val Thr Pro Ala
 180 185 190
 Leu Asp Glu Leu Lys Thr Tyr Asp Leu Ile Pro Tyr Gly Gln Ala Leu
 195 200 205
 Ser Glu Thr Asp Gly Ala Val Met Val Gly His Met Ile Val Pro Gly
 210 215 220
 Leu Gly Thr Asp Gly Val Pro Ser Ser Ile Asp Pro Ala Thr Tyr Gln
 225 230 235 240
 Leu Leu Arg Ser Gly Asp Tyr Pro Gly Gly Val Pro Phe Asp Gly Val
 245 250 255
 Ile Tyr Thr Asp Asp Leu Ser Gly Met Ser Ala Ile Ser Ala Thr His
 260 265 270
 Ser Pro Ala Glu Ala Val Leu Ala Ser Leu Lys Ala Gly Ala Asp Gln
 275 280 285

Ala Leu Trp Ile Asp Tyr Gly Ser Leu Gly Ser Ala Ile Asp Arg Val
 290 295 300

Asp Ala Ala Val Ser Ser Gly Glu Tyr Pro Gln Glu Gln Met Leu Ala
 305 310 315 320

Ser Ala Leu Arg Val Gln Leu Leu Tyr Ile Thr Arg Leu Glu Gln Lys
 325 330 335

<210> 491

<211> 1038

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (1)..(1008)

<223> RXS03215

<400> 491

atc gat gtt gtc agc gtc gtg gtg gct aac ttc ctg cac cgc gaa atc 48
 Ile Asp Val Val Ser Val Val Val Ala Asn Phe Leu His Arg Glu Ile
 1 5 10 15

gtg gaa gca ctt ctg gca tcc ggc aag cat gtg ctg tgc gag aag cca 96
 Val Glu Ala Leu Leu Ala Ser Gly Lys His Val Leu Cys Glu Lys Pro
 20 25 30

ctg tca gac acc atc gaa gat gca gaa gcc atg att gag gca gcc ggc 144
 Leu Ser Asp Thr Ile Glu Asp Ala Glu Ala Met Ile Glu Ala Ala Gly
 35 40 45

cgt gca gca aca aat ggc acc atc gcc cgc atc gga ctg acc tac cgc 192
 Arg Ala Ala Thr Asn Gly Thr Ile Ala Arg Ile Gly Leu Thr Tyr Arg
 50 55 60

cgt tcc cca ggc gtg gca cac atc cgt gat ctc gtg cag tcc ggc gag 240
 Arg Ser Pro Gly Val Ala His Ile Arg Asp Leu Val Gln Ser Gly Glu
 65 70 75 80

ctt ggc aag gtt cta cac gtc acc ggc cac tac tgg acc gac tac gga 288
 Leu Gly Lys Val Leu His Val Thr Gly His Tyr Trp Thr Asp Tyr Gly
 85 90 95

tcc aat gca cag gca cca atc agc tgg cgt tac aag ggg cca aac ggc 336
 Ser Asn Ala Gln Ala Pro Ile Ser Trp Arg Tyr Lys Gly Pro Asn Gly
 100 105 110

tcc ggc gca ctg gca gat gtg gga agc cac ctc acc tac ctg gca gaa 384
 Ser Gly Ala Leu Ala Asp Val Gly Ser His Leu Thr Tyr Leu Ala Glu
 115 120 125

ttc gtt gca gga tct gac ttc gcc gcc gtc cgt ggt ggc cag ttg tcc 432
 Phe Val Ala Gly Ser Asp Phe Ala Ala Val Arg Gly Gly Gln Leu Ser
 130 135 140

acc gtg atc acc gag cgc ccc aag cca ctc ggc gcg att gtc ggc cac 480

Thr Val Ile Thr Glu Arg Pro Lys Pro Leu Gly Ala Ile Val Gly His	
145 150 155 160	
gaa ggc ggc gca gtt tcc gat gaa tac gaa gca gtg gaa aat gat gac	528
Glu Gly Gly Ala Val Ser Asp Glu Tyr Glu Ala Val Glu Asn Asp Asp	
165 170 175	
att gca tca ttc tcc gga tcc ttc atc ggt ggc gga acc gca acc ctc	576
Ile Ala Ser Phe Ser Gly Ser Phe Ile Gly Gly Gly Thr Ala Thr Leu	
180 185 190	
cag gtc agc cgc att tcc cag gga cac cca aac acc cta ggt ttt gaa	624
Gln Val Ser Arg Ile Ser Gln Gly His Pro Asn Thr Leu Gly Phe Glu	
195 200 205	
gtg ttc tgt gaa aag ggc tcc gtg ctc ttt gat ttc cgc aac tca ggc	672
Val Phe Cys Glu Lys Gly Ser Val Leu Phe Asp Phe Arg Asn Ser Gly	
210 215 220	
gaa ttc aaa atc ttc acc cca gca acc tcc ggt gac atc agc caa gaa	720
Glu Phe Lys Ile Phe Thr Pro Ala Thr Ser Gly Asp Ile Ser Gln Glu	
225 230 235 240	
gcc ggc tac cgc acc atc acc atc gga cca aag cac cca tac tgg cgc	768
Ala Gly Tyr Arg Thr Ile Thr Ile Gly Pro Lys His Pro Tyr Trp Arg	
245 250 255	
ggc ggc ctt gca atg gat gca cca ggc gtg gga att ggc caa aac gaa	816
Gly Gly Leu Ala Met Asp Ala Pro Gly Val Gly Ile Gly Gln Asn Glu	
260 265 270	
ggc ttc gtt ttc cag gcg cgc gca ttc ctc gaa gaa atc gca gga atc	864
Gly Phe Val Phe Gln Ala Arg Ala Phe Leu Glu Glu Ile Ala Gly Ile	
275 280 285	
tcc gaa gct gaa agc ctg cca cgc tgc gca act ttg gaa gaa ggg cta	912
Ser Glu Ala Glu Ser Leu Pro Arg Cys Ala Thr Leu Glu Glu Gly Leu	
290 295 300	
cac aat atg cag ctc att gat gct gta tca cag tca gct gca gca ggt	960
His Asn Met Gln Leu Ile Asp Ala Val Ser Gln Ser Ala Ala Ala Gly	
305 310 315 320	
ggc gaa acc gtt gcg gtc cca gcg gct gct ctg atc cct gca aac aac	1008
Gly Glu Thr Val Ala Val Pro Ala Ala Leu Ile Pro Ala Asn Asn	
325 330 335	
tagaaactat tcagaaagca tcaccatgaa	1038
<210> 492	
<211> 336	
<212> PRT	
<213> Corynebacterium glutamicum	
<400> 492	
Ile Asp Val Val Ser Val Val Val Ala Asn Phe Leu His Arg Glu Ile	
1 5 10 15	
Val Glu Ala Leu Leu Ala Ser Gly Lys His Val Leu Cys Glu Lys Pro	
20 25 30	

Leu Ser Asp Thr Ile Glu Asp Ala Glu Ala Met Ile Glu Ala Ala Gly
 35 40 45
 Arg Ala Ala Thr Asn Gly Thr Ile Ala Arg Ile Gly Leu Thr Tyr Arg
 50 55 60
 Arg Ser Pro Gly Val Ala His Ile Arg Asp Leu Val Gln Ser Gly Glu
 65 70 75 80
 Leu Gly Lys Val Leu His Val Thr Gly His Tyr Trp Thr Asp Tyr Gly
 85 90 95
 Ser Asn Ala Gln Ala Pro Ile Ser Trp Arg Tyr Lys Gly Pro Asn Gly
 100 105 110
 Ser Gly Ala Leu Ala Asp Val Gly Ser His Leu Thr Tyr Leu Ala Glu
 115 120 125
 Phe Val Ala Gly Ser Asp Phe Ala Ala Val Arg Gly Gly Gln Leu Ser
 130 135 140
 Thr Val Ile Thr Glu Arg Pro Lys Pro Leu Gly Ala Ile Val Gly His
 145 150 155 160
 Glu Gly Gly Ala Val Ser Asp Glu Tyr Glu Ala Val Glu Asn Asp Asp
 165 170 175
 Ile Ala Ser Phe Ser Gly Ser Phe Ile Gly Gly Gly Thr Ala Thr Leu
 180 185 190
 Gln Val Ser Arg Ile Ser Gln Gly His Pro Asn Thr Leu Gly Phe Glu
 195 200 205
 Val Phe Cys Glu Lys Gly Ser Val Leu Phe Asp Phe Arg Asn Ser Gly
 210 215 220
 Glu Phe Lys Ile Phe Thr Pro Ala Thr Ser Gly Asp Ile Ser Gln Glu
 225 230 235 240
 Ala Gly Tyr Arg Thr Ile Thr Ile Gly Pro Lys His Pro Tyr Trp Arg
 245 250 255
 Gly Gly Leu Ala Met Asp Ala Pro Gly Val Gly Ile Gly Gln Asn Glu
 260 265 270
 Gly Phe Val Phe Gln Ala Arg Ala Phe Leu Glu Glu Ile Ala Gly Ile
 275 280 285
 Ser Glu Ala Glu Ser Leu Pro Arg Cys Ala Thr Leu Glu Glu Gly Leu
 290 295 300
 His Asn Met Gln Leu Ile Asp Ala Val Ser Gln Ser Ala Ala Ala Gly
 305 310 315 320
 Gly Glu Thr Val Ala Val Pro Ala Ala Ala Leu Ile Pro Ala Asn Asn
 325 330 335

<210> 493
 <211> 1031
 <212> DNA
 <213> *Corynebacterium glutamicum*

<220>
 <221> CDS
 <222> (1)..(1008)
 <223> FRXA01915

<400> 493

atc gat gtt gtc agc gtc gtg gtg gct aac ttc ctg cac cgc gaa atc	48
Ile Asp Val Val Ser Val Val Val Ala Asn Phe Leu His Arg Glu Ile	
1 5 10 15	
gtg gaa gca ctt ctg gca tcc ggc aag cat gtg ctg tgc gag aag cca	96
Val Glu Ala Leu Leu Ala Ser Gly Lys His Val Leu Cys Glu Lys Pro	
20 25 30	
ctg tca gac acc atc gaa gat gca gaa gcc atg att gag gca gcc ggc	144
Leu Ser Asp Thr Ile Glu Asp Ala Glu Ala Met Ile Glu Ala Ala Gly	
35 40 45	
cgt gca gca aca aat ggc acc atc gcc cgc atc gga ctg acc tac cgc	192
Arg Ala Ala Thr Asn Gly Thr Ile Ala Arg Ile Gly Leu Thr Tyr Arg	
50 55 60	
cgt tcc cca ggc gtg gca cac atc cgt gat ctc gtg cag tcc ggc gag	240
Arg Ser Pro Gly Val Ala His Ile Arg Asp Leu Val Gln Ser Gly Glu	
65 70 75 80	
ctt ggc aag gtt cta cac gtc acc ggc cac tac tgg acc gac tac gga	288
Leu Gly Lys Val Leu His Val Thr Gly His Tyr Trp Thr Asp Tyr Gly	
85 90 95	
tcc aat gca cag gca cca atc agc tgg cgt tac aag ggg cca aac ggc	336
Ser Asn Ala Gln Ala Pro Ile Ser Trp Arg Tyr Lys Gly Pro Asn Gly	
100 105 110	
tcc ggc gca ctg gca gat gtg gga agc cac ctc acc tac ctg gca gaa	384
Ser Gly Ala Leu Ala Asp Val Gly Ser His Leu Thr Tyr Leu Ala Glu	
115 120 125	
ttc gtt gca gga tct gac ttc gcc gcc gtc cgt ggt ggc cag ttg tcc	432
Phe Val Ala Gly Ser Asp Phe Ala Ala Val Arg Gly Gly Gln Leu Ser	
130 135 140	
acc gtg atc acc gag cgc ccc aag cca ctc ggc gcg att gtc ggc cac	480
Thr Val Ile Thr Glu Arg Pro Lys Pro Leu Gly Ala Ile Val Gly His	
145 150 155 160	
gaa ggc ggc gca gtt tcc gat gaa tac gaa gca gtg gaa aat gat gac	528
Glu Gly Gly Ala Val Ser Asp Glu Tyr Glu Ala Val Glu Asn Asp Asp	
165 170 175	
att gca tca ttc tcc gga tcc ttc atc ggt ggc gga acc gca acc ctc	576
Ile Ala Ser Phe Ser Gly Ser Phe Ile Gly Gly Gly Thr Ala Thr Leu	
180 185 190	
cag gtc agc cgc att tcc cag gga cac cca aac acc cta ggt ttt gaa	624

Gln Val Ser Arg Ile Ser Gln Gly His Pro Asn Thr Leu Gly Phe Glu
 195 200 205
 gtg ttc tgt gaa aag ggc tcc gtg ctc ttt gat ttc cgc aac tca ggc 672
 Val Phe Cys Glu Lys Gly Ser Val Leu Phe Asp Phe Arg Asn Ser Gly
 210 215 220
 gaa ttc aaa atc ttc acc cca gca acc tcc ggt gac atc agc caa gaa 720
 Glu Phe Lys Ile Phe Thr Pro Ala Thr Ser Gly Asp Ile Ser Gln Glu
 225 230 235 240
 gcc ggc tac cgc acc atc acc atc gga cca aag cac cca tac tgg cgc 768
 Ala Gly Tyr Arg Thr Ile Thr Ile Gly Pro Lys His Pro Tyr Trp Arg
 245 250 255
 ggc ggc ctt gca atg gat gca cca ggc gtg gga att ggc caa aac gaa 816
 Gly Gly Leu Ala Met Asp Ala Pro Gly Val Gly Ile Gly Gln Asn Glu
 260 265 270
 ggc ttc gtt ttc cag gcg cgc gca ttc ctc gaa gaa atc gca gga atc 864
 Gly Phe Val Phe Gln Ala Arg Ala Phe Leu Glu Glu Ile Ala Gly Ile
 275 280 285
 tcc gaa gct gaa agc ctg cca cgc tgc gca act ttg gaa gaa ggg cta 912
 Ser Glu Ala Glu Ser Leu Pro Arg Cys Ala Thr Leu Glu Glu Gly Leu
 290 295 300
 cac aat atg cag ctc att gat gct gta tca cag tca gct gca gca ggt 960
 His Asn Met Gln Leu Ile Asp Ala Val Ser Gln Ser Ala Ala Ala Gly
 305 310 315 320
 ggc gaa acc gtt gcg gtc cca gcg gct gct ctg atc cct gca aac aac 1008
 Gly Glu Thr Val Ala Val Pro Ala Ala Leu Ile Pro Ala Asn Asn
 325 330 335
 tagaaactat tcagaaagca tca 1031

 <210> 494
 <211> 336
 <212> PRT
 <213> Corynebacterium glutamicum

 <400> 494
 Ile Asp Val Val Ser Val Val Val Ala Asn Phe Leu His Arg Glu Ile
 1 5 10 15
 Val Glu Ala Leu Leu Ala Ser Gly Lys His Val Leu Cys Glu Lys Pro
 20 25 30
 Leu Ser Asp Thr Ile Glu Asp Ala Glu Ala Met Ile Glu Ala Ala Gly
 35 40 45
 Arg Ala Ala Thr Asn Gly Thr Ile Ala Arg Ile Gly Leu Thr Tyr Arg
 50 55 60
 Arg Ser Pro Gly Val Ala His Ile Arg Asp Leu Val Gln Ser Gly Glu
 65 70 75 80
 Leu Gly Lys Val Leu His Val Thr Gly His Tyr Trp Thr Asp Tyr Gly
 85 90 95

Ser Asn Ala Gln Ala Pro Ile Ser Trp Arg Tyr Lys Gly Pro Asn Gly
 100 105 110
 Ser Gly Ala Leu Ala Asp Val Gly Ser His Leu Thr Tyr Leu Ala Glu
 115 120 125
 Phe Val Ala Gly Ser Asp Phe Ala Ala Val Arg Gly Gly Gln Leu Ser
 130 135 140
 Thr Val Ile Thr Glu Arg Pro Lys Pro Leu Gly Ala Ile Val Gly His
 145 150 155 160
 Glu Gly Gly Ala Val Ser Asp Glu Tyr Glu Ala Val Glu Asn Asp Asp
 165 170 175
 Ile Ala Ser Phe Ser Gly Ser Phe Ile Gly Gly Gly Thr Ala Thr Leu
 180 185 190
 Gln Val Ser Arg Ile Ser Gln Gly His Pro Asn Thr Leu Gly Phe Glu
 195 200 205
 Val Phe Cys Glu Lys Gly Ser Val Leu Phe Asp Phe Arg Asn Ser Gly
 210 215 220
 Glu Phe Lys Ile Phe Thr Pro Ala Thr Ser Gly Asp Ile Ser Gln Glu
 225 230 235 240
 Ala Gly Tyr Arg Thr Ile Thr Ile Gly Pro Lys His Pro Tyr Trp Arg
 245 250 255
 Gly Gly Leu Ala Met Asp Ala Pro Gly Val Gly Ile Gly Gln Asn Glu
 260 265 270
 Gly Phe Val Phe Gln Ala Arg Ala Phe Leu Glu Glu Ile Ala Gly Ile
 275 280 285
 Ser Glu Ala Glu Ser Leu Pro Arg Cys Ala Thr Leu Glu Glu Gly Leu
 290 295 300
 His Asn Met Gln Leu Ile Asp Ala Val Ser Gln Ser Ala Ala Ala Gly
 305 310 315 320
 Gly Glu Thr Val Ala Val Pro Ala Ala Ala Leu Ile Pro Ala Asn Asn
 325 330 335

<210> 495
 <211> 1288
 <212> DNA
 <213> *Corynebacterium glutamicum*

<220>
 <221> CDS
 <222> (101)..(1258)
 <223> RXS03224

<400> 495

acgattgtgc tgtcgtttgc gttggtgaat agttctggac cgggtatttt gcggcgcaca 60

tggaactcat tgaacgccgc gcccggttaa ggtgggaggc atg agt ttt gct gaa 115
Met Ser Phe Ala Glu
1 5

cat gcg atc atc tgg cac gtc tac ccc ctg ggc gct ttg ggt gct ccc 163
His Ala Ile Ile Trp His Val Tyr Pro Leu Gly Ala Leu Gly Ala Pro
10 15 20

atc cgg cct gaa gcc ccc gca cct gtc aca cat cgg ctc ccc aat cta 211
Ile Arg Pro Glu Ala Pro Ala Pro Val Thr His Arg Leu Pro Asn Leu
25 30 35

att ggg tgg ctg gat tat gtt gtc gaa cta ggc tgc aac gcc ctc atg 259
Ile Gly Trp Leu Asp Tyr Val Val Glu Leu Gly Cys Asn Ala Leu Met
40 45 50

ctg gga ccg gta ttc gag tcc gtc agc cac ggc tac gac acc ctc gat 307
Leu Gly Pro Val Phe Glu Ser Val Ser His Gly Tyr Asp Thr Leu Asp
55 60 65

ttc tac cgc atc gac ccg cgc ctc ggc acc gag gaa gac atg gac gcg 355
Phe Tyr Arg Ile Asp Pro Arg Leu Gly Thr Glu Glu Asp Met Asp Ala
70 75 80 85

ctg ctg gag gct gcg aat cag cgg ggc att gga gtg ctt ttc gac ggc 403
Leu Leu Glu Ala Ala Asn Gln Arg Gly Ile Gly Val Leu Phe Asp Gly
90 95 100

gtc ttc aat cat gtt tcc agt tcc tct aaa tat ctc gac ctg acc acc 451
Val Phe Asn His Val Ser Ser Ser Ser Lys Tyr Leu Asp Leu Thr Thr
105 110 115

ggg gcg tca ttt gaa ggc cac gac atc ctg gcg gaa ctc gac cac acg 499
Gly Ala Ser Phe Glu Gly His Asp Ile Leu Ala Glu Leu Asp His Thr
120 125 130

aat ccc gcc gta gtg gat ctg gtt gtc gat gtc atg aac cac tgg ctc 547
Asn Pro Ala Val Val Asp Leu Val Val Asp Val Met Asn His Trp Leu
135 140 145

gac cgc gga atc gca ggc tgg cga ctc gac gct gtc tac gcc atc gcc 595
Asp Arg Gly Ile Ala Gly Trp Arg Leu Asp Ala Val Tyr Ala Ile Ala
150 155 160 165

cct gaa ttt tgg gaa aaa gtc ctg cca gaa gtg cga cga aaa cac cca 643
Pro Glu Phe Trp Glu Lys Val Leu Pro Glu Val Arg Arg Lys His Pro
170 175 180

cac gca tgg atc gtg ggg gag atg atc cat gga gat tac tcc gac tac 691
His Ala Trp Ile Val Gly Glu Met Ile His Gly Asp Tyr Ser Asp Tyr
185 190 195

gtg aaa agc tcc ggc att gat tcc gtt acc gaa tac gaa ctg tgg aaa 739
Val Lys Ser Ser Gly Ile Asp Ser Val Thr Glu Tyr Glu Leu Trp Lys
200 205 210

gcc att tgg agc agc atc aaa gag cgc aat ttc ttt gaa ctc gaa tgg 787
Ala Ile Trp Ser Ser Ile Lys Glu Arg Asn Phe Phe Glu Leu Glu Trp
215 220 225

act ttg agt cgc cac aat gaa ttc ctc gat act ttc gta ccg cag aca 835
 Thr Leu Ser Arg His Asn Glu Phe Leu Asp Thr Phe Val Pro Gln Thr
 230 235 240 245

ttc att ggt aac cat gac gtc acc cgc att gcc acc cga atc ggt caa 883
 Phe Ile Gly Asn His Asp Val Thr Arg Ile Ala Thr Arg Ile Gly Gln
 250 255 260

tca aat gcg atc ctg gcc gca gcg atc ctc ttc acg gtc gga gga acc 931
 Ser Asn Ala Ile Leu Ala Ala Ala Ile Leu Phe Thr Val Gly Gly Thr
 265 270 275

cca agc att tac tac ggc gat gag cag ggc ttt acg gga ttg aaa gag 979
 Pro Ser Ile Tyr Tyr Gly Asp Glu Gln Gly Phe Thr Gly Leu Lys Glu
 280 285 290

gat aac gtt ttc ggt gac gat gcc att agg cca cct ctt cct gcc gag 1027
 Asp Asn Val Phe Gly Asp Asp Ala Ile Arg Pro Pro Leu Pro Ala Glu
 295 300 305

ttt tct cca ctg ggc acc tgg att gaa aac att tat aag gct ctg atc 1075
 Phe Ser Pro Leu Gly Thr Trp Ile Glu Asn Ile Tyr Lys Ala Leu Ile
 310 315 320 325

gcg ctg cgc agg caa cac ccg tgg ttg tat cag gcg cac acc gaa gtc 1123
 Ala Leu Arg Arg Gln His Pro Trp Leu Tyr Gln Ala His Thr Glu Val
 330 335 340

ctt gag att gct aat gaa gcg atg acc tat aag tcc gtc ggt ctt gga 1171
 Leu Glu Ile Ala Asn Glu Ala Met Thr Tyr Lys Ser Val Gly Leu Gly
 345 350 355

ggt gaa gag ctg aca gtg cat ctt gat ttg gaa gag gtg tct gtt cgg 1219
 Gly Glu Glu Leu Thr Val His Leu Asp Leu Glu Glu Val Ser Val Arg
 360 365 370

atc ctt gat ggc gag aag gtg ctg ttt cag tac agc gct tagttgtcgg 1268
 Ile Leu Asp Gly Glu Lys Val Leu Phe Gln Tyr Ser Ala
 375 380 385

ttcaagggtg ggggaacaaa 1288

<210> 496

<211> 386

<212> PRT

<213> Corynebacterium glutamicum

<400> 496

Met Ser Phe Ala Glu His Ala Ile Ile Trp His Val Tyr Pro Leu Gly
 1 5 10 15

Ala Leu Gly Ala Pro Ile Arg Pro Glu Ala Pro Ala Pro Val Thr His
 20 25 30

Arg Leu Pro Asn Leu Ile Gly Trp Leu Asp Tyr Val Val Glu Leu Gly
 35 40 45

Cys Asn Ala Leu Met Leu Gly Pro Val Phe Glu Ser Val Ser His Gly
 50 55 60

Tyr Asp Thr Leu Asp Phe Tyr Arg Ile Asp Pro Arg Leu Gly Thr Glu
 65 70 75 80
 Glu Asp Met Asp Ala Leu Leu Glu Ala Ala Asn Gln Arg Gly Ile Gly
 85 90 95
 Val Leu Phe Asp Gly Val Phe Asn His Val Ser Ser Ser Ser Lys Tyr
 100 105 110
 Leu Asp Leu Thr Thr Gly Ala Ser Phe Glu Gly His Asp Ile Leu Ala
 115 120 125
 Glu Leu Asp His Thr Asn Pro Ala Val Val Asp Leu Val Val Asp Val
 130 135 140
 Met Asn His Trp Leu Asp Arg Gly Ile Ala Gly Trp Arg Leu Asp Ala
 145 150 155 160
 Val Tyr Ala Ile Ala Pro Glu Phe Trp Glu Lys Val Leu Pro Glu Val
 165 170 175
 Arg Arg Lys His Pro His Ala Trp Ile Val Gly Glu Met Ile His Gly
 180 185 190
 Asp Tyr Ser Asp Tyr Val Lys Ser Ser Gly Ile Asp Ser Val Thr Glu
 195 200 205
 Tyr Glu Leu Trp Lys Ala Ile Trp Ser Ser Ile Lys Glu Arg Asn Phe
 210 215 220
 Phe Glu Leu Glu Trp Thr Leu Ser Arg His Asn Glu Phe Leu Asp Thr
 225 230 235 240
 Phe Val Pro Gln Thr Phe Ile Gly Asn His Asp Val Thr Arg Ile Ala
 245 250 255
 Thr Arg Ile Gly Gln Ser Asn Ala Ile Leu Ala Ala Ala Ile Leu Phe
 260 265 270
 Thr Val Gly Gly Thr Pro Ser Ile Tyr Tyr Gly Asp Glu Gln Gly Phe
 275 280 285
 Thr Gly Leu Lys Glu Asp Asn Val Phe Gly Asp Asp Ala Ile Arg Pro
 290 295 300
 Pro Leu Pro Ala Glu Phe Ser Pro Leu Gly Thr Trp Ile Glu Asn Ile
 305 310 315 320
 Tyr Lys Ala Leu Ile Ala Leu Arg Arg Gln His Pro Trp Leu Tyr Gln
 325 330 335
 Ala His Thr Glu Val Leu Glu Ile Ala Asn Glu Ala Met Thr Tyr Lys
 340 345 350
 Ser Val Gly Leu Gly Gly Glu Glu Leu Thr Val His Leu Asp Leu Glu
 355 360 365
 Glu Val Ser Val Arg Ile Leu Asp Gly Glu Lys Val Leu Phe Gln Tyr
 370 375 380

Ser Ala
385

<210> 497
<211> 1281
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1258)
<223> FRXA00038

<400> 497
acgattgtgc tgctgtttgc gttggtgaat agttctggac cgggtatttt gcggcgcaca 60
tggaactcat tgaacgccgc gcccggttaa ggtgggaggc atg agt ttt gct gaa 115
Met Ser Phe Ala Glu
1 5
cat gcg atc atc tgg cac gtc tac ccc ctg ggc gct ttg ggt gct ccc 163
His Ala Ile Ile Trp His Val Tyr Pro Leu Gly Ala Leu Gly Ala Pro
10 15 20
atc cgg cct gaa gcc ccc gca cct gtc aca cat cgg ctc ccc aat cta 211
Ile Arg Pro Glu Ala Pro Ala Pro Val Thr His Arg Leu Pro Asn Leu
25 30 35
att ggg tgg ctg gat tat gtt gtc gaa cta ggc tgc aac gcc ctc atg 259
Ile Gly Trp Leu Asp Tyr Val Val Glu Leu Gly Cys Asn Ala Leu Met
40 45 50
ctg gga cgg gta ttc gag tcc gtc agc cac ggc tac gac acc ctc gat 307
Leu Gly Pro Val Phe Glu Ser Val Ser His Gly Tyr Asp Thr Leu Asp
55 60 65
ttc tac cgc atc gac ccg cgc ctc ggc acc gag gaa gac atg gac gcg 355
Phe Tyr Arg Ile Asp Pro Arg Leu Gly Thr Glu Glu Asp Met Asp Ala
70 75 80 85
ctg ctg gag gct gcg aat cag cgg ggc att gga gtg ctt ttc gac ggc 403
Leu Leu Glu Ala Ala Asn Gln Arg Gly Ile Gly Val Leu Phe Asp Gly
90 95 100
gtc ttc aat cat gtt tcc agt tcc tct aaa tat ctc gac ctg acc acc 451
Val Phe Asn His Val Ser Ser Ser Ser Lys Tyr Leu Asp Leu Thr Thr
105 110 115
ggg gcg tca ttt gaa ggc cac gac atc ctg gcg gaa ctc gac cac acg 499
Gly Ala Ser Phe Glu Gly His Asp Ile Leu Ala Glu Leu Asp His Thr
120 125 130
aat ccc gcc gta gtg gat ctg gtt gtc gat gtc atg aac cac tgg ctc 547
Asn Pro Ala Val Val Asp Leu Val Val Asp Val Met Asn His Trp Leu
135 140 145
gac cgc gga atc gca ggc tgg cga ctc gac gct gtc tac gcc atc gcc 595
Asp Arg Gly Ile Ala Gly Trp Arg Leu Asp Ala Val Tyr Ala Ile Ala
150 155 160 165

cct gaa ttt tgg gaa aaa gtc ctg cca gaa gtg cga cga aaa cac cca 643
 Pro Glu Phe Trp Glu Lys Val Leu Pro Glu Val Arg Arg Lys His Pro
 170 175 180

cac gca tgg atc gtg ggg gag atg atc cat gga gat tac tcc gac tac 691
 His Ala Trp Ile Val Gly Glu Met Ile His Gly Asp Tyr Ser Asp Tyr
 185 190 195

gtg aaa agc tcc ggc att gat tcc gtt acc gaa tac gaa ctg tgg aaa 739
 Val Lys Ser Ser Gly Ile Asp Ser Val Thr Glu Tyr Glu Leu Trp Lys
 200 205 210

gcc att tgg agc agc atc aaa gag cgc aat ttc ttt gaa ctc gaa tgg 787
 Ala Ile Trp Ser Ser Ile Lys Glu Arg Asn Phe Phe Glu Leu Glu Trp
 215 220 225

act ttg agt cgc cac aat gaa ttc ctc gat act ttc gta ccg cag aca 835
 Thr Leu Ser Arg His Asn Glu Phe Leu Asp Thr Phe Val Pro Gln Thr
 230 235 240 245

ttc att ggt aac cat gac gtc acc cgc att gcc acc cga atc ggt caa 883
 Phe Ile Gly Asn His Asp Val Thr Arg Ile Ala Thr Arg Ile Gly Gln
 250 255 260

tca aat gcg atc ctg gcc gca gcg atc ctc ttc acg gtc gga gga acc 931
 Ser Asn Ala Ile Leu Ala Ala Ala Ile Leu Phe Thr Val Gly Gly Thr
 265 270 275

cca agc att tac tac ggc gat gag cag ggc ttt acg gga ttg aaa gag 979
 Pro Ser Ile Tyr Tyr Gly Asp Glu Gln Gly Phe Thr Gly Leu Lys Glu
 280 285 290

gat aac gtt ttc ggt gac gat gcc att agg cca cct ctt cct gcc gag 1027
 Asp Asn Val Phe Gly Asp Asp Ala Ile Arg Pro Pro Leu Pro Ala Glu
 295 300 305

ttt tct cca ctg ggc acc tgg att gaa aac att tat aag gct ctg atc 1075
 Phe Ser Pro Leu Gly Thr Trp Ile Glu Asn Ile Tyr Lys Ala Leu Ile
 310 315 320 325

gcg ctg cgc agg caa cac ccg tgg ttg tat cag gcg cac acc gaa gtc 1123
 Ala Leu Arg Arg Gln His Pro Trp Leu Tyr Gln Ala His Thr Glu Val
 330 335 340

ctt gag att gct aat gaa gcg atg acc tat aag tcc gtc ggt ctt gga 1171
 Leu Glu Ile Ala Asn Glu Ala Met Thr Tyr Lys Ser Val Gly Leu Gly
 345 350 355

ggt gaa gag ctg aca gtg cat ctt gat ttg gaa gag gtg tct gtt cgg 1219
 Gly Glu Glu Leu Thr Val His Leu Asp Leu Glu Glu Val Ser Val Arg
 360 365 370

atc ctt gat ggc gag aag gtg ctg ttt cag tac agc gct tagttgtcgg 1268
 Ile Leu Asp Gly Glu Lys Val Leu Phe Gln Tyr Ser Ala
 375 380 385

ttcaagggtgta ggg 1281

<210> 498

<211> 386

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 498

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 1           5           10           15

Ala Leu Gly Ala Pro Ile Arg Pro Glu Ala Pro Ala Pro Val Thr His
      20           25           30

Arg Leu Pro Asn Leu Ile Gly Trp Leu Asp Tyr Val Val Glu Leu Gly
      35           40           45

Cys Asn Ala Leu Met Leu Gly Pro Val Phe Glu Ser Val Ser His Gly
      50           55           60

Tyr Asp Thr Leu Asp Phe Tyr Arg Ile Asp Pro Arg Leu Gly Thr Glu
      65           70           75           80

Glu Asp Met Asp Ala Leu Leu Glu Ala Ala Asn Gln Arg Gly Ile Gly
      85           90           95

Val Leu Phe Asp Gly Val Phe Asn His Val Ser Ser Ser Ser Lys Tyr
      100          105          110

Leu Asp Leu Thr Thr Gly Ala Ser Phe Glu Gly His Asp Ile Leu Ala
      115          120          125

Glu Leu Asp His Thr Asn Pro Ala Val Val Asp Leu Val Val Asp Val
      130          135          140

Met Asn His Trp Leu Asp Arg Gly Ile Ala Gly Trp Arg Leu Asp Ala
      145          150          155          160

Val Tyr Ala Ile Ala Pro Glu Phe Trp Glu Lys Val Leu Pro Glu Val
      165          170          175

Arg Arg Lys His Pro His Ala Trp Ile Val Gly Glu Met Ile His Gly
      180          185          190

Asp Tyr Ser Asp Tyr Val Lys Ser Ser Gly Ile Asp Ser Val Thr Glu
      195          200          205

Tyr Glu Leu Trp Lys Ala Ile Trp Ser Ser Ile Lys Glu Arg Asn Phe
      210          215          220

Phe Glu Leu Glu Trp Thr Leu Ser Arg His Asn Glu Phe Leu Asp Thr
      225          230          235          240

Phe Val Pro Gln Thr Phe Ile Gly Asn His Asp Val Thr Arg Ile Ala
      245          250          255

Thr Arg Ile Gly Gln Ser Asn Ala Ile Leu Ala Ala Ala Ile Leu Phe
      260          265          270

Thr Val Gly Gly Thr Pro Ser Ile Tyr Tyr Gly Asp Glu Gln Gly Phe
      275          280          285

Thr Gly Leu Lys Glu Asp Asn Val Phe Gly Asp Asp Ala Ile Arg Pro
      290          295          300

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Pro Leu Pro Ala Glu Phe Ser Pro Leu Gly Thr Trp Ile Glu Asn Ile
305 310 315 320

Tyr Lys Ala Leu Ile Ala Leu Arg Arg Gln His Pro Trp Leu Tyr Gln
325 330 335

Ala His Thr Glu Val Leu Glu Ile Ala Asn Glu Ala Met Thr Tyr Lys
340 345 350

Ser Val Gly Leu Gly Gly Glu Glu Leu Thr Val His Leu Asp Leu Glu
355 360 365

Glu Val Ser Val Arg Ile Leu Asp Gly Glu Lys Val Leu Phe Gln Tyr
370 375 380

Ser Ala
385

<210> 499

<211> 517

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(517)

<223> RXC00233

<400> 499

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aatagcgctt tagacacaga ctcatgacag aatagaagac atg agt gtg aat gaa 115
Met Ser Val Asn Glu
1 5

gca gat ctg aac gct gtc gaa gag caa ttg gga agg gcc cca cga ggt 163
Ala Asp Leu Asn Ala Val Glu Glu Gln Leu Gly Arg Ala Pro Arg Gly
10 15 20

gtc ctc gat att tct tac cgc agc cct gat gga gta ccc ggt gtg gtg 211
Val Leu Asp Ile Ser Tyr Arg Ser Pro Asp Gly Val Pro Gly Val Val
25 30 35

atg acc gca cca aaa ctg gat gac gga acc cca ttc cca acc ctg tac 259
Met Thr Ala Pro Lys Leu Asp Asp Gly Thr Pro Phe Pro Thr Leu Tyr
40 45 50

tac ttg aca gat cca cgc ctg acc acc gag gca tcc cgc ctc gag gtc 307
Tyr Leu Thr Asp Pro Arg Leu Thr Thr Glu Ala Ser Arg Leu Glu Val
55 60 65

gca ttg gta atg aag tgg atg act gat cgc ctt tcc acc gac gaa gag 355
Ala Leu Val Met Lys Trp Met Thr Asp Arg Leu Ser Thr Asp Glu Glu
70 75 80 85

ctt cgt gcc gac tac cag cgc gcc cac gag cac ttc ctg gca aag cgc 403
Leu Arg Ala Asp Tyr Gln Arg Ala His Glu His Phe Leu Ala Lys Arg
90 95 100

aac gca att gaa gat ctc ggc acg gat ttt tcc ggc ggt ggc atg cct 451

Asn Ala Ile Glu Asp Leu Gly Thr Asp Phe Ser Gly Gly Gly Met Pro
 105 110 115
 gac cga gtg aag tgc ctt cac gtc ctc att gac tat gca ctg gca gaa 499
 Asp Arg Val Lys Cys Leu His Val Leu Ile Asp Tyr Ala Leu Ala Glu
 120 125 130
 ggc cca cac cat ttc ctt 517
 Gly Pro His His Phe Leu
 135

<210> 500
 <211> 139
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 500
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 20 25 30
 Val Pro Gly Val Val Met Thr Ala Pro Lys Leu Asp Asp Gly Thr Pro
 35 40 45
 Phe Pro Thr Leu Tyr Tyr Leu Thr Asp Pro Arg Leu Thr Thr Glu Ala
 50 55 60
 Ser Arg Leu Glu Val Ala Leu Val Met Lys Trp Met Thr Asp Arg Leu
 65 70 75 80
 Ser Thr Asp Glu Glu Leu Arg Ala Asp Tyr Gln Arg Ala His Glu His
 85 90 95
 Phe Leu Ala Lys Arg Asn Ala Ile Glu Asp Leu Gly Thr Asp Phe Ser
 100 105 110
 Gly Gly Gly Met Pro Asp Arg Val Lys Cys Leu His Val Leu Ile Asp
 115 120 125
 Tyr Ala Leu Ala Glu Gly Pro His His Phe Leu
 130 135

<210> 501
 <211> 849
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
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 <222> (101)..(826)
 <223> RXC00236

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 agcaatggga tttggatgcg gttcggtttt ggccgtcatc atg gtg atc tca ttt 115
 Met Val Ile Ser Phe

	1	5	
gtt gga tgg gcg ctc agc ttc atg gat gga acg gca cct att cgc caa			163
Val Gly Trp Ala Leu Ser Phe Met Asp Gly Thr Ala Pro Ile Arg Gln			
	10	20	
ctc cag caa atc cct gaa gat gtt ccg ccg gcg cgt ggt gta gaa gtt			211
Leu Gln Gln Ile Pro Glu Asp Val Pro Pro Ala Arg Gly Val Glu Val			
	25	35	
ccg caa att gat aca gag gca gat gga cgc aca tcc aac cat ttg cgt			259
Pro Gln Ile Asp Thr Glu Ala Asp Gly Arg Thr Ser Asn His Leu Arg			
	40	50	
ttt tgg gcg gaa cca att gct caa gat act ggt gtg tcc gct caa gcg			307
Phe Trp Ala Glu Pro Ile Ala Gln Asp Thr Gly Val Ser Ala Gln Ala			
	55	65	
att gcg gct tat gga aac gca gag ctc atc gcg agt act gcg tgg cct			355
Ile Ala Ala Tyr Gly Asn Ala Glu Leu Ile Ala Ser Thr Ala Trp Pro			
	70	80	85
ggc tgc aat ctg ggg tgg aat acc ttg gca ggt atc ggc cag gtg gaa			403
Gly Cys Asn Leu Gly Trp Asn Thr Leu Ala Gly Ile Gly Gln Val Glu			
	90	95	100
acc cgt cac ggt acc tac aac ggc aaa atg ttc ggg ggc agt tcc ctg			451
Thr Arg His Gly Thr Tyr Asn Gly Lys Met Phe Gly Gly Ser Ser Leu			
	105	110	115
gat gaa aat gga gtt gca acc cct cca atc atc ggc gtt cca ctt gat			499
Asp Glu Asn Gly Val Ala Thr Pro Pro Ile Ile Gly Val Pro Leu Asp			
	120	125	130
ggt tca ccg ggg ttt gcg gaa att ccc gac act gat ggt ggg gaa tta			547
Gly Ser Pro Gly Phe Ala Glu Ile Pro Asp Thr Asp Gly Gly Glu Leu			
	135	140	145
gat ggc gat act gaa tat gat cgc gcg gta ggt ccc atg cag ttc att			595
Asp Gly Asp Thr Glu Tyr Asp Arg Ala Val Gly Pro Met Gln Phe Ile			
	150	155	160
ccg gaa acg tgg cga ctt atg gga ttg gat gca aac ggt gat ggg gta			643
Pro Glu Thr Trp Arg Leu Met Gly Leu Asp Ala Asn Gly Asp Gly Val			
	170	175	180
gcg gac ccc aac caa att gat gac gca gca ttg agt gcc gca aac ctg			691
Ala Asp Pro Asn Gln Ile Asp Asp Ala Ala Leu Ser Ala Ala Asn Leu			
	185	190	195
ttg tgt tcc aac gat cgt gac ttg tcc act cct gaa gga tgg acc gca			739
Leu Cys Ser Asn Asp Arg Asp Leu Ser Thr Pro Glu Gly Trp Thr Ala			
	200	205	210
gct gtt cat tct tac aac atg tct aat cag tat ttg atg gac gtt cga			787
Ala Val His Ser Tyr Asn Met Ser Asn Gln Tyr Leu Met Asp Val Arg			
	215	220	225
gat gct gcc gcg tcc tac gct tta cga cag ccg gcg atc taaaacttaa			836
Asp Ala Ala Ala Ser Tyr Ala Leu Arg Gln Pro Ala Ile			
	230	235	240

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849

<210> 502

<211> 242

<212> PRT

<213> Corynebacterium glutamicum

<400> 502

Met Val Ile Ser Phe Val Gly Trp Ala Leu Ser Phe Met Asp Gly Thr
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 20 25 30

Arg Gly Val Glu Val Pro Gln Ile Asp Thr Glu Ala Asp Gly Arg Thr
 35 40 45

Ser Asn His Leu Arg Phe Trp Ala Glu Pro Ile Ala Gln Asp Thr Gly
 50 55 60

Val Ser Ala Gln Ala Ile Ala Ala Tyr Gly Asn Ala Glu Leu Ile Ala
 65 70 75 80

Ser Thr Ala Trp Pro Gly Cys Asn Leu Gly Trp Asn Thr Leu Ala Gly
 85 90 95

Ile Gly Gln Val Glu Thr Arg His Gly Thr Tyr Asn Gly Lys Met Phe
 100 105 110

Gly Gly Ser Ser Leu Asp Glu Asn Gly Val Ala Thr Pro Pro Ile Ile
 115 120 125

Gly Val Pro Leu Asp Gly Ser Pro Gly Phe Ala Glu Ile Pro Asp Thr
 130 135 140

Asp Gly Gly Glu Leu Asp Gly Asp Thr Glu Tyr Asp Arg Ala Val Gly
 145 150 155 160

Pro Met Gln Phe Ile Pro Glu Thr Trp Arg Leu Met Gly Leu Asp Ala
 165 170 175

Asn Gly Asp Gly Val Ala Asp Pro Asn Gln Ile Asp Asp Ala Ala Leu
 180 185 190

Ser Ala Ala Asn Leu Leu Cys Ser Asn Asp Arg Asp Leu Ser Thr Pro
 195 200 205

Glu Gly Trp Thr Ala Ala Val His Ser Tyr Asn Met Ser Asn Gln Tyr
 210 215 220

Leu Met Asp Val Arg Asp Ala Ala Ala Ser Tyr Ala Leu Arg Gln Pro
 225 230 235 240

Ala Ile

<210> 503

<211> 1113

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(1090)

<223> RXC00271

<400> 503

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tctgccccctt tttgaaaata acactttaag gagatgtgcc atg ttt tct tcc cgt 115
                               Met Phe Ser Ser Arg
                               1           5

tcg aag gta ctc gca agc atc ttt act gtt ggc gcc ttg gcg ttg gct 163
Ser Lys Val Leu Ala Ser Ile Phe Thr Val Gly Ala Leu Ala Leu Ala
          10          15          20

tcg tgc tca agc gat tcc agt gac agc tcc acc tcc act gat gct gca 211
Ser Cys Ser Ser Asp Ser Ser Asp Ser Ser Thr Ser Thr Asp Ala Ala
          25          30          35

ggt ggc gac tct tac cga gtt ggc atc aac cag ctt gtt cag cac cct 259
Gly Gly Asp Ser Tyr Arg Val Gly Ile Asn Gln Leu Val Gln His Pro
          40          45          50

gca ctt gat gca gcg acc act ggt ttc aag gaa gct ttt gaa gag gca 307
Ala Leu Asp Ala Ala Thr Thr Gly Phe Lys Glu Ala Phe Glu Glu Ala
          55          60          65

ggc gtt gac gtc acc ttt gat gag caa aac gct aac ggc gag cag ggc 355
Gly Val Asp Val Thr Phe Asp Glu Gln Asn Ala Asn Gly Glu Gln Gly
          70          75          80          85

act gca ctg act att tct cag cag ttc gct tct gac aat ttg gat ctc 403
Thr Ala Leu Thr Ile Ser Gln Gln Phe Ala Ser Asp Asn Leu Asp Leu
          90          95          100

gtg ttg gct gtt gca act cca gca gca cag gca act gcg cag aat atc 451
Val Leu Ala Val Ala Thr Pro Ala Ala Gln Ala Thr Ala Gln Asn Ile
          105          110          115

act gat atc cca gtc ctg ttc acc gca gtt acc gat gca gtg tcg gca 499
Thr Asp Ile Pro Val Leu Phe Thr Ala Val Thr Asp Ala Val Ser Ala
          120          125          130

gag ctg gtg gat tct aat gaa gca cct ggc gga aac gtc acc ggt act 547
Glu Leu Val Asp Ser Asn Glu Ala Pro Gly Gly Asn Val Thr Gly Thr
          135          140          145

tct gat atc gca ccg att gag cag cag ttg gag ctt ttg cag cag ctg 595
Ser Asp Ile Ala Pro Ile Glu Gln Gln Leu Glu Leu Leu Gln Gln Leu
          150          155          160          165

gtt cct gac gca aag tcc atc ggc atc gtc tac gcg tct ggt gag gtc 643
Val Pro Asp Ala Lys Ser Ile Gly Ile Val Tyr Ala Ser Gly Glu Val
          170          175          180

aac tct cag gtg cag gtc gat gag gtc acc aag gct gct gag cca ctg 691
Asn Ser Gln Val Gln Val Asp Glu Val Thr Lys Ala Ala Glu Pro Leu

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185	190	195	
ggg ctg tcc gtt aat act cag act gtc act acc gtg aac gag att cag			739
Gly Leu Ser Val Asn Thr Gln Thr Val Thr Thr Val Asn Glu Ile Gln			
200	205	210	
cag gct gtt gaa gct ctc ggc gat gtt gat gtc atc tac gtt cca act			787
Gln Ala Val Glu Ala Leu Ser Gly Asp Val Asp Val Ile Tyr Val Pro Thr			
215	220	225	
gac aac atg gtt gtt tcc ggt att tct tct ctg gtt cag gtt gct gag			835
Asp Asn Met Val Val Ser Gly Ile Ser Ser Leu Val Gln Val Ala Glu			
230	235	240	245
cag aag cag atc cct gtg atc ggc gct gag tcc ggc act gtt gag ggt			883
Gln Lys Gln Ile Pro Val Ile Gly Ala Glu Ser Gly Thr Val Glu Gly			
250	255	260	
ggc gca ctg gca acc ctg ggt atc gat tac acc gag ctt ggc cgc cag			931
Gly Ala Leu Ala Thr Leu Gly Ile Asp Tyr Thr Glu Leu Gly Arg Gln			
265	270	275	
act ggt gag atg gct ctg cgt att ctg cag gac ggc gaa gac cca gca			979
Thr Gly Glu Met Ala Leu Arg Ile Leu Gln Asp Gly Glu Asp Pro Ala			
280	285	290	
acc atg cct gtg gag act gca act gag ttc acc tac gtg atc aac gaa			1027
Thr Met Pro Val Glu Thr Ala Thr Glu Phe Thr Tyr Val Ile Asn Glu			
295	300	305	
gat gca gca gag cgc cag ggc gtg gag atc cct caa gag att ttg gat			1075
Asp Ala Ala Glu Arg Gln Gly Val Glu Ile Pro Gln Glu Ile Leu Asp			
310	315	320	325
aag gcc gaa cgc gta tgcacggcgc ttttgagttc gga			1113
Lys Ala Glu Arg Val			
330			

<210> 504

<211> 330

<212> PRT

<213> Corynebacterium glutamicum

<400> 504

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20 25 30	
Ser Thr Asp Ala Ala Gly Gly Asp Ser Tyr Arg Val Gly Ile Asn Gln	
35 40 45	
Leu Val Gln His Pro Ala Leu Asp Ala Ala Thr Thr Gly Phe Lys Glu	
50 55 60	
Ala Phe Glu Glu Ala Gly Val Asp Val Thr Phe Asp Glu Gln Asn Ala	
65 70 75 80	
Asn Gly Glu Gln Gly Thr Ala Leu Thr Ile Ser Gln Gln Phe Ala Ser	

85										90					95				
Asp	Asn	Leu	Asp	Leu	Val	Leu	Ala	Val	Ala	Thr	Pro	Ala	Ala	Gln	Ala				
			100						105					110					
Thr	Ala	Gln	Asn	Ile	Thr	Asp	Ile	Pro	Val	Leu	Phe	Thr	Ala	Val	Thr				
		115					120					125							
Asp	Ala	Val	Ser	Ala	Glu	Leu	Val	Asp	Ser	Asn	Glu	Ala	Pro	Gly	Gly				
		130				135					140								
Asn	Val	Thr	Gly	Thr	Ser	Asp	Ile	Ala	Pro	Ile	Glu	Gln	Gln	Leu	Glu				
145					150					155					160				
Leu	Leu	Gln	Gln	Leu	Val	Pro	Asp	Ala	Lys	Ser	Ile	Gly	Ile	Val	Tyr				
				165					170					175					
Ala	Ser	Gly	Glu	Val	Asn	Ser	Gln	Val	Gln	Val	Asp	Glu	Val	Thr	Lys				
		180						185					190						
Ala	Ala	Glu	Pro	Leu	Gly	Leu	Ser	Val	Asn	Thr	Gln	Thr	Val	Thr	Thr				
		195					200					205							
Val	Asn	Glu	Ile	Gln	Gln	Ala	Val	Glu	Ala	Leu	Gly	Asp	Val	Asp	Val				
	210					215					220								
Ile	Tyr	Val	Pro	Thr	Asp	Asn	Met	Val	Val	Ser	Gly	Ile	Ser	Ser	Leu				
225					230					235					240				
Val	Gln	Val	Ala	Glu	Gln	Lys	Gln	Ile	Pro	Val	Ile	Gly	Ala	Glu	Ser				
			245						250					255					
Gly	Thr	Val	Glu	Gly	Gly	Ala	Leu	Ala	Thr	Leu	Gly	Ile	Asp	Tyr	Thr				
		260					265						270						
Glu	Leu	Gly	Arg	Gln	Thr	Gly	Glu	Met	Ala	Leu	Arg	Ile	Leu	Gln	Asp				
		275					280					285							
Gly	Glu	Asp	Pro	Ala	Thr	Met	Pro	Val	Glu	Thr	Ala	Thr	Glu	Phe	Thr				
	290					295					300								
Tyr	Val	Ile	Asn	Glu	Asp	Ala	Ala	Glu	Arg	Gln	Gly	Val	Glu	Ile	Pro				
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Gln	Glu	Ile	Leu	Asp	Lys	Ala	Glu	Arg	Val										
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<210> 505

<211> 1263

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1240)

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	Val Ser Asp Val Thr	
	1 5	
gtt ggc gat att cgc cgc att ttg gat gag gct tat ccg ccg gcg ttg	163	
Val Gly Asp Ile Arg Arg Ile Leu Asp Glu Ala Tyr Pro Pro Ala Leu		
	10 15 20	
gcg gaa agc tgg gac aaa gtg ggg ctg atc tgc ggt gat cca aca gag	211	
Ala Glu Ser Trp Asp Lys Val Gly Leu Ile Cys Gly Asp Pro Thr Glu		
	25 30 35	
tcg gtg aag cgt gtc ggt tta gca ctc gat tgc acc cag gca gtg gcc	259	
Ser Val Lys Arg Val Gly Leu Ala Leu Asp Cys Thr Gln Ala Val Ala		
	40 45 50	
gac aag gct gtg gac atg ggt ttg gac atg ctg atc att cac cac cca	307	
Asp Lys Ala Val Asp Met Gly Leu Asp Met Leu Ile Ile His His Pro		
	55 60 65	
ttg ctg ctg cgt ggg gtg acg tct gtt gct gcg gat gag cca aaa ggc	355	
Leu Leu Leu Arg Gly Val Thr Ser Val Ala Ala Asp Glu Pro Lys Gly		
	70 75 80 85	
aag gtc att cac acc cta att cgc ggc ggg gtg gca ctg ttt tcc gcg	403	
Lys Val Ile His Thr Leu Ile Arg Gly Gly Val Ala Leu Phe Ser Ala		
	90 95 100	
cac act aat gcg gat tcc gcg cgc cca ggt gtc aac gat aaa ctc gcc	451	
His Thr Asn Ala Asp Ser Ala Arg Pro Gly Val Asn Asp Lys Leu Ala		
	105 110 115	
gag ctc gtc ggc atc acg gcc ggg cga ccc atc gcg aca cgg ctt tta	499	
Glu Leu Val Gly Ile Thr Ala Gly Arg Pro Ile Ala Thr Arg Leu Leu		
	120 125 130	
ggc ggc atg gac aaa tgg ggc gtg cac gtt ctg ccc aag gat gca gcg	547	
Gly Gly Met Asp Lys Trp Gly Val His Val Leu Pro Lys Asp Ala Ala		
	135 140 145	
tac cta aag aag atg ctt ttc gac gca ggt gcc ggt gcg atc ggc gac	595	
Tyr Leu Lys Lys Met Leu Phe Asp Ala Gly Ala Gly Ala Ile Gly Asp		
	150 155 160 165	
tac cga gag tgt gcc ttt gag atc gaa gga acc ggg cag ttt agg ccc	643	
Tyr Arg Glu Cys Ala Phe Glu Ile Glu Gly Thr Gly Gln Phe Arg Pro		
	170 175 180	
gtg gag ggg gcg aat ccg gca gag ggg gac gtc gat aag ctt ttt aaa	691	
Val Glu Gly Ala Asn Pro Ala Glu Gly Asp Val Asp Lys Leu Phe Lys		
	185 190 195	
tcc ctt gag ctg cgc atc gag ttt gtt gca ccg cgc aac ctg cgc gcc	739	
Ser Leu Glu Leu Arg Ile Glu Phe Val Ala Pro Arg Asn Leu Arg Ala		
	200 205 210	
cgg ctc acg tcg gtg ctg cgg gag gct cat ccg tat gag gag cct gcc	787	
Arg Leu Thr Ser Val Leu Arg Glu Ala His Pro Tyr Glu Glu Pro Ala		
	215 220 225	
ttc gat att gtt gaa atg cac agc gct gag agt tta gaa aat gcg acc	835	

Phe Asp Ile Val Glu Met His Ser Ala Glu Ser Leu Glu Asn Ala Thr
 230 235 240 245
 gga ttg ggt cgt gtg ggt gaa ttg ccg gag ccg atg cgc ctc gcg gat 883
 Gly Leu Gly Arg Val Gly Glu Leu Pro Glu Pro Met Arg Leu Ala Asp
 250 255 260
 ttc gtg caa caa gtg gcc aac aac ctg cct gtc acc gaa tgg ggc gtg 931
 Phe Val Gln Gln Val Ala Asn Asn Leu Pro Val Thr Glu Trp Gly Val
 265 270 275
 cgc gct acc ggc gat cct gaa caa atg gtg tcc cgt gtg gcg gtt tca 979
 Arg Ala Thr Gly Asp Pro Glu Gln Met Val Ser Arg Val Ala Val Ser
 280 285 290
 tca ggg tcg ggt gac agt ttc tta aac gat gtg att aag ctc gga gtg 1027
 Ser Gly Ser Gly Asp Ser Phe Leu Asn Asp Val Ile Lys Leu Gly Val
 295 300 305
 gac gtt tat gtc act tct gat ctg cgc cac cat cca gtt gat gaa tat 1075
 Asp Val Tyr Val Thr Ser Asp Leu Arg His His Pro Val Asp Glu Tyr
 310 315 320 325
 ctc cga gaa ggt ggc cct gca gta atc gat act gca cac tgg gcc agc 1123
 Leu Arg Glu Gly Gly Pro Ala Val Ile Asp Thr Ala His Trp Ala Ser
 330 335 340
 gaa ttt cca tgg act tcc caa gcc caa gaa att ttg cag gac aaa gcc 1171
 Glu Phe Pro Trp Thr Ser Gln Ala Gln Glu Ile Leu Gln Asp Lys Ala
 345 350 355
 cca cag gtt gaa gtt gat gtg att tcg atc cgc aca gac ccc tgg acc 1219
 Pro Gln Val Glu Val Asp Val Ile Ser Ile Arg Thr Asp Pro Trp Thr
 360 365 370
 atg tct gcg cga gca gtg aac taaattcttg agaactaaaa aag 1263
 Met Ser Ala Arg Ala Val Asn
 375 380

<210> 506

<211> 380

<212> PRT

<213> Corynebacterium glutamicum

<400> 506

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 Tyr Pro Pro Ala Leu Ala Glu Ser Trp Asp Lys Val Gly Leu Ile Cys
 20 25 30
 Gly Asp Pro Thr Glu Ser Val Lys Arg Val Gly Leu Ala Leu Asp Cys
 35 40 45
 Thr Gln Ala Val Ala Asp Lys Ala Val Asp Met Gly Leu Asp Met Leu
 50 55 60
 Ile Ile His His Pro Leu Leu Leu Arg Gly Val Thr Ser Val Ala Ala
 65 70 75 80

Asp Glu Pro Lys Gly Lys Val Ile His Thr Leu Ile Arg Gly Gly Val
 85 90 95
 Ala Leu Phe Ser Ala His Thr Asn Ala Asp Ser Ala Arg Pro Gly Val
 100 105 110
 Asn Asp Lys Leu Ala Glu Leu Val Gly Ile Thr Ala Gly Arg Pro Ile
 115 120 125
 Ala Thr Arg Leu Leu Gly Gly Met Asp Lys Trp Gly Val His Val Leu
 130 135 140
 Pro Lys Asp Ala Ala Tyr Leu Lys Lys Met Leu Phe Asp Ala Gly Ala
 145 150 155 160
 Gly Ala Ile Gly Asp Tyr Arg Glu Cys Ala Phe Glu Ile Glu Gly Thr
 165 170 175
 Gly Gln Phe Arg Pro Val Glu Gly Ala Asn Pro Ala Glu Gly Asp Val
 180 185 190
 Asp Lys Leu Phe Lys Ser Leu Glu Leu Arg Ile Glu Phe Val Ala Pro
 195 200 205
 Arg Asn Leu Arg Ala Arg Leu Thr Ser Val Leu Arg Glu Ala His Pro
 210 215 220
 Tyr Glu Glu Pro Ala Phe Asp Ile Val Glu Met His Ser Ala Glu Ser
 225 230 235 240
 Leu Glu Asn Ala Thr Gly Leu Gly Arg Val Gly Glu Leu Pro Glu Pro
 245 250 255
 Met Arg Leu Ala Asp Phe Val Gln Gln Val Ala Asn Asn Leu Pro Val
 260 265 270
 Thr Glu Trp Gly Val Arg Ala Thr Gly Asp Pro Glu Gln Met Val Ser
 275 280 285
 Arg Val Ala Val Ser Ser Gly Ser Gly Asp Ser Phe Leu Asn Asp Val
 290 295 300
 Ile Lys Leu Gly Val Asp Val Tyr Val Thr Ser Asp Leu Arg His His
 305 310 315 320
 Pro Val Asp Glu Tyr Leu Arg Glu Gly Gly Pro Ala Val Ile Asp Thr
 325 330 335
 Ala His Trp Ala Ser Glu Phe Pro Trp Thr Ser Gln Ala Gln Glu Ile
 340 345 350
 Leu Gln Asp Lys Ala Pro Gln Val Glu Val Asp Val Ile Ser Ile Arg
 355 360 365
 Thr Asp Pro Trp Thr Met Ser Ala Arg Ala Val Asn
 370 375 380

<210> 507

<211> 1470

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1447)

<223> RXC00362

<400> 507

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aacatgctacgggttttttcggtcacttaaa  ggaggcgctt  atg gga atc att gct  115
                                         Met Gly Ile Ile Ala
                                         1                               5

ctg ctc gtt ttt atc gca att gcc gtg ata ttg aat gtg ttt ttg aaa  163
Leu Leu Val Phe Ile Ala Ile Ala Val Ile Leu Asn Val Phe Leu Lys
                        10                        15                        20

cga gat att tca gaa gca ttg cta gtt gga tta gta gga act gcg ctt  211
Arg Asp Ile Ser Glu Ala Leu Leu Val Gly Leu Val Gly Thr Ala Leu
                        25                        30                        35

gtc ggc ggt gta aat gca ccg aca tta ctg att gat gct gta gtg gat  259
Val Gly Gly Val Asn Ala Pro Thr Leu Leu Ile Asp Ala Val Val Asp
                        40                        45                        50

gct gct cag tcg gaa gtt act ttc gca ggt atg gcc ttt gtt ttc atg  307
Ala Ala Gln Ser Glu Val Thr Phe Ala Gly Met Ala Phe Val Phe Met
                        55                        60                        65

ggc atc gtt gtg caa tca act gga ttg att gat cga tta atc gca atc  355
Gly Ile Val Val Gln Ser Thr Gly Leu Ile Asp Arg Leu Ile Ala Ile
                        70                        75                        80                        85

ctt aac tcg att ttt ggt cgg ctt cga ggt ggc gca ggt tat gtt tcc  403
Leu Asn Ser Ile Phe Gly Arg Leu Arg Gly Gly Ala Gly Tyr Val Ser
                        90                        95                        100

act ctt gga tct gcg ctc att gga ctc atc gct gga tca acg gct gga  451
Thr Leu Gly Ser Ala Leu Ile Gly Leu Ile Ala Gly Ser Thr Ala Gly
                        105                        110                        115

aac tcc gcg acg gtt ggc tca gtg acg atc cct tgg atg aaa aag acg  499
Asn Ser Ala Thr Val Gly Ser Val Thr Ile Pro Trp Met Lys Lys Thr
                        120                        125                        130

gga tgg act gct gaa agg tcc gca acg tta gtc gcg ggc aac tct ggc  547
Gly Trp Thr Ala Glu Arg Ser Ala Thr Leu Val Ala Gly Asn Ser Gly
                        135                        140                        145

ctt ggt gtt gcg ttg cct ccc aat tca aca atg ttc atc att ttg gca  595
Leu Gly Val Ala Leu Pro Pro Asn Ser Thr Met Phe Ile Ile Leu Ala
                        150                        155                        160                        165

ttg cca gct gca gca gct tct tcg gcc tct cag gtg tac att gct ttg  643
Leu Pro Ala Ala Ala Ala Ser Ser Ala Ser Gln Val Tyr Ile Ala Leu
                        170                        175                        180

gct tgt ggt ggt gcg tat gca gtg ctc tac cgc tta gcg gtc gtc ttt  691
Ala Cys Gly Gly Ala Tyr Ala Val Leu Tyr Arg Leu Ala Val Val Phe
                        185                        190                        195

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tac tgg aca cgt aaa gat aaa att cct gcc acc cct gat gat caa cgg	739
Tyr Trp Thr Arg Lys Asp Lys Ile Pro Ala Thr Pro Asp Asp Gln Arg	
200 205 210	
gtg tca ttc ggt gag gca atg aag act gga tgg cgt tca ccg ttg atc	787
Val Ser Phe Gly Glu Ala Met Lys Thr Gly Trp Arg Ser Pro Leu Ile	
215 220 225	
ttc ctt gga att ttg atc ccc gta atc ctc aca atc ggc cca ttg tct	835
Phe Leu Gly Ile Leu Ile Pro Val Ile Leu Thr Ile Gly Pro Leu Ser	
230 235 240 245	
gaa tgg tta aag aca cat gga gtt ggg gag tct ggt gtt aaa tcg atg	883
Glu Trp Leu Lys Thr His Gly Val Gly Glu Ser Gly Val Lys Ser Met	
250 255 260	
tcg atc atc gtg tgg gtg cca att ctg att acg gca att gct ctg att	931
Ser Ile Ile Val Trp Val Pro Ile Leu Ile Thr Ala Ile Ala Leu Ile	
265 270 275	
gaa ggg cgt aaa cga att gct aac aac atg gca cac ttt agg gtt cag	979
Glu Gly Arg Lys Arg Ile Ala Asn Asn Met Ala His Phe Arg Val Gln	
280 285 290	
atc tcc aag gac ttg cca caa ttt gcc acc gta gga att tcg ttg ttt	1027
Ile Ser Lys Asp Leu Pro Gln Phe Ala Thr Val Gly Ile Ser Leu Phe	
295 300 305	
tct gcg ctt gca gca gcg aac atc atg gaa gaa ctg ggt gtt ggc ccg	1075
Ser Ala Leu Ala Ala Ala Asn Ile Met Glu Glu Leu Gly Val Gly Pro	
310 315 320 325	
cag ttg tct aac tgg ctt gat tcc atg gac cta cct aag tct gtc atg	1123
Gln Leu Ser Asn Trp Leu Asp Ser Met Asp Leu Pro Lys Ser Val Met	
330 335 340	
gtg atc att gtc tgc atc atg tgc att gtg gtg gca acg cca ctg tcg	1171
Val Ile Ile Val Cys Ile Met Cys Ile Val Val Ala Thr Pro Leu Ser	
345 350 355	
tca aca gca acc gcg gct gcg att ggt gct ccc gct gtc gct gcg ttg	1219
Ser Thr Ala Thr Ala Ala Ala Ile Gly Ala Pro Ala Val Ala Ala Leu	
360 365 370	
gct gcg gta ggt att gat cca act gtg gcg atc gta gtg atc ttg ctg	1267
Ala Ala Val Gly Ile Asp Pro Thr Val Ala Ile Val Val Ile Leu Leu	
375 380 385	
tgc act tcc act gaa ggt gca tcc ccg ccg gtg ggc gcg ccg att tac	1315
Cys Thr Ser Thr Glu Gly Ala Ser Pro Pro Val Gly Ala Pro Ile Tyr	
390 395 400 405	
ctt tct gct gcg atc gcc gat gca aac cca acg aaa atg ttc gta cca	1363
Leu Ser Ala Ala Ile Ala Asp Ala Asn Pro Thr Lys Met Phe Val Pro	
410 415 420	
ctg att acg tac ttt gtt gtc ccc atg att ctg ctt gct tgg cta gtt	1411
Leu Ile Thr Tyr Phe Val Val Pro Met Ile Leu Leu Ala Trp Leu Val	
425 430 435	

gga atg gga ttc tta cca gtg att gtt cct acg ggt taaaggggta 1457
 Gly Met Gly Phe Leu Pro Val Ile Val Pro Thr Gly
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aaaatgaact caa 1470

<210> 508

<211> 449

<212> PRT

<213> Corynebacterium glutamicum

<400> 508

Met Gly Ile Ile Ala Leu Leu Val Phe Ile Ala Ile Ala Val Ile Leu
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Asn Val Phe Leu Lys Arg Asp Ile Ser Glu Ala Leu Leu Val Gly Leu
 20 25 30

Val Gly Thr Ala Leu Val Gly Gly Val Asn Ala Pro Thr Leu Leu Ile
 35 40 45

Asp Ala Val Val Asp Ala Ala Gln Ser Glu Val Thr Phe Ala Gly Met
 50 55 60

Ala Phe Val Phe Met Gly Ile Val Val Gln Ser Thr Gly Leu Ile Asp
 65 70 75 80

Arg Leu Ile Ala Ile Leu Asn Ser Ile Phe Gly Arg Leu Arg Gly Gly
 85 90 95

Ala Gly Tyr Val Ser Thr Leu Gly Ser Ala Leu Ile Gly Leu Ile Ala
 100 105 110

Gly Ser Thr Ala Gly Asn Ser Ala Thr Val Gly Ser Val Thr Ile Pro
 115 120 125

Trp Met Lys Lys Thr Gly Trp Thr Ala Glu Arg Ser Ala Thr Leu Val
 130 135 140

Ala Gly Asn Ser Gly Leu Gly Val Ala Leu Pro Pro Asn Ser Thr Met
 145 150 155 160

Phe Ile Ile Leu Ala Leu Pro Ala Ala Ala Ala Ser Ser Ala Ser Gln
 165 170 175

Val Tyr Ile Ala Leu Ala Cys Gly Gly Ala Tyr Ala Val Leu Tyr Arg
 180 185 190

Leu Ala Val Val Phe Tyr Trp Thr Arg Lys Asp Lys Ile Pro Ala Thr
 195 200 205

Pro Asp Asp Gln Arg Val Ser Phe Gly Glu Ala Met Lys Thr Gly Trp
 210 215 220

Arg Ser Pro Leu Ile Phe Leu Gly Ile Leu Ile Pro Val Ile Leu Thr
 225 230 235 240

Ile Gly Pro Leu Ser Glu Trp Leu Lys Thr His Gly Val Gly Glu Ser
 245 250 255

Gly

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<220>  
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<222> (101)..(1180)  
<223> RXC00412
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Val Ser His Thr Ala
1 5

tcc aca ccg acg cca gag gaa tac tcc gcg cag caa ccc agc acc cag 163
Ser Thr Pro Thr Pro Glu Glu Tyr Ser Ala Gln Gln Pro Ser Thr Gln
10 15 20

ggc act cgc gtt gag ttc cgc ggc ata acc aaa gtc ttt agc aac aat	211
Gly Thr Arg Val Glu Phe Arg Gly Ile Thr Lys Val Phe Ser Asn Asn	
25 30 35	
aaa tct gct aaa acc acc gcg ctt gat aat gtc act ctc acc gta gaa	259
Lys Ser Ala Lys Thr Thr Ala Leu Asp Asn Val Thr Leu Thr Val Glu	
40 45 50	
ccc ggt gag gta atc ggc atc atc ggt tac tct ggc gcc ggc aag tcc	307
Pro Gly Glu Val Ile Gly Ile Ile Gly Tyr Ser Gly Ala Gly Lys Ser	
55 60 65	
act ctt gtc cgc ctc atc aat ggc ctt gac tcc ccc acg agc ggt tcg	355
Thr Leu Val Arg Leu Ile Asn Gly Leu Asp Ser Pro Thr Ser Gly Ser	
70 75 80 85	
ttg ctg ctc aac ggc acc gac atc gtc gga atg ccc gag tct aag ctg	403
Leu Leu Leu Asn Gly Thr Asp Ile Val Gly Met Pro Glu Ser Lys Leu	
90 95 100	
cgt aaa ctg cgc agt aat atc ggc atg att ttc cag cag ttc aac ctg	451
Arg Lys Leu Arg Ser Asn Ile Gly Met Ile Phe Gln Gln Phe Asn Leu	
105 110 115	
ttc cag tcg cgt act gcg gct gga aat gtg gag tac ccg ctg gaa gtt	499
Phe Gln Ser Arg Thr Ala Ala Gly Asn Val Glu Tyr Pro Leu Glu Val	
120 125 130	
gcc aag atg gac aag gca gct cgt aaa gct cgc gtg caa gaa atg ctc	547
Ala Lys Met Asp Lys Ala Ala Arg Lys Ala Arg Val Gln Glu Met Leu	
135 140 145	
gag ttc gtc ggc ctg ggc gac aaa ggc aaa aac tac ccc gag cag ctg	595
Glu Phe Val Gly Leu Gly Asp Lys Gly Lys Asn Tyr Pro Glu Gln Leu	
150 155 160 165	
tcg ggc ggc cag aag cag cgc gtc ggc att gcc cgt gca ctg gcc acc	643
Ser Gly Gly Gln Lys Gln Arg Val Gly Ile Ala Arg Ala Leu Ala Thr	
170 175 180	
aat cca acg ctt ttg ctt gcc gac gaa gcc acc tcc gct ttg gac cca	691
Asn Pro Thr Leu Leu Ala Asp Glu Ala Thr Ser Ala Leu Asp Pro	
185 190 195	
gaa acc acc cat gaa gtt ctg gag ctg ctg cgc aag gta aac cgc gaa	739
Glu Thr Thr His Glu Val Leu Glu Leu Leu Arg Lys Val Asn Arg Glu	
200 205 210	
ctg ggc atc acc atc gtt gtg atc acc cac gaa atg gaa gtt gtg cgt	787
Leu Gly Ile Thr Ile Val Val Ile Thr His Glu Met Glu Val Val Arg	
215 220 225	
tcc atc gca gac aag gtt gct gtg atg gaa tcc ggc aaa gtt gtg gaa	835
Ser Ile Ala Asp Lys Val Ala Val Met Glu Ser Gly Lys Val Val Glu	
230 235 240 245	
tac ggc agc gtc tac gag gtg ttc tcc aat cca caa aca cag gtt gct	883
Tyr Gly Ser Val Tyr Glu Val Phe Ser Asn Pro Gln Thr Gln Val Ala	
250 255 260	
caa aag ttc gtg gcc acc gcg ctg cgt aac acc cca gac caa gtg gaa	931

Gln Lys Phe Val Ala Thr Ala Leu Arg Asn Thr Pro Asp Gln Val Glu
 265 270 275

tcg gaa gat ctg ctt agc cat gag gga cgt ctg ttc acc att gat ctg 979
 Ser Glu Asp Leu Leu Ser His Glu Gly Arg Leu Phe Thr Ile Asp Leu
 280 285 290

act gaa acg tcc ggc ttc ttt gca gca acc gct cgt gct gcc gaa caa 1027
 Thr Glu Thr Ser Gly Phe Phe Ala Ala Thr Ala Arg Ala Ala Glu Gln
 295 300 305

ggc gct ttt gtc aac atc gtt cac ggt ggc gtg acc acc ttg caa cgc 1075
 Gly Ala Phe Val Asn Ile Val His Gly Gly Val Thr Thr Leu Gln Arg
 310 315 320 325

caa tca ttt ggc aaa atg act gtt cga ctc acc ggc aac acc gct gcg 1123
 Gln Ser Phe Gly Lys Met Thr Val Arg Leu Thr Gly Asn Thr Ala Ala
 330 335 340

att gaa gag ttc tat caa acc ttg acc aag acc acg acc atc aag gag 1171
 Ile Glu Glu Phe Tyr Gln Thr Leu Thr Lys Thr Thr Thr Ile Lys Glu
 345 350 355

atc acc cga tgaacgagat gaccccgca gct 1203
 Ile Thr Arg
 360

<210> 510

<211> 360

<212> PRT

<213> Corynebacterium glutamicum

<400> 510

Val Ser His Thr Ala Ser Thr Pro Thr Pro Glu Glu Tyr Ser Ala Gln
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Gln Pro Ser Thr Gln Gly Thr Arg Val Glu Phe Arg Gly Ile Thr Lys
 20 25 30

Val Phe Ser Asn Asn Lys Ser Ala Lys Thr Thr Ala Leu Asp Asn Val
 35 40 45

Thr Leu Thr Val Glu Pro Gly Glu Val Ile Gly Ile Ile Gly Tyr Ser
 50 55 60

Gly Ala Gly Lys Ser Thr Leu Val Arg Leu Ile Asn Gly Leu Asp Ser
 65 70 75 80

Pro Thr Ser Gly Ser Leu Leu Leu Asn Gly Thr Asp Ile Val Gly Met
 85 90 95

Pro Glu Ser Lys Leu Arg Lys Leu Arg Ser Asn Ile Gly Met Ile Phe
 100 105 110

Gln Gln Phe Asn Leu Phe Gln Ser Arg Thr Ala Ala Gly Asn Val Glu
 115 120 125

Tyr Pro Leu Glu Val Ala Lys Met Asp Lys Ala Ala Arg Lys Ala Arg
 130 135 140

Val Gln Glu Met Leu Glu Phe Val Gly Leu Gly Asp Lys Gly Lys Asn
 145 150 155 160
 Tyr Pro Glu Gln Leu Ser Gly Gly Gln Lys Gln Arg Val Gly Ile Ala
 165 170 175
 Arg Ala Leu Ala Thr Asn Pro Thr Leu Leu Leu Ala Asp Glu Ala Thr
 180 185 190
 Ser Ala Leu Asp Pro Glu Thr Thr His Glu Val Leu Glu Leu Leu Arg
 195 200 205
 Lys Val Asn Arg Glu Leu Gly Ile Thr Ile Val Val Ile Thr His Glu
 210 215 220
 Met Glu Val Val Arg Ser Ile Ala Asp Lys Val Ala Val Met Glu Ser
 225 230 235 240
 Gly Lys Val Val Glu Tyr Gly Ser Val Tyr Glu Val Phe Ser Asn Pro
 245 250 255
 Gln Thr Gln Val Ala Gln Lys Phe Val Ala Thr Ala Leu Arg Asn Thr
 260 265 270
 Pro Asp Gln Val Glu Ser Glu Asp Leu Leu Ser His Glu Gly Arg Leu
 275 280 285
 Phe Thr Ile Asp Leu Thr Glu Thr Ser Gly Phe Phe Ala Ala Thr Ala
 290 295 300
 Arg Ala Ala Glu Gln Gly Ala Phe Val Asn Ile Val His Gly Gly Val
 305 310 315 320
 Thr Thr Leu Gln Arg Gln Ser Phe Gly Lys Met Thr Val Arg Leu Thr
 325 330 335
 Gly Asn Thr Ala Ala Ile Glu Glu Phe Tyr Gln Thr Leu Thr Lys Thr
 340 345 350
 Thr Thr Ile Lys Glu Ile Thr Arg
 355 360

<210> 511
 <211> 813
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(790)
 <223> RXC00526

<400> 511
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 cgtttctgcc aagcaaaccg tgggccaggt gatttagcct atg agc ctc atc gaa 115
 Met Ser Leu Ile Glu
 1 5
 atg cga aat att gtc aag acc tac aac att gga tct gaa ggt gaa ctc 163

Met	Arg	Asn	Ile	Val	Lys	Thr	Tyr	Asn	Ile	Gly	Ser	Glu	Gly	Glu	Leu		
				10					15					20			
acc	gtg	ttg	cac	ggt	gtg	gat	ttc	cat	gtg	gac	cgt	ggc	gaa	ttc	gtg	211	
Thr	Val	Leu	His	Gly	Val	Asp	Phe	His	Val	Asp	Arg	Gly	Glu	Phe	Val		
			25					30					35				
tcg	gtt	gtg	ggt	acg	tcc	ggc	tca	ggt	aaa	tca	acg	atg	atg	aac	atc	259	
Ser	Val	Val	Gly	Thr	Ser	Gly	Ser	Gly	Lys	Ser	Thr	Met	Met	Asn	Ile		
		40					45					50					
att	ggg	ttg	ttg	gat	aag	cca	act	gat	ggc	acg	tac	acc	ttg	gat	ggc	307	
Ile	Gly	Leu	Leu	Asp	Lys	Pro	Thr	Asp	Gly	Thr	Tyr	Thr	Leu	Asp	Gly		
	55					60					65						
gtg	gat	gtg	ttg	gat	atc	agc	gat	gat	gct	ttg	gcg	agc	cac	cgc	gct	355	
Val	Asp	Val	Leu	Asp	Ile	Ser	Asp	Asp	Ala	Leu	Ala	Ser	His	Arg	Ala		
	70				75					80					85		
aaa	tcg	att	ggt	ttt	gtg	ttt	cag	aac	ttc	aat	ctg	att	ggc	cgg	atc	403	
Lys	Ser	Ile	Gly	Phe	Val	Phe	Gln	Asn	Phe	Asn	Leu	Ile	Gly	Arg	Ile		
				90				95						100			
gat	gcg	ttg	aag	aat	gtg	gaa	atg	ccc	atg	atg	tat	gcg	ggc	att	ccg	451	
Asp	Ala	Leu	Lys	Asn	Val	Glu	Met	Pro	Met	Met	Tyr	Ala	Gly	Ile	Pro		
			105					110					115				
gct	aag	cag	cgg	aga	agt	cgt	gcg	gtt	gaa	tta	ttg	gaa	atg	gtc	ggg	499	
Ala	Lys	Gln	Arg	Arg	Ser	Arg	Ala	Val	Glu	Leu	Leu	Glu	Met	Val	Gly		
		120					125						130				
atg	ggt	gag	cgt	ctc	aac	cat	gag	ccc	aat	gag	ctt	tcg	ggt	ggt	cag	547	
Met	Gly	Glu	Arg	Leu	Asn	His	Glu	Pro	Asn	Glu	Leu	Ser	Gly	Gly	Gln		
	135					140					145						
aag	cag	cgc	gtg	gcc	att	gct	cgc	gcg	ttg	gcg	aac	gat	cct	gag	atc	595	
Lys	Gln	Arg	Val	Ala	Ile	Ala	Arg	Ala	Leu	Ala	Asn	Asp	Pro	Glu	Ile		
	150				155				160						165		
att	ctt	gct	gat	gaa	cca	act	ggt	gcg	ttg	gat	tct	gca	acg	ggc	cgg	643	
Ile	Leu	Ala	Asp	Glu	Pro	Thr	Gly	Ala	Leu	Asp	Ser	Ala	Thr	Gly	Arg		
				170				175						180			
atg	gtg	atg	gat	att	ttc	cac	cag	ctc	aac	aag	gag	cag	ggc	aaa	acc	691	
Met	Val	Met	Asp	Ile	Phe	His	Gln	Leu	Asn	Lys	Glu	Gln	Gly	Lys	Thr		
			185					190					195				
atc	gtg	ttt	att	act	cac	aac	cct	gag	ctt	gct	gat	gaa	tct	gat	cgg	739	
Ile	Val	Phe	Ile	Thr	His	Asn	Pro	Glu	Leu	Ala	Asp	Glu	Ser	Asp	Arg		
		200					205					210					
gtg	gtc	acc	atg	gtt	gac	ggg	cgc	atc	att	ggg	tct	gag	gtg	aaa	cac	787	
Val	Val	Thr	Met	Val	Asp	Gly	Arg	Ile	Ile	Gly	Ser	Glu	Val	Lys	His		
	215					220				225							
tca	tgagccttg	agaatcaatt	ctt													813	
Ser																	
230																	

<210> 512

<211> 230

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 512

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Ser Glu Gly Glu Leu Thr Val Leu His Gly Val Asp Phe His Val Asp
 20 25 30

Arg Gly Glu Phe Val Ser Val Val Gly Thr Ser Gly Ser Gly Lys Ser
 35 40 45

Thr Met Met Asn Ile Ile Gly Leu Leu Asp Lys Pro Thr Asp Gly Thr
 50 55 60

Tyr Thr Leu Asp Gly Val Asp Val Leu Asp Ile Ser Asp Asp Ala Leu
 65 70 75 80

Ala Ser His Arg Ala Lys Ser Ile Gly Phe Val Phe Gln Asn Phe Asn
 85 90 95

Leu Ile Gly Arg Ile Asp Ala Leu Lys Asn Val Glu Met Pro Met Met
 100 105 110

Tyr Ala Gly Ile Pro Ala Lys Gln Arg Arg Ser Arg Ala Val Glu Leu
 115 120 125

Leu Glu Met Val Gly Met Gly Glu Arg Leu Asn His Glu Pro Asn Glu
 130 135 140

Leu Ser Gly Gly Gln Lys Gln Arg Val Ala Ile Ala Arg Ala Leu Ala
 145 150 155 160

Asn Asp Pro Glu Ile Ile Leu Ala Asp Glu Pro Thr Gly Ala Leu Asp
 165 170 175

Ser Ala Thr Gly Arg Met Val Met Asp Ile Phe His Gln Leu Asn Lys
 180 185 190

Glu Gln Gly Lys Thr Ile Val Phe Ile Thr His Asn Pro Glu Leu Ala
 195 200 205

Asp Glu Ser Asp Arg Val Val Thr Met Val Asp Gly Arg Ile Ile Gly
 210 215 220

Ser Glu Val Lys His Ser
 225 230

<210> 513

<211> 1185

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(1162)

<223> RXC01004

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                               Val Ser Ile Trp Ala
                               1           5

act gtc ctt cta att atc gtc ctt ctt tcc gcc aac gcc ttc ttc gtg 163
Thr Val Leu Leu Ile Ile Val Leu Leu Ser Ala Asn Ala Phe Phe Val
                10                15                20

gcc gcg gag ttc gca ctg att tcc tcg cgc cgg gac cgc ctg gat tcc 211
Ala Ala Glu Phe Ala Leu Ile Ser Ser Arg Arg Asp Arg Leu Asp Ser
                25                30                35

ctg gta tcc cag ggt aaa aag gga gct gaa aag gtt ctc tac gca acc 259
Leu Val Ser Gln Gly Lys Lys Gly Ala Glu Lys Val Leu Tyr Ala Thr
                40                45                50

gag cac ctc tcc atc atg ttg gcg ggc gct cag ttc ggt att acg gtc 307
Glu His Leu Ser Ile Met Leu Ala Gly Ala Gln Phe Gly Ile Thr Val
                55                60                65

tgt tct ctg att ctg ggt aaa gtc gca gaa cct gcg atc gcc cac ttc 355
Cys Ser Leu Ile Leu Gly Lys Val Ala Glu Pro Ala Ile Ala His Phe
                70                75                80                85

att gag gtg cct ttc acc tcc tgg ggt gtt cca aat gat ttg atc cac 403
Ile Glu Val Pro Phe Thr Ser Trp Gly Val Pro Asn Asp Leu Ile His
                90                95                100

cca att tcc ttc gtc atc gca ctg gcg atc atc acc tgg ttg cac att 451
Pro Ile Ser Phe Val Ile Ala Leu Ala Ile Ile Thr Trp Leu His Ile
                105                110                115

ctc ttt ggt gaa atg gtg cca aag aac atc gct att gct ggc cct gaa 499
Leu Phe Gly Glu Met Val Pro Lys Asn Ile Ala Ile Ala Gly Pro Glu
                120                125                130

acc tta ggc atg tgg ctt gct cca gtg ctc att gcg ttt gtg aag att 547
Thr Leu Gly Met Trp Leu Ala Pro Val Leu Ile Ala Phe Val Lys Ile
                135                140                145

acc cgc ccg ttg atc gag ttc atg aac tgg atc gcc cgt ctg acc ctt 595
Thr Arg Pro Leu Ile Glu Phe Met Asn Trp Ile Ala Arg Leu Thr Leu
                150                155                160                165

cgc gcc ttt ggt gtg gag caa aaa aac gag ctg gat tcc acc gtg gac 643
Arg Ala Phe Gly Val Glu Gln Lys Asn Glu Leu Asp Ser Thr Val Asp
                170                175                180

cca gag cag ctg gca tca atg att tcc gag tcc cgt tcc gaa ggc ctc 691
Pro Glu Gln Leu Ala Ser Met Ile Ser Glu Ser Arg Ser Glu Gly Leu
                185                190                195

ctt gat gct gaa gag cac gcc cgc ctg tcc aag gcg ctg cgc tct gag 739
Leu Asp Ala Glu Glu His Ala Arg Leu Ser Lys Ala Leu Arg Ser Glu
                200                205                210

cag cgt tcc atc aag gaa ctg gtg att aag gat gag gac gtg cgc acg 787
Gln Arg Ser Ile Lys Glu Leu Val Ile Lys Asp Glu Asp Val Arg Thr

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215	220	225	
ctg gcg ttc ggt aaa tct ggc ccg acc ttg cac cag ttg gag gaa gca			835
Leu Ala Phe Gly Lys Ser Gly Pro Thr Leu His Gln Leu Glu Glu Ala			
230	235	240	245
gtc cgc gag acc ggt ttc tcc cgc ttc cct gtc acc ggc cgc gat gga			883
Val Arg Glu Thr Gly Phe Ser Arg Phe Pro Val Thr Gly Arg Asp Gly			
	250	255	260
tcc tac ttg ggt tat atc cac atc aag gat att ttg cct cgt ctg gct			931
Ser Tyr Leu Gly Tyr Ile His Ile Lys Asp Ile Leu Pro Arg Leu Ala			
	265	270	275
gat cct gag atg gat ccc tcc gag acc att ccg cgt tct gca ctg cgc			979
Asp Pro Glu Met Asp Pro Ser Glu Thr Ile Pro Arg Ser Ala Leu Arg			
	280	285	290
cct ttg agc aat gtg gat gcc gac ggc ctc atg gat gac gtc ttg gat			1027
Pro Leu Ser Asn Val Asp Ala Asp Gly Leu Met Asp Asp Val Leu Asp			
	295	300	305
ttt atg cac tac cgc tcc gcg cac atg gct cag gtt cgc ctc aaa ggt			1075
Phe Met His Tyr Arg Ser Ala His Met Ala Gln Val Arg Leu Lys Gly			
	310	315	320
gag ctt ctc ggc gtg att acg ctg gag gat ctc atc gaa gaa tac gtg			1123
Glu Leu Leu Gly Val Ile Thr Leu Glu Asp Leu Ile Glu Glu Tyr Val			
	330	335	340
ggc acc gtc aac gat tgg act cac gaa agc tcc gac gac tagaaatagt			1172
Gly Thr Val Asn Asp Trp Thr His Glu Ser Ser Asp Asp			
	345	350	
aactgtgttg gac			1185

<210> 514

<211> 354

<212> PRT

<213> Corynebacterium glutamicum

<400> 514

Val Ser Ile Trp Ala Thr Val Leu Leu Ile Ile Val Leu Leu Ser Ala
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Asn Ala Phe Phe Val Ala Ala Glu Phe Ala Leu Ile Ser Ser Arg Arg
20 25 30

Asp Arg Leu Asp Ser Leu Val Ser Gln Gly Lys Lys Gly Ala Glu Lys
35 40 45

Val Leu Tyr Ala Thr Glu His Leu Ser Ile Met Leu Ala Gly Ala Gln
50 55 60

Phe Gly Ile Thr Val Cys Ser Leu Ile Leu Gly Lys Val Ala Glu Pro
65 70 75 80

Ala Ile Ala His Phe Ile Glu Val Pro Phe Thr Ser Trp Gly Val Pro
85 90 95

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Asn Asp Leu Ile His Pro Ile Ser Phe Val Ile Ala Leu Ala Ile Ile
    100                      105                      110

Thr Trp Leu His Ile Leu Phe Gly Glu Met Val Pro Lys Asn Ile Ala
    115                      120                      125

Ile Ala Gly Pro Glu Thr Leu Gly Met Trp Leu Ala Pro Val Leu Ile
    130                      135                      140

Ala Phe Val Lys Ile Thr Arg Pro Leu Ile Glu Phe Met Asn Trp Ile
    145                      150                      155                      160

Ala Arg Leu Thr Leu Arg Ala Phe Gly Val Glu Gln Lys Asn Glu Leu
    165                      170                      175

Asp Ser Thr Val Asp Pro Glu Gln Leu Ala Ser Met Ile Ser Glu Ser
    180                      185                      190

Arg Ser Glu Gly Leu Leu Asp Ala Glu Glu His Ala Arg Leu Ser Lys
    195                      200                      205

Ala Leu Arg Ser Glu Gln Arg Ser Ile Lys Glu Leu Val Ile Lys Asp
    210                      215                      220

Glu Asp Val Arg Thr Leu Ala Phe Gly Lys Ser Gly Pro Thr Leu His
    225                      230                      235                      240

Gln Leu Glu Glu Ala Val Arg Glu Thr Gly Phe Ser Arg Phe Pro Val
    245                      250                      255

Thr Gly Arg Asp Gly Ser Tyr Leu Gly Tyr Ile His Ile Lys Asp Ile
    260                      265                      270

Leu Pro Arg Leu Ala Asp Pro Glu Met Asp Pro Ser Glu Thr Ile Pro
    275                      280                      285

Arg Ser Ala Leu Arg Pro Leu Ser Asn Val Asp Ala Asp Gly Leu Met
    290                      295                      300

Asp Asp Val Leu Asp Phe Met His Tyr Arg Ser Ala His Met Ala Gln
    305                      310                      315                      320

Val Arg Leu Lys Gly Glu Leu Leu Gly Val Ile Thr Leu Glu Asp Leu
    325                      330                      335

Ile Glu Glu Tyr Val Gly Thr Val Asn Asp Trp Thr His Glu Ser Ser
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Asp Asp

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 <211> 732
 <212> DNA
 <213> *Corynebacterium glutamicum*

<220>
 <221> CDS
 <222> (101)..(709)
 <223> RXC01017

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agtgtggatt gctagaaaac tttaagaaag aggaaataat atg gct caa aaa gta 115
                                         Met Ala Gln Lys Val
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acc ttc tgg ttc gat acc acc tgc cca ttc tgc tgg gtc acc tcc cgc 163
Thr Phe Trp Phe Asp Thr Thr Cys Pro Phe Cys Trp Val Thr Ser Arg
                        10                        15                        20

tgg att aag gaa gtc gaa caa gtc cgc gat att gaa atc cag tgg gtt 211
Trp Ile Lys Glu Val Glu Gln Val Arg Asp Ile Glu Ile Gln Trp Val
                        25                        30                        35

cca atg agc ctc gct gtc cta aac gaa ggc cgt gat ctc cca gag gat 259
Pro Met Ser Leu Ala Val Leu Asn Glu Gly Arg Asp Leu Pro Glu Asp
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tac aag gag cgc atg aag gct gca tgg gga cca gca cgc gtt ttc gca 307
Tyr Lys Glu Arg Met Lys Ala Ala Trp Gly Pro Ala Arg Val Phe Ala
                        55                        60                        65

gct gtc gcc acc gac cat gct gac aag ctc ggc gac ctg tac acc gca 355
Ala Val Ala Thr Asp His Ala Asp Lys Leu Gly Asp Leu Tyr Thr Ala
                        70                        75                        80                        85

atg ggt acc cgc atc cac aac gac ggt cgc gga cca atc gaa ggt tcc 403
Met Gly Thr Arg Ile His Asn Asp Gly Arg Gly Pro Ile Glu Gly Ser
                        90                        95                        100

ttc aat gat gtc atc gca gag gca ctt gaa gag gtc ggc cta gac gct 451
Phe Asn Asp Val Ile Ala Glu Ala Leu Glu Glu Val Gly Leu Asp Ala
                        105                        110                        115

gca ctt ggt gaa gtt gca gac acc acc gaa tgg gac gac gca ctt cgc 499
Ala Leu Gly Glu Val Ala Asp Thr Thr Glu Trp Asp Asp Ala Leu Arg
                        120                        125                        130

gca ttc cac cag acc gca atg gac gag gtc ggc aac gat gtc gga acc 547
Ala Phe His Gln Thr Ala Met Asp Glu Val Gly Asn Asp Val Gly Thr
                        135                        140                        145

cca gtg gtc aag ctc ggc gac acc gct ttc ttc ggc cca gtg ctc acc 595
Pro Val Val Lys Leu Gly Asp Thr Ala Phe Phe Gly Pro Val Leu Thr
                        150                        155                        160                        165

cgc atc cca cgc ggc gag gaa gca gga gag atc ttc gac gct tcc ttc 643
Arg Ile Pro Arg Gly Glu Glu Ala Gly Glu Ile Phe Asp Ala Ser Phe
                        170                        175                        180

aag ctc gca agc tat ccc cac ttc ttt gaa atc aag cgc agc cgc act 691
Lys Leu Ala Ser Tyr Pro His Phe Phe Glu Ile Lys Arg Ser Arg Thr
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gag aac cca cag ttc gac taattaacgc tgtctctgct tat 732
Glu Asn Pro Gln Phe Asp
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Met Ser Ser Ser Glu

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agc	tcg	cgt	tcc	gaa	ggc	tcg	cag	cca	gca	ccg	tct	gta	cag	cct	gaa	163																
Ser	Ser	Arg	Ser	Glu	Gly	Ser	Gln	Pro	Ala	Pro	Ser	Val	Gln	Pro	Glu																	
				10					15					20																		
cgc	cgt	gct	gat	tca	acg	ggg	gct	cct	gcg	gca	gct	tcc	aag	gaa	gct	211																
Arg	Arg	Ala	Asp	Ser	Thr	Gly	Ala	Pro	Ala	Ala	Ala	Ser	Lys	Glu	Ala																	
				25					30					35																		
tcc	caa	caa	atg	gac	gct	gcc	gga	gtt	ctt	gag	tgg	gcc	agg	acc	gct	259																
Ser	Gln	Gln	Met	Asp	Ala	Ala	Gly	Val	Leu	Glu	Trp	Ala	Arg	Thr	Ala																	
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gtc	gag	cag	ctt	tct	gaa	cgt	cgt	gca	gag	atc	aat	gca	ctg	aat	gtc	307																
Val	Glu	Gln	Leu	Ser	Glu	Arg	Arg	Ala	Glu	Ile	Asn	Ala	Leu	Asn	Val																	
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Phe	Pro	Val	Pro	Asp	Ala	Asp	Thr	Gly	Ser	Asn	Met	Thr	Tyr	Thr	Met																	
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aca	gct	gcg	ttg	gat	gaa	gcg	ctg	aaa	ctg	ggg	gag	ttg	ggt	gat	gtc	403																
Thr	Ala	Ala	Leu	Asp	Glu	Ala	Leu	Lys	Leu	Gly	Glu	Leu	Gly	Asp	Val																	
				90					95					100																		
gca	agg	att	act	gag	gct	ttg	gct	gtt	ggt	tct	gtg	cgt	gga	gcc	cga	451																
Ala	Arg	Ile	Thr	Glu	Ala	Leu	Ala	Val	Gly	Ser	Val	Arg	Gly	Ala	Arg																	
				105					110					115																		
gga	aat	tct	gga	gta	gtc	ctt	agt	cag	gtc	ctt	cgc	gct	att	gct	cag	499																
Gly	Asn	Ser	Gly	Val	Val	Leu	Ser	Gln	Val	Leu	Arg	Ala	Ile	Ala	Gln																	
				120					125					130																		
gca	gct	gct	gac	ggg	gtt	att	gat	ggc	cac	aca	atc	caa	gaa	gcg	cta	547																
Ala	Ala	Ala	Asp	Gly	Val	Ile	Asp	Gly	His	Thr	Ile	Gln	Glu	Ala	Leu																	
				135					140					145																		
tcc	att	gct	cgc	tcc	cta	gtt	gat	cgc	gca	att	aca	gat	cct	gtg	gag	595																
Ser	Ile	Ala	Arg	Ser	Leu	Val	Asp	Arg	Ala	Ile	Thr	Asp	Pro	Val	Glu																	
				150					155					160																		
ggc	act	gtt	gtc	act	gtg	ttg	cgt	tct								622																
Gly	Thr	Val	Val	Thr	Val	Leu	Arg	Ser																								
				170																												

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<211> 174

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 518

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Ser	Val	Gln	Pro	Glu	Arg	Arg	Ala	Asp	Ser	Thr	Gly	Ala	Pro	Ala	Ala
			20					25					30		

Ala	Ser	Lys	Glu	Ala	Ser	Gln	Gln	Met	Asp	Ala	Ala	Gly	Val	Leu	Glu
		35					40					45			

Trp Ala Arg Thr Ala Val Glu Gln Leu Ser Glu Arg Arg Ala Glu Ile
 50 55 60

Asn Ala Leu Asn Val Phe Pro Val Pro Asp Ala Asp Thr Gly Ser Asn
 65 70 75 80

Met Thr Tyr Thr Met Thr Ala Ala Leu Asp Glu Ala Leu Lys Leu Gly
 85 90 95

Glu Leu Gly Asp Val Ala Arg Ile Thr Glu Ala Leu Ala Val Gly Ser
 100 105 110

Val Arg Gly Ala Arg Gly Asn Ser Gly Val Val Leu Ser Gln Val Leu
 115 120 125

Arg Ala Ile Ala Gln Ala Ala Ala Asp Gly Val Ile Asp Gly His Thr
 130 135 140

Ile Gln Glu Ala Leu Ser Ile Ala Arg Ser Leu Val Asp Arg Ala Ile
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Thr Asp Pro Val Glu Gly Thr Val Val Thr Val Leu Arg Ser
 165 170

<210> 519
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 <212> DNA
 <213> Corynebacterium glutamicum

<220>
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 <222> (101)..(1024)
 <223> RXC01212

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 Met Pro Met Thr Thr
 1 5

aca cca gca atc gac gta aca gac ctc gtg aga acc tac ggc gac tac 163
 Thr Pro Ala Ile Asp Val Thr Asp Leu Val Arg Thr Tyr Gly Asp Tyr
 10 15 20

acc gca gtc aag ggc ctg aat ttc cat gta cag cgc ggt gaa gta ttt 211
 Thr Ala Val Lys Gly Leu Asn Phe His Val Gln Arg Gly Glu Val Phe
 25 30 35

ggg ctg ctc ggc acc aac ggg gcc ggc aaa acc tcc acc ttg gaa gtc 259
 Gly Leu Leu Gly Thr Asn Gly Ala Gly Lys Thr Ser Thr Leu Glu Val
 40 45 50

atc gaa gga ctt tcc gca ccc agc tcc ggc acc gtg cgc atc tcc ggg 307
 Ile Glu Gly Leu Ser Ala Pro Ser Ser Gly Thr Val Arg Ile Ser Gly
 55 60 65

ctt gac ccc gtt gcc gac cgc gcg atc ctg cgc ccc gag ctc ggc atc 355
 Leu Asp Pro Val Ala Asp Arg Ala Ile Leu Arg Pro Glu Leu Gly Ile

70	75							80							85				
atg ctg caa tca ggc ggc ctg cca tca cag ctc acc gtc gcc gaa acc																			403
Met Leu Gln Ser Gly Gly Leu Pro Ser Gln Leu Thr Val Ala Glu Thr																			
	90							95							100				
atg gac atg tgg cac ggc acc tgc acg tat ccg cgc gcc att aaa gat																			451
Met Asp Met Trp His Gly Thr Cys Thr Tyr Pro Arg Ala Ile Lys Asp																			
	105							110							115				
gtg ctt gcc gac gtc gac ctc cta cac cgc gaa aac gtc aag gtc ggc																			499
Val Leu Ala Asp Val Asp Leu Leu His Arg Glu Asn Val Lys Val Gly																			
	120							125							130				
gcg ctt tcc gga ggc gaa caa cga cgc ctt gat ttg gcc tgc gca ctg																			547
Ala Leu Ser Gly Gly Glu Gln Arg Arg Leu Asp Leu Ala Cys Ala Leu																			
	135							140							145				
ctt ggc gac ccc tca att ttg ttc ctc gac gaa ccc acc acc ggc ctc																			595
Leu Gly Asp Pro Ser Ile Leu Phe Leu Asp Glu Pro Thr Thr Gly Leu																			
	150							155							160				165
gac cca gaa tct agg cgc cac acc tgg caa ctc ctg ctg gac ctg aaa																			643
Asp Pro Glu Ser Arg Arg His Thr Trp Gln Leu Leu Leu Asp Leu Lys																			
	170							175							180				
cag cgc ggc gtc acc atg atg ctg acc acc cac tac ctg gag gaa gcc																			691
Gln Arg Gly Val Thr Met Met Leu Thr Thr His Tyr Leu Glu Glu Ala																			
	185							190							195				
gaa ttc ctc tgc gac cgg att gcc atc atg aac gcc ggt gag atc gca																			739
Glu Phe Leu Cys Asp Arg Ile Ala Ile Met Asn Ala Gly Glu Ile Ala																			
	200							205							210				
gtg gaa ggc acc ttg gat gaa ctg gtg gcc cgc gag aag tcg atc atc																			787
Val Glu Gly Thr Leu Asp Glu Leu Val Ala Arg Glu Lys Ser Ile Ile																			
	215							220							225				
agt ttc gtg ctg cgt ggc ggg cag gtg gag ttg ccg gtc ttg agt ggg																			835
Ser Phe Val Leu Arg Gly Gly Gln Val Glu Leu Pro Val Leu Ser Gly																			
	230							235							240				245
gct gaa atc atc cgc gac aac aac cac gtc cgc atc gcc acc acc acc																			883
Ala Glu Ile Ile Arg Asp Asn Asn His Val Arg Ile Ala Thr Thr Thr																			
	250							255							260				
ctg cag cag cac acc tta gaa ata ctt acc tgg gct gca gag acc ggg																			931
Leu Gln Gln His Thr Leu Glu Ile Leu Thr Trp Ala Ala Glu Thr Gly																			
	265							270							275				
atc gcg ctg gaa ggc ttc gct gca aaa ccc gcc acc ttg gaa tcc gta																			979
Ile Ala Leu Glu Gly Phe Ala Ala Lys Pro Ala Thr Leu Glu Ser Val																			
	280							285							290				
ttc atg gac atc gcc tca ctc gag aac acc tcg ctg caa acc gcc																			1024
Phe Met Asp Ile Ala Ser Leu Glu Asn Thr Ser Leu Gln Thr Ala																			
	295							300							305				
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<210> 520
 <211> 308
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 520

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Thr Tyr Gly Asp Tyr Thr Ala Val Lys Gly Leu Asn Phe His Val Gln
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Arg Gly Glu Val Phe Gly Leu Leu Gly Thr Asn Gly Ala Gly Lys Thr
      35              40              45

Ser Thr Leu Glu Val Ile Glu Gly Leu Ser Ala Pro Ser Ser Gly Thr
      50              55              60

Val Arg Ile Ser Gly Leu Asp Pro Val Ala Asp Arg Ala Ile Leu Arg
      65              70              75              80

Pro Glu Leu Gly Ile Met Leu Gln Ser Gly Gly Leu Pro Ser Gln Leu
      85              90              95

Thr Val Ala Glu Thr Met Asp Met Trp His Gly Thr Cys Thr Tyr Pro
      100              105              110

Arg Ala Ile Lys Asp Val Leu Ala Asp Val Asp Leu Leu His Arg Glu
      115              120              125

Asn Val Lys Val Gly Ala Leu Ser Gly Gly Glu Gln Arg Arg Leu Asp
      130              135              140

Leu Ala Cys Ala Leu Leu Gly Asp Pro Ser Ile Leu Phe Leu Asp Glu
      145              150              155              160

Pro Thr Thr Gly Leu Asp Pro Glu Ser Arg Arg His Thr Trp Gln Leu
      165              170              175

Leu Leu Asp Leu Lys Gln Arg Gly Val Thr Met Met Leu Thr Thr His
      180              185              190

Tyr Leu Glu Glu Ala Glu Phe Leu Cys Asp Arg Ile Ala Ile Met Asn
      195              200              205

Ala Gly Glu Ile Ala Val Glu Gly Thr Leu Asp Glu Leu Val Ala Arg
      210              215              220

Glu Lys Ser Ile Ile Ser Phe Val Leu Arg Gly Gly Gln Val Glu Leu
      225              230              235              240

Pro Val Leu Ser Gly Ala Glu Ile Ile Arg Asp Asn Asn His Val Arg
      245              250              255

Ile Ala Thr Thr Thr Leu Gln Gln His Thr Leu Glu Ile Leu Thr Trp
      260              265              270

Ala Ala Glu Thr Gly Ile Ala Leu Glu Gly Phe Ala Ala Lys Pro Ala
      275              280              285

Thr Leu Glu Ser Val Phe Met Asp Ile Ala Ser Leu Glu Asn Thr Ser

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290

295

300

Leu Gln Thr Ala
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<210> 521

<211> 1131

<212> DNA

<213> Corynebacterium glutamicum

<220>

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<222> (101)..(1108)

<223> RXC01306

<400> 521

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Met Thr Glu Trp Tyr
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gtc gtt tta ccc gcc act att cta ctc atc gcg ctg tct gcg ttt ttc 163
Val Val Leu Pro Ala Thr Ile Leu Leu Ala Leu Ser Ala Phe Phe
10 15 20

gtc atc att gag ttc gct ttg ctt gca gct agg cgg aac cgg tta gag 211
Val Ile Ile Glu Phe Ala Leu Leu Ala Ala Arg Arg Asn Arg Leu Glu
25 30 35

gag act gtg gaa acc tcg cgg tct tcc cgc gct gcg ttg cga agc ctc 259
Glu Thr Val Glu Thr Ser Arg Ser Ser Arg Ala Ala Leu Arg Ser Leu
40 45 50

aat gaa ctt act ctc atg ctc gcg ggc gcg cag ttg gga atc acc atg 307
Asn Glu Leu Thr Leu Met Leu Ala Gly Ala Gln Leu Gly Ile Thr Met
55 60 65

gtg act ttc gcg ttg ggt gct atc acg aag ccg tgg gtt cat tat gct 355
Val Thr Phe Ala Leu Gly Ala Ile Thr Lys Pro Trp Val His Tyr Ala
70 75 80 85

ttg atg ccg ctc ttc gaa tgg gcg cgt ata ccg ctg gtt atg gca gat 403
Leu Met Pro Leu Phe Glu Trp Ala Arg Ile Pro Leu Val Met Ala Asp
90 95 100

gtc att gcg ttt att ttg tcg ctg ttt atc gta acg ttt ctg cac ttg 451
Val Ile Ala Phe Ile Leu Ser Leu Phe Ile Val Thr Phe Leu His Leu
105 110 115

gtc atc ggc gaa atg gct ccg aaa tcc tgg gca atc gcg cat ccg gag 499
Val Ile Gly Glu Met Ala Pro Lys Ser Trp Ala Ile Ala His Pro Glu
120 125 130

acg gca ctt cga act atc gcg att ccc gca cgg ggc ttc att aac ctg 547
Thr Ala Leu Arg Thr Ile Ala Ile Pro Ala Arg Gly Phe Ile Asn Leu
135 140 145

ttt cgt cca ttg ctg cag tgg atc aac aaa atg gcg aac gat ttg gtc 595
Phe Arg Pro Leu Leu Gln Trp Ile Asn Lys Met Ala Asn Asp Leu Val

150	155	160	165	
cgc aaa gtt ggt gaa act ccc gtt gat cga gct gca gct ggt ggc tat				643
Arg Lys Val Gly Glu Thr Pro Val Asp Arg Ala Ala Ala Gly Gly Tyr	170	175	180	
gac acc gat acc ctc cat gcc ctc att gag cat tcc cga gaa act ggc				691
Asp Thr Asp Thr Leu His Ala Leu Ile Glu His Ser Arg Glu Thr Gly	185	190	195	
gct ctg gat cag caa tcc gcc gcc caa atc agc gga att atc aag ctg				739
Ala Leu Asp Gln Gln Ser Ala Ala Gln Ile Ser Gly Ile Ile Lys Leu	200	205	210	
gat aaa atc acg gtc ggt caa acc ctg acc gca tct cca ttt acg cac				787
Asp Lys Ile Thr Val Gly Gln Thr Leu Thr Ala Ser Pro Phe Thr His	215	220	225	
agc gcc agc gcc acg gtt gct gag gtg caa gcc gca gct cag cgc agt				835
Ser Ala Ser Ala Thr Val Ala Glu Val Gln Ala Ala Ala Gln Arg Ser	230	235	240	245
ggc agc ttg cgt gtg ctt atc gac gcc ccc tcc cac ctt ttc cca cac				883
Gly Ser Leu Arg Val Leu Ile Asp Ala Pro Ser His Leu Phe Pro His	250	255	260	
gtc att cat gtg cga gac acc ctt ggt gcc tcg cca gac gag aag gct				931
Val Ile His Val Arg Asp Thr Leu Gly Ala Ser Pro Asp Glu Lys Ala	265	270	275	
tcg aag tgg tct cgc cca atc ctc acc gtt gct gag acc gac acg tta				979
Ser Lys Trp Ser Arg Pro Ile Leu Thr Val Ala Glu Thr Asp Thr Leu	280	285	290	
cac caa gcg ctg gaa tac atg cgg gag cat aac gag cag atc agt gcg				1027
His Gln Ala Leu Glu Tyr Met Arg Glu His Asn Glu Gln Ile Ser Ala	295	300	305	
gtg ctt tcc gct gat ggg aaa acg gtg ctt ggt gta ata act tgg gat				1075
Val Leu Ser Ala Asp Gly Lys Thr Val Leu Gly Val Ile Thr Trp Asp	310	315	320	325
cac atc ttg aaa tac ctg tgg cct gca tcg gtg tagctaattt gaggtgcgct				1128
His Ile Leu Lys Tyr Leu Trp Pro Ala Ser Val	330	335		
gaa				1131
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20	25	30		

Arg Asn Arg Leu Glu Glu Thr Val Glu Thr Ser Arg Ser Ser Arg Ala
 35 40 45
 Ala Leu Arg Ser Leu Asn Glu Leu Thr Leu Met Leu Ala Gly Ala Gln
 50 55 60
 Leu Gly Ile Thr Met Val Thr Phe Ala Leu Gly Ala Ile Thr Lys Pro
 65 70 75 80
 Trp Val His Tyr Ala Leu Met Pro Leu Phe Glu Trp Ala Arg Ile Pro
 85 90 95
 Leu Val Met Ala Asp Val Ile Ala Phe Ile Leu Ser Leu Phe Ile Val
 100 105 110
 Thr Phe Leu His Leu Val Ile Gly Glu Met Ala Pro Lys Ser Trp Ala
 115 120 125
 Ile Ala His Pro Glu Thr Ala Leu Arg Thr Ile Ala Ile Pro Ala Arg
 130 135 140
 Gly Phe Ile Asn Leu Phe Arg Pro Leu Leu Gln Trp Ile Asn Lys Met
 145 150 155 160
 Ala Asn Asp Leu Val Arg Lys Val Gly Glu Thr Pro Val Asp Arg Ala
 165 170 175
 Ala Ala Gly Gly Tyr Asp Thr Asp Thr Leu His Ala Leu Ile Glu His
 180 185 190
 Ser Arg Glu Thr Gly Ala Leu Asp Gln Gln Ser Ala Ala Gln Ile Ser
 195 200 205
 Gly Ile Ile Lys Leu Asp Lys Ile Thr Val Gly Gln Thr Leu Thr Ala
 210 215 220
 Ser Pro Phe Thr His Ser Ala Ser Ala Thr Val Ala Glu Val Gln Ala
 225 230 235 240
 Ala Ala Gln Arg Ser Gly Ser Leu Arg Val Leu Ile Asp Ala Pro Ser
 245 250 255
 His Leu Phe Pro His Val Ile His Val Arg Asp Thr Leu Gly Ala Ser
 260 265 270
 Pro Asp Glu Lys Ala Ser Lys Trp Ser Arg Pro Ile Leu Thr Val Ala
 275 280 285
 Glu Thr Asp Thr Leu His Gln Ala Leu Glu Tyr Met Arg Glu His Asn
 290 295 300
 Glu Gln Ile Ser Ala Val Leu Ser Ala Asp Gly Lys Thr Val Leu Gly
 305 310 315 320
 Val Ile Thr Trp Asp His Ile Leu Lys Tyr Leu Trp Pro Ala Ser Val
 325 330 335

<400> 524
Val Ser Gln Phe Arg Arg Cys Ser Arg Pro Gly Cys Gly Lys Pro Ala
1 5 10 15

Val Ala Thr Leu Thr Tyr Ala Tyr Ser Asp Ser Thr Ala Val Val Gly
 20 25 30

Pro Leu Ala Pro Ala Ala Glu Pro His Ser Trp Asp Leu Cys Glu His
 35 40 45

His Ala Glu Arg Ile Thr Ala Pro Leu Gly Trp Glu Met Leu Arg Val
 50 55 60

Asn Asp Ile Lys Val Asp Asp Asp Glu Asp Leu Thr Ala Leu Ala Gln
 65 70 75 80

Ala Val Arg Glu Ala Gly Arg Thr Val Ser Gly Leu Val Pro Glu Asp
 85 90 95

Glu Val Gly Gly Asn His Pro Val Asn Arg Ser Ala Arg Ile Ala Glu
 100 105 110

Gln Lys Val His Arg Arg Gly His Leu Tyr Val Val Pro Asp Gln Asp
 115 120 125

Glu Ser
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<210> 525
 <211> 614
 <212> DNA
 <213> *Corynebacterium glutamicum*

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 <222> (1)..(591)
 <223> RXC01372

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 Gln Asp Thr Phe Val Leu Pro Thr Leu Pro Thr Ala Ala Gly Leu Ser
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cct gcc cgc atc gtg gcg tcg ata agc act ctt tta gat ctt tta gaa 96
 Pro Ala Arg Ile Val Ala Ser Ile Ser Thr Leu Leu Asp Leu Leu Glu
 20 25 30

gca gac ccc agc att att tcc gac cgc ttg gaa cac ctc gcc gac tgc 144
 Ala Asp Pro Ser Ile Ile Ser Asp Arg Leu Glu His Leu Ala Asp Cys
 35 40 45

att gat gag gaa gtg gaa tcg cta tcg ccg gaa cgt gac gaa cta gtc 192
 Ile Asp Glu Glu Val Glu Ser Leu Ser Pro Glu Arg Asp Glu Leu Val
 50 55 60

aat ccc ggc cga aaa ctg cgc gca tac gta gat cac gca cgg atc gtg 240
 Asn Pro Gly Arg Lys Leu Arg Ala Tyr Val Asp His Ala Arg Ile Val
 65 70 75 80

cat acc ggc cga act gat gtg gga ctc gcg att gcc aac gtt atc gcc 288
 His Thr Gly Arg Thr Asp Val Gly Leu Ala Ile Ala Asn Val Ile Ala
 85 90 95

cca atc tgg acc cga cga ggc ctg gta tca gcc gtg ctg gat ttt ccc 336

Pro Ile Trp Thr Arg Arg Gly Leu Val Ser Ala Val Leu Asp Phe Pro
 100 105 110

gag ctc atg gaa tca ttg ccg gaa ctc cgc gga ccc gag cca att acc 384
 Glu Leu Met Glu Ser Leu Pro Glu Leu Arg Gly Pro Glu Pro Ile Thr
 115 120 125

gac gat ata ttc cat gac cca ttc ata gat gac gaa ccc ggg gtg gta 432
 Asp Asp Ile Phe His Asp Pro Phe Ile Asp Asp Glu Pro Gly Val Val
 130 135 140

ccg ttt agg gct gtt gtc tgg gcc gaa gag gaa ccc gga atc ccc gat 480
 Pro Phe Arg Ala Val Trp Ala Glu Glu Glu Pro Gly Ile Pro Asp
 145 150 155 160

gcc atg gcg caa agc tgc gac gga cct agc aaa ggg gcg ctg aca caa 528
 Ala Met Ala Gln Ser Cys Asp Gly Pro Ser Lys Gly Ala Leu Thr Gln
 165 170 175

gca ctg cgt ttg ctg gtg cgc gga cag tca gcc acg acc tat tcc att 576
 Ala Leu Arg Leu Leu Val Arg Gly Gln Ser Ala Thr Thr Tyr Ser Ile
 180 185 190

gaa gaa aag gac ttg taaatggagc tattggaagg ctc 614
 Glu Glu Lys Asp Leu
 195

<210> 526
 <211> 197
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 526
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Pro Ala Arg Ile Val Ala Ser Ile Ser Thr Leu Leu Asp Leu Leu Glu
 20 25 30

Ala Asp Pro Ser Ile Ile Ser Asp Arg Leu Glu His Leu Ala Asp Cys
 35 40 45

Ile Asp Glu Glu Val Glu Ser Leu Ser Pro Glu Arg Asp Glu Leu Val
 50 55 60

Asn Pro Gly Arg Lys Leu Arg Ala Tyr Val Asp His Ala Arg Ile Val
 65 70 75 80

His Thr Gly Arg Thr Asp Val Gly Leu Ala Ile Ala Asn Val Ile Ala
 85 90 95

Pro Ile Trp Thr Arg Arg Gly Leu Val Ser Ala Val Leu Asp Phe Pro
 100 105 110

Glu Leu Met Glu Ser Leu Pro Glu Leu Arg Gly Pro Glu Pro Ile Thr
 115 120 125

Asp Asp Ile Phe His Asp Pro Phe Ile Asp Asp Glu Pro Gly Val Val
 130 135 140

Pro Phe Arg Ala Val Val Trp Ala Glu Glu Glu Pro Gly Ile Pro Asp
 145 150 155 160

Ala Met Ala Gln Ser Cys Asp Gly Pro Ser Lys Gly Ala Leu Thr Gln
 165 170 175

Ala Leu Arg Leu Leu Val Arg Gly Gln Ser Ala Thr Thr Tyr Ser Ile
 180 185 190

Glu Glu Lys Asp Leu
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 <212> DNA
 <213> Corynebacterium glutamicum

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 <222> (101)..(646)
 <223> RXC01659

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tgcagattga taccgtctct ggattccgcc tgctcagtac gtg gcg ggg gtt gcg 115
 Val Ala Gly Val Ala
 1 5

cag cgt ttt gtc gac gag cgc att cac gtc ggt ttg gat tcc atg cca 163
 Gln Arg Phe Val Asp Glu Arg Ile His Val Gly Leu Asp Ser Met Pro
 10 15 20

gaa gct gtg act gct gtg tgg atg gaa tct gat tgg gtg ttg gcg gaa 211
 Glu Ala Val Thr Ala Val Trp Met Glu Ser Asp Trp Val Leu Ala Glu
 25 30 35

acc atc aag ggt tcc acg cct tcc gat tgg gaa gag att ttg cgg ccg 259
 Thr Ile Lys Gly Ser Thr Pro Ser Asp Trp Glu Glu Ile Leu Arg Pro
 40 45 50

ttg gcg ctg ctc acg gac gcg tct ttc acg ttg cca cct cgt tcc acg 307
 Leu Ala Leu Leu Thr Asp Ala Ser Phe Thr Leu Pro Pro Arg Ser Thr
 55 60 65

cgt gcg caa acc ttg gat ttg aag cat ttg gaa cca agc cgt ctg aag 355
 Arg Ala Gln Thr Leu Asp Leu Lys His Leu Glu Pro Ser Arg Leu Lys
 70 75 80 85

ccg gag cag cca gaa aag cca gcg ttt act ccc aat gct tcg gaa gaa 403
 Pro Glu Gln Pro Glu Lys Pro Ala Phe Thr Pro Asn Ala Ser Glu Glu
 90 95 100

gat ttg tct cag ccg ttg gtg atc cgc ccc gag gag ccg ttg cag atg 451
 Asp Leu Ser Gln Pro Leu Val Ile Arg Pro Glu Glu Pro Leu Gln Met
 105 110 115

ccg gtt cgc ggt gtg cag gaa agc cgc gga gtg gtc gag cca cgg tca 499
 Pro Val Arg Gly Val Gln Glu Ser Arg Gly Val Val Glu Pro Arg Ser
 120 125 130

ttg ggt gcg gat gat gtg gag tcg att gcg gag ggc gat cca gag cgt 547
 Leu Gly Ala Asp Asp Val Glu Ser Ile Ala Glu Gly Asp Pro Glu Arg
 135 140 145
 ccg agc gat ctt tat ggc acg cgt gtg ctg cgt gat ctc aat ggt cag 595
 Pro Ser Asp Leu Tyr Gly Thr Arg Val Leu Arg Asp Leu Asn Gly Gln
 150 155 160 165
 tcc agt att ttc caa gat tcc acc gac gcg gat gag cca cca aaa aag 643
 Ser Ser Ile Phe Gln Asp Ser Thr Asp Ala Asp Glu Pro Pro Lys Lys
 170 175 180
 tgg tagaaaactg gtgttttttcg gcc 669
 Trp

<210> 528

<211> 182

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 528

Val Ala Gly Val Ala Gln Arg Phe Val Asp Glu Arg Ile His Val Gly
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 20 25 30
 Trp Val Leu Ala Glu Thr Ile Lys Gly Ser Thr Pro Ser Asp Trp Glu
 35 40 45
 Glu Ile Leu Arg Pro Leu Ala Leu Leu Thr Asp Ala Ser Phe Thr Leu
 50 55 60
 Pro Pro Arg Ser Thr Arg Ala Gln Thr Leu Asp Leu Lys His Leu Glu
 65 70 75 80
 Pro Ser Arg Leu Lys Pro Glu Gln Pro Glu Lys Pro Ala Phe Thr Pro
 85 90 95
 Asn Ala Ser Glu Glu Asp Leu Ser Gln Pro Leu Val Ile Arg Pro Glu
 100 105 110
 Glu Pro Leu Gln Met Pro Val Arg Gly Val Gln Glu Ser Arg Gly Val
 115 120 125
 Val Glu Pro Arg Ser Leu Gly Ala Asp Asp Val Glu Ser Ile Ala Glu
 130 135 140
 Gly Asp Pro Glu Arg Pro Ser Asp Leu Tyr Gly Thr Arg Val Leu Arg
 145 150 155 160
 Asp Leu Asn Gly Gln Ser Ser Ile Phe Gln Asp Ser Thr Asp Ala Asp
 165 170 175
 Glu Pro Pro Lys Lys Trp
 180


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<211> 981
<212> DNA
<213> Corynebacterium glutamicum
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<222> (101)..(958)  
<223> RXC01663
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cgtggcttga gtacgcactg ccagtaaggt gtgtgatgtg atg gaa ata agt gtc 115
Met Glu Ile Ser Val
1 5

ttg atc atc gcc gca ctg atc ttg gtg gca ggc atc gta ctg tgg cgc 163
Leu Ile Ile Ala Ala Leu Ile Leu Val Ala Gly Ile Val Leu Trp Arg
10 15 20

gcg gac tcg tct aaa cag gca gct aaa aaq gct gaa tca cct gtg ggc 211
Ala Asp Ser Ser Lys Gln Ala Ala Lys Lys Ala Glu Ser Pro Val Gly
25 30 35

tca gtc gca cct gcg ccc gtg ctg gtt gaa gaa gag ccg gac cct gag 259
Ser Val Ala Pro Ala Pro Val Leu Val Glu Glu Glu Pro Asp Pro Glu
40 45 50

ttt gag cca gaa ctg gac cct gaa cca gaa gcg caa cca gaa cca gag 307
Phe Glu Pro Glu Leu Asp Pro Glu Pro Glu Ala Gln Pro Glu Pro Glu
55 60 65

ctg gaa gtt gcg cct aga ttt gcg cca gaa cca gtt caa gat ctt gag 355
Leu Glu Val Ala Pro Arg Phe Ala Pro Glu Pro Val Gln Asp Leu Glu
70 75 80 85

ccg gat cag gct gag gac att tat ttt gat gat tcc cct gaa ctc gat 403
Pro Asp Gln Ala Glu Asp Ile Tyr Phe Asp Asp Ser Pro Glu Leu Asp
90 95 100

gct gat gtt gaa aat gcc ttg gct gag ctt act gag gta gaa gac tac 451
Ala Asp Val Glu Asn Ala Leu Ala Glu Leu Thr Glu Val Glu Asp Tyr
105 110 115

ccg gaa gag cca gtg cag tct gag caa cct caa gcc cct gcc acg gcg 499
Pro Glu Glu Pro Val Gln Ser Glu Gln Pro Gln Ala Pro Ala Thr Ala
120 125 130

gag gta gct gcg gac gag gag caa cgg ggc gtc gat aag cat tcg ttt 547
Glu Val Ala Ala Asp Glu Glu Gln Arg Gly Val Asp Lys His Ser Phe
135 140 145

ttg agc tct ttg cct ggt tcg cag cgc cgg gag cgc cga aac tgg gcg 595
Leu Ser Ser Leu Pro Gly Ser Gln Arg Arg Glu Arg Arg Asn Trp Ala
150 155 160 165

gcg aag cac cac ttc gat ttc atc aag gaa gat gcc ttt ttg acc gat 643
Ala Lys His His Phe Asp Phe Ile Lys Glu Asp Ala Phe Leu Thr Asp
170 175 180

gaa tgg tca agg ggt gcg gca tcg act ggt gcc gtt gca cgt gat gtg 691
 Glu Trp Ser Arg Gly Ala Ala Ser Thr Gly Ala Val Ala Arg Asp Val
 185 190 195

gtc agt ggc atg gct gaa gga tat gaa acg cat ctg gtg gat ttg gcg 739
 Val Ser Gly Met Ala Glu Gly Tyr Glu Thr His Leu Val Asp Leu Ala
 200 205 210

ggc gtg ccc gtg atg gcg atg cgc cgt gga att acc tct gac gtg gtc 787
 Gly Val Pro Val Met Ala Met Arg Arg Gly Ile Thr Ser Asp Val Val
 215 220 225

att gat gcg cgc cgc ggt gag cag cct gcc gat cca gag cgt gaa gaa 835
 Ile Asp Ala Arg Arg Gly Glu Gln Pro Ala Asp Pro Glu Arg Glu Glu
 230 235 240 245

tct gat gat tta gtc gag att gat acc gtc tct gga ttc cgc ctg ctc 883
 Ser Asp Asp Leu Val Glu Ile Asp Thr Val Ser Gly Phe Arg Leu Leu
 250 255 260

agt acg tgg cgg ggg ttg cgc agc gtt ttg tcg acg agc gca ttc acg 931
 Ser Thr Trp Arg Gly Leu Arg Ser Val Leu Ser Thr Ser Ala Phe Thr
 265 270 275

tcg gtt tgg att cca tgc cag aag ctg tgactgctgt gtggatggaa 978
 Ser Val Trp Ile Pro Cys Gln Lys Leu
 280 285

tct 981

<210> 530

<211> 286

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 530

Met Glu Ile Ser Val Leu Ile Ile Ala Ala Leu Ile Leu Val Ala Gly
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Ile Val Leu Trp Arg Ala Asp Ser Ser Lys Gln Ala Ala Lys Lys Ala
 20 25 30

Glu Ser Pro Val Gly Ser Val Ala Pro Ala Pro Val Leu Val Glu Glu
 35 40 45

Glu Pro Asp Pro Glu Phe Glu Pro Glu Leu Asp Pro Glu Pro Glu Ala
 50 55 60

Gln Pro Glu Pro Glu Leu Glu Val Ala Pro Arg Phe Ala Pro Glu Pro
 65 70 75 80

Val Gln Asp Leu Glu Pro Asp Gln Ala Glu Asp Ile Tyr Phe Asp Asp
 85 90 95

Ser Pro Glu Leu Asp Ala Asp Val Glu Asn Ala Leu Ala Glu Leu Thr
 100 105 110

Glu Val Glu Asp Tyr Pro Glu Glu Pro Val Gln Ser Glu Gln Pro Gln
 115 120 125

Ala Pro Ala Thr Ala Glu Val Ala Ala Asp Glu Glu Gln Arg Gly Val
 130 135 140

Asp Lys His Ser Phe Leu Ser Ser Leu Pro Gly Ser Gln Arg Arg Glu
 145 150 155 160

Arg Arg Asn Trp Ala Ala Lys His His Phe Asp Phe Ile Lys Glu Asp
 165 170 175

Ala Phe Leu Thr Asp Glu Trp Ser Arg Gly Ala Ala Ser Thr Gly Ala
 180 185 190

Val Ala Arg Asp Val Val Ser Gly Met Ala Glu Gly Tyr Glu Thr His
 195 200 205

Leu Val Asp Leu Ala Gly Val Pro Val Met Ala Met Arg Arg Gly Ile
 210 215 220

Thr Ser Asp Val Val Ile Asp Ala Arg Arg Gly Glu Gln Pro Ala Asp
 225 230 235 240

Pro Glu Arg Glu Glu Ser Asp Asp Leu Val Glu Ile Asp Thr Val Ser
 245 250 255

Gly Phe Arg Leu Leu Ser Thr Trp Arg Gly Leu Arg Ser Val Leu Ser
 260 265 270

Thr Ser Ala Phe Thr Ser Val Trp Ile Pro Cys Gln Lys Leu
 275 280 285

<210> 531
 <211> 1545
 <212> DNA
 <213> Corynebacterium glutamicum

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 <222> (101)..(1522)
 <223> RXC01693

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gtcccaacaa ttgccagaac ccgaacacta ggcttgaacc atg aat act gca cct 115
 Met Asn Thr Ala Pro
 1 5

ttc aaa ctc gaa gct gac ttc gca tca gcc ctg ccc acc atg gca gcc 163
 Phe Lys Leu Glu Ala Asp Phe Ala Ser Ala Leu Pro Thr Met Ala Ala
 10 15 20

ccc tgg caa ggt gag gaa gcc ccc aac cct gag ctc gtg att tta aat 211
 Pro Trp Gln Gly Glu Glu Ala Pro Asn Pro Glu Leu Val Ile Leu Asn
 25 30 35

gac gac ctc gcc tac agc ctc ggg ctt gat ccg aca tgg ctt cgc aca 259
 Asp Asp Leu Ala Tyr Ser Leu Gly Leu Asp Pro Thr Trp Leu Arg Thr
 40 45 50

cct gag ggc gtt caa ttt ctt ctc gga ctc aac ccc gag ccc tta aca 307

Pro	Glu	Gly	Val	Gln	Phe	Leu	Leu	Gly	Leu	Asn	Pro	Glu	Pro	Leu	Thr		
	55					60					65						
aaa	gca	gtt	gcg	cag	gcc	tat	tcc	ggc	cac	caa	ttc	gga	cag	ttt	gtg	355	
Lys	Ala	Val	Ala	Gln	Ala	Tyr	Ser	Gly	His	Gln	Phe	Gly	Gln	Phe	Val		
70					75					80					85		
gca	agc	ctt	ggt	gat	ggc	cga	gcg	ctt	ctt	ctc	ggc	gaa	gcc	cgc	tca	403	
Ala	Ser	Leu	Gly	Asp	Gly	Arg	Ala	Leu	Leu	Leu	Gly	Glu	Ala	Arg	Ser		
				90					95					100			
gct	gac	ggc	gta	ctg	cat	gat	atc	cac	ctc	aaa	gga	tct	gga	cga	acc	451	
Ala	Asp	Gly	Val	Leu	His	Asp	Ile	His	Leu	Lys	Gly	Ser	Gly	Arg	Thr		
			105					110					115				
caa	ttc	tcc	cga	gga	gcc	gat	gga	cgc	gcc	gtc	ctt	ggc	ccc	gtc	tta	499	
Gln	Phe	Ser	Arg	Gly	Ala	Asp	Gly	Arg	Ala	Val	Leu	Gly	Pro	Val	Leu		
		120					125					130					
cgc	gaa	tac	atc	atc	tcc	gaa	gcg	atg	cat	gca	ctt	ggt	ggt	ccc	acc	547	
Arg	Glu	Tyr	Ile	Ile	Ser	Glu	Ala	Met	His	Ala	Leu	Gly	Val	Pro	Thr		
	135					140					145						
acc	agg	tca	ctt	gca	gta	att	agc	acc	ggt	agg	aaa	atc	caa	cga	gga	595	
Thr	Arg	Ser	Leu	Ala	Val	Ile	Ser	Thr	Gly	Arg	Lys	Ile	Gln	Arg	Gly		
150					155					160					165		
agc	gta	gcc	cca	ggc	gca	gtc	ctt	ggt	cga	gta	gca	acc	agc	ctc	att	643	
Ser	Val	Ala	Pro	Gly	Ala	Val	Leu	Val	Arg	Val	Ala	Thr	Ser	Leu	Ile		
				170					175					180			
cga	gtc	gga	tcc	ttc	caa	tac	tcc	aac	atc	tct	ggt	ggc	atc	gaa	cta	691	
Arg	Val	Gly	Ser	Phe	Gln	Tyr	Ser	Asn	Ile	Ser	Gly	Gly	Ile	Glu	Leu		
			185					190					195				
tct	caa	cac	ctg	gcg	aac	tat	acg	atc	acc	agg	cat	ttc	cct	tcg	ttg	739	
Ser	Gln	His	Leu	Ala	Asn	Tyr	Thr	Ile	Thr	Arg	His	Phe	Pro	Ser	Leu		
		200					205					210					
gta	gct	gaa	cta	tcc	gca	cca	acc	ccc	gca	act	tat	gta	tca	ctg	ttt	787	
Val	Ala	Glu	Leu	Ser	Ala	Pro	Thr	Pro	Ala	Thr	Tyr	Val	Ser	Leu	Phe		
	215					220					225						
aaa	gcg	att	ctt	cag	cgc	caa	gca	gac	acc	ggt	gga	aaa	tgg	acc	agg	835	
Lys	Ala	Ile	Leu	Gln	Arg	Gln	Ala	Asp	Thr	Val	Gly	Lys	Trp	Thr	Arg		
230					235					240					245		
ctg	ggt	ttc	ggt	cac	gga	gcc	ctc	aac	aca	gac	aac	acg	ttg	ata	tcc	883	
Leu	Gly	Phe	Val	His	Gly	Ala	Leu	Asn	Thr	Asp	Asn	Thr	Leu	Ile	Ser		
				250					255					260			
gga	gaa	act	ggt	gac	tac	ggc	cca	tgc	gct	ttc	atg	gag	cgc	tac	cgt	931	
Gly	Glu	Thr	Val	Asp	Tyr	Gly	Pro	Cys	Ala	Phe	Met	Glu	Arg	Tyr	Arg		
			265				270						275				
ggc	gac	gcg	aaa	ttt	agc	tcc	atc	gac	act	tat	ggt	cgc	tac	aaa	ttt	979	
Gly	Asp	Ala	Lys	Phe	Ser	Ser	Ile	Asp	Thr	Tyr	Gly	Arg	Tyr	Lys	Phe		
		280					285					290					
gaa	aac	caa	cct	atg	atc	ctc	gga	tgg	aac	atg	gcc	cgc	ctc	gta	gaa	1027	
Glu	Asn	Gln	Pro	Met	Ile	Leu	Gly	Trp	Asn	Met	Ala	Arg	Leu	Val	Glu		

	295						300				305							
acc ctc ctc cca ctc ctg ggc gcc aca cca gac gaa ggc atg aca gca																		1075
Thr Leu Leu Pro Leu Leu Gly Ala Thr Pro Asp Glu Gly Met Thr Ala																		
310	315						320				325							
gcc caa gaa gct ctc gta gaa ttc gat gac ctc tgc gaa caa gca atc																		1123
Ala Gln Glu Ala Leu Val Glu Phe Asp Asp Leu Cys Glu Gln Ala Ile																		
	330						335				340							
cga aaa gaa ttc gcc act gca ctg ggc ctt gac gag tca gac acc ggc																		1171
Arg Lys Glu Phe Ala Thr Ala Leu Gly Leu Asp Glu Ser Asp Thr Gly																		
	345						350				355							
acg gta gag cag ttc cgt gaa ctg ctc tac ctc cat aac ccc gac atc																		1219
Thr Val Glu Gln Phe Arg Glu Leu Leu Tyr Leu His Asn Pro Asp Ile																		
	360						365				370							
acc acg ctg ctg cgc gca ctc acc gac aac acc gca cca ccg agt ggc																		1267
Thr Thr Leu Leu Arg Ala Leu Thr Asp Asn Thr Ala Pro Pro Ser Gly																		
	375						380				385							
ttt gaa gca ttc gtt cac gac tgg aaa acc caa gac cca gat atc gaa																		1315
Phe Glu Ala Phe Val His Asp Trp Lys Thr Gln Asp Pro Asp Ile Glu																		
	395						400				405							
gca atg cga gca gtaaat cca ctt ttc att cca cgc aat cac ctc gtg																		1363
Ala Met Arg Ala Val Asn Pro Leu Phe Ile Pro Arg Asn His Leu Val																		
	410						415				420							
gaa gct gct ctc gca gac gca gtt gaa ggg aat cta gaa aag ttc cac																		1411
Glu Ala Ala Leu Ala Asp Ala Val Glu Gly Asn Leu Glu Lys Phe His																		
	425						430				435							
gaa ctc ctc gct gct gtc acc aat cct ttt gat cca act gcg ggc ccc																		1459
Glu Leu Leu Ala Ala Val Thr Asn Pro Phe Asp Pro Thr Ala Gly Pro																		
	440						445				450							
gat gaa cta cgc ctg cca agc gaa gaa gga ttt gaa gaa gac tac atg																		1507
Asp Glu Leu Arg Leu Pro Ser Glu Glu Gly Phe Glu Glu Asp Tyr Met																		
	455						460				465							
acc ttc tgc ggt acc taggacagat ggtggggcag acg															1545			
Thr Phe Cys Gly Thr																		
470																		

<210> 532

<211> 474

<212> PRT

<213> Corynebacterium glutamicum

<400> 532

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Leu Val Ile Leu Asn Asp Asp Leu Ala Tyr Ser Leu Gly Leu Asp Pro
35 40 45

Thr Trp Leu Arg Thr Pro Glu Gly Val Gln Phe Leu Leu Gly Leu Asn
 50 55 60
 Pro Glu Pro Leu Thr Lys Ala Val Ala Gln Ala Tyr Ser Gly His Gln
 65 70 75 80
 Phe Gly Gln Phe Val Ala Ser Leu Gly Asp Gly Arg Ala Leu Leu Leu
 85 90 95
 Gly Glu Ala Arg Ser Ala Asp Gly Val Leu His Asp Ile His Leu Lys
 100 105 110
 Gly Ser Gly Arg Thr Gln Phe Ser Arg Gly Ala Asp Gly Arg Ala Val
 115 120 125
 Leu Gly Pro Val Leu Arg Glu Tyr Ile Ile Ser Glu Ala Met His Ala
 130 135 140
 Leu Gly Val Pro Thr Thr Arg Ser Leu Ala Val Ile Ser Thr Gly Arg
 145 150 155 160
 Lys Ile Gln Arg Gly Ser Val Ala Pro Gly Ala Val Leu Val Arg Val
 165 170 175
 Ala Thr Ser Leu Ile Arg Val Gly Ser Phe Gln Tyr Ser Asn Ile Ser
 180 185 190
 Gly Gly Ile Glu Leu Ser Gln His Leu Ala Asn Tyr Thr Ile Thr Arg
 195 200 205
 His Phe Pro Ser Leu Val Ala Glu Leu Ser Ala Pro Thr Pro Ala Thr
 210 215 220
 Tyr Val Ser Leu Phe Lys Ala Ile Leu Gln Arg Gln Ala Asp Thr Val
 225 230 235 240
 Gly Lys Trp Thr Arg Leu Gly Phe Val His Gly Ala Leu Asn Thr Asp
 245 250 255
 Asn Thr Leu Ile Ser Gly Glu Thr Val Asp Tyr Gly Pro Cys Ala Phe
 260 265 270
 Met Glu Arg Tyr Arg Gly Asp Ala Lys Phe Ser Ser Ile Asp Thr Tyr
 275 280 285
 Gly Arg Tyr Lys Phe Glu Asn Gln Pro Met Ile Leu Gly Trp Asn Met
 290 295 300
 Ala Arg Leu Val Glu Thr Leu Leu Pro Leu Leu Gly Ala Thr Pro Asp
 305 310 315 320
 Glu Gly Met Thr Ala Ala Gln Glu Ala Leu Val Glu Phe Asp Asp Leu
 325 330 335
 Cys Glu Gln Ala Ile Arg Lys Glu Phe Ala Thr Ala Leu Gly Leu Asp
 340 345 350
 Glu Ser Asp Thr Gly Thr Val Glu Gln Phe Arg Glu Leu Leu Tyr Leu
 355 360 365

His Asn Pro Asp Ile Thr Thr Leu Leu Arg Ala Leu Thr Asp Asn Thr
 370 375 380
 Ala Pro Pro Ser Gly Phe Glu Ala Phe Val His Asp Trp Lys Thr Gln
 385 390 395 400
 Asp Pro Asp Ile Glu Ala Met Arg Ala Val Asn Pro Leu Phe Ile Pro
 405 410 415
 Arg Asn His Leu Val Glu Ala Ala Leu Ala Asp Ala Val Glu Gly Asn
 420 425 430
 Leu Glu Lys Phe His Glu Leu Leu Ala Ala Val Thr Asn Pro Phe Asp
 435 440 445
 Pro Thr Ala Gly Pro Asp Glu Leu Arg Leu Pro Ser Glu Glu Gly Phe
 450 455 460
 Glu Glu Asp Tyr Met Thr Phe Cys Gly Thr
 465 470

<210> 533
 <211> 1236
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1213)
 <223> RXC01703

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 cgcgagggtt tgggggtctgc ctcgaacaaa tcttggggttt gtg gca tgg cca tcc 115
 Val Ala Trp Pro Ser
 1 5
 aac gcc aaa gaa aaa ctg ttt atc cac tgg cac tac tgg tgg caa gcg 163
 Asn Ala Lys Glu Lys Leu Phe Ile His Trp His Tyr Trp Trp Gln Ala
 10 15 20
 cat tat cta gac tgc ctg gtg gat gct gct cgt cga cgc acc aca aag 211
 His Tyr Leu Asp Cys Leu Val Asp Ala Ala Arg Arg Arg Thr Thr Lys
 25 30 35
 gcc cgt cgc gac cgc atc agg gac acc atc cgc ggc att tcg gtg cgc 259
 Ala Arg Arg Asp Arg Ile Arg Asp Thr Ile Arg Gly Ile Ser Val Arg
 40 45 50
 aat gtg ggc aag ctg acc tcg aat cgt tat tac gac gac aaa gct tgg 307
 Asn Val Gly Lys Leu Thr Ser Asn Arg Tyr Tyr Asp Asp Lys Ala Trp
 55 60 65
 ctg gcc ctt gct ctt ggg cgt gcc gga aaa gtg cga aag gtg cgc aca 355
 Leu Ala Leu Ala Leu Gly Arg Ala Gly Lys Val Arg Lys Val Arg Thr
 70 75 80 85
 cca aaa tca ttg ccc tcg ttg gaa caa aac atc gtc gat ggc att gat 403
 Pro Lys Ser Leu Pro Ser Leu Glu Gln Asn Ile Val Asp Gly Ile Asp

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gtt ccc tcc aac ggt cct gct gcg atc atg atg gcc cgc acc gac cgt Val Pro Ser Asn Gly Pro Ala Ala Ile Met Met Ala Arg Thr Asp Arg 120 125 130			499
ttg gac gag gct atg aaa atc acc gat tgg att ttt gac aac ctg atc Leu Asp Glu Ala Met Lys Ile Thr Asp Trp Ile Phe Asp Asn Leu Ile 135 140 145			547
gat ggc gac ggc ctt gtg atg gac gga ttg cgc atg cgc atg cac gga Asp Gly Asp Gly Leu Val Met Asp Gly Leu Arg Met Arg Met His Gly 150 155 160 165			595
cct gag ctt gtc cgt tcc atc cac ccg tat tgc caa ggt gtc gcc att Pro Glu Leu Val Arg Ser Ile His Pro Tyr Cys Gln Gly Val Ala Ile 170 175 180			643
ggt gcg tgt ttg gaa att gct ctc aaa ctg cgt gag cgc gca ggc ttg Gly Ala Cys Leu Glu Ile Ala Leu Lys Leu Arg Glu Arg Ala Gly Leu 185 190 195			691
acc act act gtg gtg gat cac tgg tcg gat gcc gat aag gca gaa gac Thr Thr Thr Val Val Asp His Trp Ser Asp Ala Asp Lys Ala Glu Asp 200 205 210			739
tcc ctc aaa tac ttt gca cac atc cac gct gtg gtt cag gct gtg tcg Ser Leu Lys Tyr Phe Ala His Ile His Ala Val Val Gln Ala Val Ser 215 220 225			787
cgg aag atg acc aac ttc cac ggc gtt att gat tgg gac acc ggt gac Arg Lys Met Thr Asn Phe His Gly Val Ile Asp Trp Asp Thr Gly Asp 230 235 240 245			835
ggc gac ggc ggt ttg ttc aag ggc att ttg gtc cgc tat tta gct gat Gly Asp Gly Gly Leu Phe Lys Gly Ile Leu Val Arg Tyr Leu Ala Asp 250 255 260			883
gtg gcc atc cgc ctg cct gac gat tca cca acc aac cgg gaa acc aaa Val Ala Ile Arg Leu Pro Asp Asp Ser Pro Thr Asn Arg Glu Thr Lys 265 270 275			931
aag att gca gca cgc ctg gta ctg gaa tcg gcg gaa agc gta tgg aac Lys Ile Ala Ala Arg Leu Val Leu Glu Ser Ala Glu Ser Val Trp Asn 280 285 290			979
cac cga ttg gaa gtt gat ggc ctt ccg gta ttc gcc aca gac tgg aca His Arg Leu Glu Val Asp Gly Leu Pro Val Phe Ala Thr Asp Trp Thr 295 300 305			1027
acg gat gca cgc ctg cca caa aac ttt ggt ttg agt tcc tct agt ttg Thr Asp Ala Arg Leu Pro Gln Asn Phe Gly Leu Ser Ser Ser Ser Leu 310 315 320 325			1075
agc gat ctg gtg agt gtt gtg cgc gtg gat gaa cgt gat ctg tcc gtg Ser Asp Leu Val Ser Val Val Arg Val Asp Glu Arg Asp Leu Ser Val 330 335 340			1123

caa ttg tcc ggt tgg atg ctc atg gaa gca gca gcg aaa gtg gcc gaa 1171
 Gln Leu Ser Gly Trp Met Leu Met Glu Ala Ala Ala Lys Val Ala Glu
 345 350 355

gaa ctg gaa aac aac ggc aat agt tac acc ggt cgc tcc cga 1213
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tagccccgat agtgtatgtg ctg 1236

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 <213> Corynebacterium glutamicum

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Tyr Trp Trp Gln Ala His Tyr Leu Asp Cys Leu Val Asp Ala Ala Arg
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Arg Arg Thr Thr Lys Ala Arg Arg Asp Arg Ile Arg Asp Thr Ile Arg
 35 40 45

Gly Ile Ser Val Arg Asn Val Gly Lys Leu Thr Ser Asn Arg Tyr Tyr
 50 55 60

Asp Asp Lys Ala Trp Leu Ala Leu Ala Leu Gly Arg Ala Gly Lys Val
 65 70 75 80

Arg Lys Val Arg Thr Pro Lys Ser Leu Pro Ser Leu Glu Gln Asn Ile
 85 90 95

Val Asp Gly Ile Asp Ser Leu Thr Gly Val Leu Pro Trp Arg Ser Gly
 100 105 110

Glu Thr Phe Tyr Asn Val Pro Ser Asn Gly Pro Ala Ala Ile Met Met
 115 120 125

Ala Arg Thr Asp Arg Leu Asp Glu Ala Met Lys Ile Thr Asp Trp Ile
 130 135 140

Phe Asp Asn Leu Ile Asp Gly Asp Gly Leu Val Met Asp Gly Leu Arg
 145 150 155 160

Met Arg Met His Gly Pro Glu Leu Val Arg Ser Ile His Pro Tyr Cys
 165 170 175

Gln Gly Val Ala Ile Gly Ala Cys Leu Glu Ile Ala Leu Lys Leu Arg
 180 185 190

Glu Arg Ala Gly Leu Thr Thr Thr Val Val Asp His Trp Ser Asp Ala
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Asp Lys Ala Glu Asp Ser Leu Lys Tyr Phe Ala His Ile His Ala Val
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Val Gln Ala Val Ser Arg Lys Met Thr Asn Phe His Gly Val Ile Asp

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<211> 800
<212> DNA
<213> *Corynebacterium glutamicum*

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<223> RXC02254
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1 5 10 15																
cgc ttc ggt gga cat ggt gcg cta gct ggt cac gcc ttg gga aac ctc	96															
Arg Phe Gly Gly His Gly Ala Leu Ala Gly His Ala Leu Gly Asn Leu																
20 25 30																
gtg atc gcg gcg ttg acc gac att ttg ggc acc tcc cag cat gcg ctt	144															
Val Ile Ala Ala Leu Thr Asp Ile Leu Gly Thr Ser Gln His Ala Leu																
35 40 45																
gat caa atc gct caa ctc gct gga gcc aaa gga cgc atc atc ccg gta	192															
Asp Gln Ile Ala Gln Leu Ala Gly Ala Lys Gly Arg Ile Ile Pro Val																
50 55 60																
tgt gct gaa cct ttg gat ctt gaa gcg gaa gta tca ggt cta gac tct	240															
Cys Ala Glu Pro Leu Asp Leu Glu Ala Glu Val Ser Gly Leu Asp Ser																
65 70 75 80																

gat gct cga gtc atg cgt caa gtt cgt ggt caa gtg gcg gta gct gca 288
Asp Ala Arg Val Met Arg Gln Val Arg Gly Gln Val Ala Val Ala Ala
85 90 95

acc ccc ggg cag gtg cga cgc gtt cga atc att ccg gac aat cca gaa 336
Thr Pro Gly Gln Val Arg Arg Val Arg Ile Ile Pro Asp Asn Pro Glu
100 105 110

ccg aac ccc gct gcc atc gag gcc att ctc gat gca gat ttg gtc acc 384
Pro Asn Pro Ala Ala Ile Glu Ala Ile Leu Asp Ala Asp Leu Val Thr
115 120 125

ctt ggc cca ggt tcc tgg ttc tcc tct gtg att cca cac att ttg gtc 432
Leu Gly Pro Gly Ser Trp Phe Ser Ser Val Ile Pro His Ile Leu Val
130 135 140

cca ggg atc gtt gat gcc ttg gcg cag aca aaa gca acc aaa acc gtg 480
Pro Gly Ile Val Asp Ala Leu Ala Gln Thr Lys Ala Thr Lys Thr Val
145 150 155 160

gtg tta aac ctg acg tcc gag cca ggg gag acc gcg gga ttc tct gca 528
Val Leu Asn Leu Thr Ser Glu Pro Gly Glu Thr Ala Gly Phe Ser Ala
165 170 175

gaa cga cac atc cat gtg ctc cgc cag cat gct cga aac ctt cag gtt 576
Glu Arg His Ile His Val Leu Arg Gln His Ala Arg Asn Leu Gln Val
180 185 190

gac caa gtc att gtc gat gcc aag aca ctg tcc tca caa acc gaa cgc 624
Asp Gln Val Ile Val Asp Ala Lys Thr Leu Ser Ser Gln Thr Glu Arg
195 200 205

aat cat gta gaa cga gct gct cgc acc ctt ggt gca gaa gtc tcc ttc 672
Asn His Val Glu Arg Ala Ala Arg Thr Leu Gly Ala Glu Val Ser Phe
210 215 220

cat gat gtc cag gct gaa gat ggc cgt ggt cga ttc acc agt att cac 720
His Asp Val Gln Ala Glu Asp Gly Arg Gly Arg Phe Thr Ser Ile His
225 230 235 240

gat cca gca aag ctg tgt gca gcg ttg ctg gca agt ttt gct gga gca 768
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Arg Lys Arg

<210> 536

<211> 259

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 536

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Arg Phe Gly Gly His Gly Ala Leu Ala Gly His Ala Leu Gly Asn Leu
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Val Ile Ala Ala Leu Thr Asp Ile Leu Gly Thr Ser Gln His Ala Leu
 35 40 45
 Asp Gln Ile Ala Gln Leu Ala Gly Ala Lys Gly Arg Ile Ile Pro Val
 50 55 60
 Cys Ala Glu Pro Leu Asp Leu Glu Ala Glu Val Ser Gly Leu Asp Ser
 65 70 75 80
 Asp Ala Arg Val Met Arg Gln Val Arg Gly Gln Val Ala Val Ala Ala
 85 90 95
 Thr Pro Gly Gln Val Arg Arg Val Arg Ile Ile Pro Asp Asn Pro Glu
 100 105 110
 Pro Asn Pro Ala Ala Ile Glu Ala Ile Leu Asp Ala Asp Leu Val Thr
 115 120 125
 Leu Gly Pro Gly Ser Trp Phe Ser Ser Val Ile Pro His Ile Leu Val
 130 135 140
 Pro Gly Ile Val Asp Ala Leu Ala Gln Thr Lys Ala Thr Lys Thr Val
 145 150 155 160
 Val Leu Asn Leu Thr Ser Glu Pro Gly Glu Thr Ala Gly Phe Ser Ala
 165 170 175
 Glu Arg His Ile His Val Leu Arg Gln His Ala Arg Asn Leu Gln Val
 180 185 190
 Asp Gln Val Ile Val Asp Ala Lys Thr Leu Ser Ser Gln Thr Glu Arg
 195 200 205
 Asn His Val Glu Arg Ala Ala Arg Thr Leu Gly Ala Glu Val Ser Phe
 210 215 220
 His Asp Val Gln Ala Glu Asp Gly Arg Gly Arg Phe Thr Ser Ile His
 225 230 235 240
 Asp Pro Ala Lys Leu Cys Ala Ala Leu Leu Ala Ser Phe Ala Gly Ala
 245 250 255
 Arg Lys Arg

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 <212> DNA
 <213> Corynebacterium glutamicum

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 <222> (101)..(1036)
 <223> RXC02255

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 Val Ala Lys Asn Ser

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gtt	cgt	gct	gcg	gaa	gtg	tct	gca	att	tta	agg	ttt	gct	ggt	gag	atg	163															
Val	Arg	Ala	Ala	Glu	Val	Ser	Ala	Ile	Leu	Arg	Phe	Ala	Gly	Glu	Met																
				10					15					20																	
caa	gct	gtc	ggc	ggc	aag	ctg	gtc	atc	gaa	gca	aat	ttg	gac	agc	atg	211															
Gln	Ala	Val	Gly	Gly	Lys	Leu	Val	Ile	Glu	Ala	Asn	Leu	Asp	Ser	Met																
				25					30					35																	
caa	gtc	ggt	atg	agg	ctt	cag	gag	ttt	atc	caa	ggt	ttg	tac	aac	tct	259															
Gln	Val	Gly	Met	Arg	Leu	Gln	Glu	Phe	Ile	Gln	Gly	Leu	Tyr	Asn	Ser																
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cga	gtc	gat	gtg	cac	acc	gtg	aac	ccg	act	gtg	agc	agg	aaa	acg	cca	307															
Arg	Val	Asp	Val	His	Thr	Val	Asn	Pro	Thr	Val	Ser	Arg	Lys	Thr	Pro																
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cgg	tat	ttg	gtg	cgc	atc	att	gac	aat	gcc	gat	gaa	att	gcg	cga	cgc	355															
Arg	Tyr	Leu	Val	Arg	Ile	Ile	Asp	Asn	Ala	Asp	Glu	Ile	Ala	Arg	Arg																
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acc	gga	ctg	gtc	acc	agg	tct	gga	cat	gtg	ggt	aaa	ggt	cta	gcg	cct	403															
Thr	Gly	Leu	Val	Thr	Arg	Ser	Gly	His	Val	Val	Lys	Gly	Leu	Ala	Pro																
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tct	gtg	gtc	agc	gga	aca	atc	agt	gac	gct	gaa	gct	gca	tgg	cgc	ggt	451															
Ser	Val	Val	Ser	Gly	Thr	Ile	Ser	Asp	Ala	Glu	Ala	Ala	Trp	Arg	Gly																
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gcg	ttt	cta	gcc	aat	gga	tct	tta	agt	gat	cca	ggt	cgt	tcc	tct	tcg	499															
Ala	Phe	Leu	Ala	Asn	Gly	Ser	Leu	Ser	Asp	Pro	Gly	Arg	Ser	Ser	Ser																
				120					125					130																	
ttg	gag	gtg	ttg	tgt	cct	ggt	caa	gaa	tca	gca	ttg	gca	ctg	gtt	gga	547															
Leu	Glu	Val	Leu	Cys	Pro	Gly	Gln	Glu	Ser	Ala	Leu	Ala	Leu	Val	Gly																
				135					140					145																	
tgt	gcg	cga	aga	att	ggg	atc	gcg	gcg	aaa	acg	aaa	gat	tct	cga	gga	595															
Cys	Ala	Arg	Arg	Ile	Gly	Ile	Ala	Ala	Lys	Thr	Lys	Asp	Ser	Arg	Gly																
				150					155					160																	
ttt	gat	cgc	gtc	aat	gtt	cgt	gat	gcg	gaa	gca	att	ggg	gca	ctg	ctc	643															
Phe	Asp	Arg	Val	Asn	Val	Arg	Asp	Ala	Glu	Ala	Ile	Gly	Ala	Leu	Leu																
				170					175					180																	
act	cga	atg	ggt	gcc	cag	aaa	act	cgc	atg	ttg	tgg	gaa	gaa	aaa	cgc	691															
Thr	Arg	Met	Gly	Ala	Gln	Lys	Thr	Arg	Met	Leu	Trp	Glu	Glu	Lys	Arg																
				185					190					195																	
atc	aag	cgg	gaa	agt	cga	act	ccg	caa	acc	ggg	ttg	gcc	aac	ttc	gac	739															
Ile	Lys	Arg	Glu	Ser	Arg	Thr	Pro	Gln	Thr	Gly	Leu	Ala	Asn	Phe	Asp																
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gat	gcc	aat	ctg	cgc	agg	tca	gcc	cga	gca	gca	gtt	gcc	gct	gca	gcg	787															
Asp	Ala	Asn	Leu	Arg	Arg	Ser	Ala	Arg	Ala	Ala	Val	Ala	Ala	Ala	Ala																
				215					220					225																	
agg	gta	gaa	cgc	gcc	atg	aag	att	ctt	ggt	gat	gat	gtt	cct	gag	cat	835															
Arg	Val	Glu	Arg	Ala	Met	Lys	Ile	Leu	Gly	Asp	Asp	Val	Pro	Glu	His																
				230					235					240																	

ttg gct gag gct gga cag ctg cgt gtg cag cac cgt cag gca tcg ttg 883
 Leu Ala Glu Ala Gly Gln Leu Arg Val Gln His Arg Gln Ala Ser Leu
 250 255 260
 gag gag ttg ggc cgg ttg gct gat cct caa atg acc aag gat gct gtg 931
 Glu Glu Leu Gly Arg Leu Ala Asp Pro Gln Met Thr Lys Asp Ala Val
 265 270 275
 gcc ggt cgt att cgt cgt ctt ttg acg atg gca gat aag cgc gcc gaa 979
 Ala Gly Arg Ile Arg Arg Leu Leu Thr Met Ala Asp Lys Arg Ala Glu
 280 285 290
 gat ctg aag att cct gat aca aat tct gtt gtg acg gaa gat ttg ttg 1027
 Asp Leu Lys Ile Pro Asp Thr Asn Ser Val Val Thr Glu Asp Leu Leu
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 gaa gaa att tagatgattg aagcctaaaa acg 1059
 Glu Glu Ile
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<210> 538

<211> 312

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 538

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 Asn Leu Asp Ser Met Gln Val Gly Met Arg Leu Gln Glu Phe Ile Gln
 35 40 45
 Gly Leu Tyr Asn Ser Arg Val Asp Val His Thr Val Asn Pro Thr Val
 50 55 60
 Ser Arg Lys Thr Pro Arg Tyr Leu Val Arg Ile Ile Asp Asn Ala Asp
 65 70 75 80
 Glu Ile Ala Arg Arg Thr Gly Leu Val Thr Arg Ser Gly His Val Val
 85 90 95
 Lys Gly Leu Ala Pro Ser Val Val Ser Gly Thr Ile Ser Asp Ala Glu
 100 105 110
 Ala Ala Trp Arg Gly Ala Phe Leu Ala Asn Gly Ser Leu Ser Asp Pro
 115 120 125
 Gly Arg Ser Ser Ser Leu Glu Val Leu Cys Pro Gly Gln Glu Ser Ala
 130 135 140
 Leu Ala Leu Val Gly Cys Ala Arg Arg Ile Gly Ile Ala Ala Lys Thr
 145 150 155 160
 Lys Asp Ser Arg Gly Phe Asp Arg Val Asn Val Arg Asp Ala Glu Ala
 165 170 175

Ile Gly Ala Leu Leu Thr Arg Met Gly Ala Gln Lys Thr Arg Met Leu
 180 185 190

Trp Glu Glu Lys Arg Ile Lys Arg Glu Ser Arg Thr Pro Gln Thr Gly
 195 200 205

Leu Ala Asn Phe Asp Asp Ala Asn Leu Arg Arg Ser Ala Arg Ala Ala
 210 215 220

Val Ala Ala Ala Ala Arg Val Glu Arg Ala Met Lys Ile Leu Gly Asp
 225 230 235 240

Asp Val Pro Glu His Leu Ala Glu Ala Gly Gln Leu Arg Val Gln His
 245 250 255

Arg Gln Ala Ser Leu Glu Glu Leu Gly Arg Leu Ala Asp Pro Gln Met
 260 265 270

Thr Lys Asp Ala Val Ala Gly Arg Ile Arg Arg Leu Leu Thr Met Ala
 275 280 285

Asp Lys Arg Ala Glu Asp Leu Lys Ile Pro Asp Thr Asn Ser Val Val
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Thr Glu Asp Leu Leu Glu Glu Ile
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 <211> 681
 <212> DNA
 <213> Corynebacterium glutamicum

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 <223> RXC02435

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 Val Thr Asp Asn Leu
 1 5

ggt tca acc agt atc ggt gac gcg tgg att ctg tac gca ccg ctg atg 163
 Gly Ser Thr Ser Ile Gly Asp Ala Trp Ile Leu Tyr Ala Pro Leu Met
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gat gat ggt ggc ttt ggt cca ctg cgt gcc atc gga gga atg ttc ctg 211
 Asp Asp Gly Gly Phe Gly Pro Leu Arg Ala Ile Gly Gly Met Phe Leu
 25 30 35

cac att ggc ccc ggg cac atg ctg ttg aac ctt gtg ttg ttg tgg ttg 259
 His Ile Gly Pro Gly His Met Leu Leu Asn Leu Val Leu Leu Trp Leu
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ctg gga aga gaa att gaa cga gac ttc ggt tct gcg ctt ttc act gcg 307
 Leu Gly Arg Glu Ile Glu Arg Asp Phe Gly Ser Ala Leu Phe Thr Ala
 55 60 65

atg tac ttt gtg ggc ggt att ggt gcg tct gca gct gtc atc tgg atg 355
 Met Tyr Phe Val Gly Gly Ile Gly Ala Ser Ala Ala Val Ile Trp Met 85
 70 75 80

gat ccc tat tca ccg aca gca ggt gct tcc ggc gcc att tac gcc atg 403
 Asp Pro Tyr Ser Pro Thr Ala Gly Ala Ser Gly Ala Ile Tyr Ala Met 100
 90 95

atg gct att ttg gtg ggg ctt ttt gtg tta aga agc gcg gat atc cga 451
 Met Ala Ile Leu Val Gly Leu Phe Val Leu Arg Ser Ala Asp Ile Arg 115
 105 110

gca ccc ttg atc ctt atc gcc atc aac atc gcc tat acc ttg atg tcc 499
 Ala Pro Leu Ile Leu Ile Ala Ile Asn Ile Ala Tyr Thr Leu Met Ser 130
 120 125

acc aat gtt tct ctg tgg gga cac ctt gga ggt ttg atc act gga gct 547
 Thr Asn Val Ser Leu Trp Gly His Leu Gly Gly Leu Ile Thr Gly Ala 145
 135 140

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 Leu Ile Thr Trp Pro Met Val Lys Ala Lys Thr Gln Arg Thr Arg Trp 165
 150 155 160

att atc gtg ctc att ggt ttt gct gta gtt gtg gct gct gtc att cta 643
 Ile Ile Val Leu Ile Gly Phe Ala Val Val Val Ala Ala Val Ile Leu 180
 170 175

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 Gly Ile Asp Arg Val 185

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<211> 186

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 540

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Tyr Ala Pro Leu Met Asp Asp Gly Gly Phe Gly Pro Leu Arg Ala Ile 30
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Gly Gly Met Phe Leu His Ile Gly Pro Gly His Met Leu Leu Asn Leu 45
 35 40

Val Leu Leu Trp Leu Leu Gly Arg Glu Ile Glu Arg Asp Phe Gly Ser 60
 50 55

Ala Leu Phe Thr Ala Met Tyr Phe Val Gly Gly Ile Gly Ala Ser Ala 80
 65 70 75

Ala Val Ile Trp Met Asp Pro Tyr Ser Pro Thr Ala Gly Ala Ser Gly 95
 85 90

Ala Ile Tyr Ala Met Met Ala Ile Leu Val Gly Leu Phe Val Leu Arg 110
 100 105

Ser Ala Asp Ile Arg Ala Pro Leu Ile Leu Ile Ala Ile Asn Ile Ala

115	120	125
Tyr Thr Leu Met Ser Thr Asn Val Ser Leu Trp Gly His Leu Gly Gly		
130	135	140
Leu Ile Thr Gly Ala Leu Ile Thr Trp Pro Met Val Lys Ala Lys Thr		
145	150	155
Gln Arg Thr Arg Trp Ile Ile Val Leu Ile Gly Phe Ala Val Val Val		
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Ala Ala Val Ile Leu Gly Ile Asp Arg Val		
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 Val Thr Asp Asn Leu
 1 5
 ggt tca acc agt atc ggt gac gcg tgg att ctg tac gca ccg ctg atg 163
 Gly Ser Thr Ser Ile Gly Asp Ala Trp Ile Leu Tyr Ala Pro Leu Met
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 gat gat ggt ggc ttt ggt cca ctg cgt gcc atc gga gga atg ttc ctg 211
 Asp Asp Gly Gly Phe Gly Pro Leu Arg Ala Ile Gly Gly Met Phe Leu
 25 30 35
 cac att ggc ccc ggg cac atg ctg ttg aac ctt gtg ttg ttg tgg ttg 259
 His Ile Gly Pro Gly His Met Leu Leu Asn Leu Val Leu Leu Trp Leu
 40 45 50
 ctg gga aga gaa att gaa cga gac ttc ggt tct gcg ctt ttc act gcg 307
 Leu Gly Arg Glu Ile Glu Arg Asp Phe Gly Ser Ala Leu Phe Thr Ala
 55 60 65
 atg tac ttt gtg ggc ggt att ggt gcg tct gca gct gtc atc tgg atg 355
 Met Tyr Phe Val Gly Gly Ile Gly Ala Ser Ala Ala Val Ile Trp Met
 70 75 80 85
 gat ccc tat tca ccg aca gca ggt gct tcc ggc gcc att tac gcc atg 403
 Asp Pro Tyr Ser Pro Thr Ala Gly Ala Ser Gly Ala Ile Tyr Ala Met
 90 95 100
 atg gct att ttg gtg ggg ctt ttt gtg tta aga agc gcg gat atc cga 451
 Met Ala Ile Leu Val Gly Leu Phe Val Leu Arg Ser Ala Asp Ile Arg
 105 110 115
 gca ccc ttg atc ctt atc gcc atc aac atc gcc tat acc ttg atg tcc 499

Ala Pro Leu Ile Leu Ile Ala Ile Asn Ile Ala Tyr Thr Leu Met Ser
 120 125 130

acc aat gtt tct ctg tgg gga cac ctt gga ggt ttg atc act gga gct 547
 Thr Asn Val Ser Leu Trp Gly His Leu Gly Gly Leu Ile Thr Gly Ala
 135 140 145

tta att act tgg cca atg gtt aaa gcg aaa act caa aga aca cgg tgg 595
 Leu Ile Thr Trp Pro Met Val Lys Ala Lys Thr Gln Arg Thr Arg Trp
 150 155 160 165

att atc gtg ctc att ggt ttt gct gta gtt gtg gct gct gtc att cta 643
 Ile Ile Val Leu Ile Gly Phe Ala Val Val Val Ala Ala Val Ile Leu
 170 175 180

gga att gac cgg gtg tagacacatt ccgcccattg ccc 681
 Gly Ile Asp Arg Val
 185

<210> 542

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<213> Corynebacterium glutamicum

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Val Thr Asp Asn Leu Gly Ser Thr Ser Ile Gly Asp Ala Trp Ile Leu
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Tyr Ala Pro Leu Met Asp Asp Gly Gly Phe Gly Pro Leu Arg Ala Ile
 20 25 30

Gly Gly Met Phe Leu His Ile Gly Pro Gly His Met Leu Leu Asn Leu
 35 40 45

Val Leu Leu Trp Leu Leu Gly Arg Glu Ile Glu Arg Asp Phe Gly Ser
 50 55 60

Ala Leu Phe Thr Ala Met Tyr Phe Val Gly Gly Ile Gly Ala Ser Ala
 65 70 75 80

Ala Val Ile Trp Met Asp Pro Tyr Ser Pro Thr Ala Gly Ala Ser Gly
 85 90 95

Ala Ile Tyr Ala Met Met Ala Ile Leu Val Gly Leu Phe Val Leu Arg
 100 105 110

Ser Ala Asp Ile Arg Ala Pro Leu Ile Leu Ile Ala Ile Asn Ile Ala
 115 120 125

Tyr Thr Leu Met Ser Thr Asn Val Ser Leu Trp Gly His Leu Gly Gly
 130 135 140

Leu Ile Thr Gly Ala Leu Ile Thr Trp Pro Met Val Lys Ala Lys Thr
 145 150 155 160

Gln Arg Thr Arg Trp Ile Ile Val Leu Ile Gly Phe Ala Val Val Val
 165 170 175

Ala Ala Val Ile Leu Gly Ile Asp Arg Val
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atccctgcaa acaactagaa actattcaga aagcatcacc atg aaa ctc ggt ctc 115
 Met Lys Leu Gly Leu
 1 5

tac aac gcg atc ttc cac gac cgc acc ctg cca gaa gcg ctc gca gcc 163
 Tyr Asn Ala Ile Phe His Asp Arg Thr Leu Pro Glu Ala Leu Ala Ala
 10 15 20

atc aaa gct gca ggt ctc acc gga att gaa ctc aac acc ggc gga ttt 211
 Ile Lys Ala Ala Gly Leu Thr Gly Ile Glu Leu Asn Thr Gly Gly Phe
 25 30 35

ttg cct gca acc cac atc ccg acc atc gat gac atc ctg gtc agc gat 259
 Leu Pro Ala Thr His Ile Pro Thr Ile Asp Asp Ile Leu Val Ser Asp
 40 45 50

gat gcc cgc gat gaa ttc ctc ggg att ttc gaa ggc acc ggc gtc gac 307
 Asp Ala Arg Asp Glu Phe Leu Gly Ile Phe Glu Gly Thr Gly Val Asp
 55 60 65

atc tac ggc ctt aac tgc aac ggc aac ccg ctt cac ccc aac aag gcg 355
 Ile Tyr Gly Leu Asn Cys Asn Gly Asn Pro Leu His Pro Asn Lys Ala
 70 75 80 85

atc ggg gac aag cat gcc gaa gac att cga cgt tcc atc cgc ctc gca 403
 Ile Gly Asp Lys His Ala Glu Asp Ile Arg Arg Ser Ile Arg Leu Ala
 90 95 100

gag cgc ctc ggc caa aac cgt gtg gtc acc atg tct ggt ctt cct ggt 451
 Glu Arg Leu Gly Gln Asn Arg Val Val Thr Met Ser Gly Leu Pro Gly
 105 110 115

ggc gaa cca ggc gcg aag tac acc aac tgg gtt gtc aac gcg tgg aac 499
 Gly Glu Pro Gly Ala Lys Tyr Thr Asn Trp Val Val Asn Ala Trp Asn
 120 125 130

tcc gca gcc ttg gat gtc ctt gat tac caa tgg gat atc gca gct gaa 547
 Ser Ala Ala Leu Asp Val Leu Asp Tyr Gln Trp Asp Ile Ala Ala Glu
 135 140 145

ttc tgg cgc gag acc gac cgc ttc gcc gca gat cac ggc gtg aaa gtg 595
 Phe Trp Arg Glu Thr Asp Arg Phe Ala Ala Asp His Gly Val Lys Val
 150 155 160 165

gct ctt gag ctg cac cca cag aac atc gtg ttc aac tcc gct gac gtg 643
 Ala Leu Glu Leu His Pro Gln Asn Ile Val Phe Asn Ser Ala Asp Val

170	175	180	
cat aag ctc atc gat ctc acc ggc gcc acc cac gtg ggc gtc gaa ctg			691
His Lys Leu Ile Asp Leu Thr Gly Ala Thr His Val Gly Val Glu Leu			
185	190	195	
gat gca tca cac ctg ttc tgg cag cag atg gac cca atc gct gtg att			739
Asp Ala Ser His Leu Phe Trp Gln Gln Met Asp Pro Ile Ala Val Ile			
200	205	210	
gat cac ctc ggc gag ctc atc ttc cac gcc gcc gcc aaa gac gtg cga			787
Asp His Leu Gly Glu Leu Ile Phe His Ala Ala Ala Lys Asp Val Arg			
215	220	225	
gtt aat aag gaa tgg gct cag ctc aac ggt gtg ctg gac aac agc ttc			835
Val Asn Lys Glu Trp Ala Gln Leu Asn Gly Val Leu Asp Asn Ser Phe			
230	235	240	245
cga cgc ctt gac cca tcc gaa aac cgc acc aac ttg ggc ggc gac gag			883
Arg Arg Leu Asp Pro Ser Glu Asn Arg Thr Asn Leu Gly Gly Asp Glu			
250	255	260	
tgg gcg aat gaa tgg cca aag aac tct gct tgg gat ttc gtt gct ctg			931
Trp Ala Asn Glu Trp Pro Lys Asn Ser Ala Trp Asp Phe Val Ala Leu			
265	270	275	
ggc cgc ggt cat gac gtt gct tac tgg acc gaa ttc ctc cgc gca ctt			979
Gly Arg Gly His Asp Val Ala Tyr Trp Thr Glu Phe Leu Arg Ala Leu			
280	285	290	
cac cgc gtc gat cca aac atg ctg gtc aac atc gaa cac gag gat gtt			1027
His Arg Val Asp Pro Asn Met Leu Val Asn Ile Glu His Glu Asp Val			
295	300	305	
tca ctc ggt cgc gaa gaa ggc gtc aac gaa gcc gct aag gtg ctg atc			1075
Ser Leu Gly Arg Glu Glu Gly Val Asn Glu Ala Ala Lys Val Leu Ile			
310	315	320	325
gag gcc aac aag gca ctc gaa gag tcc ctg gtt tct taaaaaaact			1121
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<213> Corynebacterium glutamicum

<400> 544

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Asn Thr Gly Gly Phe Leu Pro Ala Thr His Ile Pro Thr Ile Asp Asp
 35 40 45

Ile Leu Val Ser Asp Asp Ala Arg Asp Glu Phe Leu Gly Ile Phe Glu

50	55	60
Gly Thr Gly Val Asp Ile Tyr Gly Leu Asn Cys Asn Gly Asn Pro Leu 65 70 75 80		
His Pro Asn Lys Ala Ile Gly Asp Lys His Ala Glu Asp Ile Arg Arg 85 90 95		
Ser Ile Arg Leu Ala Glu Arg Leu Gly Gln Asn Arg Val Val Thr Met 100 105 110		
Ser Gly Leu Pro Gly Gly Glu Pro Gly Ala Lys Tyr Thr Asn Trp Val 115 120 125		
Val Asn Ala Trp Asn Ser Ala Ala Leu Asp Val Leu Asp Tyr Gln Trp 130 135 140		
Asp Ile Ala Ala Glu Phe Trp Arg Glu Thr Asp Arg Phe Ala Ala Asp 145 150 155 160		
His Gly Val Lys Val Ala Leu Glu Leu His Pro Gln Asn Ile Val Phe 165 170 175		
Asn Ser Ala Asp Val His Lys Leu Ile Asp Leu Thr Gly Ala Thr His 180 185 190		
Val Gly Val Glu Leu Asp Ala Ser His Leu Phe Trp Gln Gln Met Asp 195 200 205		
Pro Ile Ala Val Ile Asp His Leu Gly Glu Leu Ile Phe His Ala Ala 210 215 220		
Ala Lys Asp Val Arg Val Asn Lys Glu Trp Ala Gln Leu Asn Gly Val 225 230 235 240		
Leu Asp Asn Ser Phe Arg Arg Leu Asp Pro Ser Glu Asn Arg Thr Asn 245 250 255		
Leu Gly Gly Asp Glu Trp Ala Asn Glu Trp Pro Lys Asn Ser Ala Trp 260 265 270		
Asp Phe Val Ala Leu Gly Arg Gly His Asp Val Ala Tyr Trp Thr Glu 275 280 285		
Phe Leu Arg Ala Leu His Arg Val Asp Pro Asn Met Leu Val Asn Ile 290 295 300		
Glu His Glu Asp Val Ser Leu Gly Arg Glu Glu Gly Val Asn Glu Ala 305 310 315 320		
Ala Lys Val Leu Ile Glu Ala Asn Lys Ala Leu Glu Glu Ser Leu Val 325 330 335		
Ser		

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<223> RXA02175

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                               1 5

aac aag gct gtc ctg cac tac ccc ggt ggc gag ttc gaa atg gac atc 163
Asn Lys Ala Val Leu His Tyr Pro Gly Gly Glu Phe Glu Met Asp Ile
                               10 15 20

atc gag gct tct gag ggt aac aac ggt gtt gtc ctg ggc aag atg ctg 211
Ile Glu Ala Ser Glu Gly Asn Asn Gly Val Val Leu Gly Lys Met Leu
                               25 30 35

tct gag act gga ctg atc act ttt gac cca ggt tat gtg agc act ggc 259
Ser Glu Thr Gly Leu Ile Thr Phe Asp Pro Gly Tyr Val Ser Thr Gly
                               40 45 50

tcc acc gag tcg aag atc acc tac atc gat ggc gat gcg gga atc ctg 307
Ser Thr Glu Ser Lys Ile Thr Tyr Ile Asp Gly Asp Ala Gly Ile Leu
                               55 60 65

cgt tac cgc ggc tat gac atc gct gat ctg gct gag aat gcc acc ttc 355
Arg Tyr Arg Gly Tyr Asp Ile Ala Asp Leu Ala Glu Asn Ala Thr Phe
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aac gag gtt tct tac cta ctt atc aac ggt gag cta cca acc cca gat 403
Asn Glu Val Ser Tyr Leu Leu Ile Asn Gly Glu Leu Pro Thr Pro Asp
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gag ctt cac aag ttt aac gac gag att cgc cac cac acc ctt ctg gac 451
Glu Leu His Lys Phe Asn Asp Glu Ile Arg His His Thr Leu Leu Asp
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gag gac ttc aag tcc cag ttc aac gtg ttc cca cgc gac gct cac cca 499
Glu Asp Phe Lys Ser Gln Phe Asn Val Phe Pro Arg Asp Ala His Pro
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atg gca acc ttg gct tcc tcg gtt aac att ttg tct acc tac tac cag 547
Met Ala Thr Leu Ala Ser Ser Val Asn Ile Leu Ser Thr Tyr Tyr Gln
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gac cag ctg aac cca ctc gat gag gca cag ctt gat aag gca acc gtt 595
Asp Gln Leu Asn Pro Leu Asp Glu Ala Gln Leu Asp Lys Ala Thr Val
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cgc ctc atg gca aag gtt cca atg ctg gct gcg tac gca cac cgc gca 643
Arg Leu Met Ala Lys Val Pro Met Leu Ala Ala Tyr Ala His Arg Ala
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cgc aag ggt gct cct tac atg tac cca gac aac tcc ctc aat gcg cgt 691
Arg Lys Gly Ala Pro Tyr Met Tyr Pro Asp Asn Ser Leu Asn Ala Arg
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atc gac cca atc atg gtc aag gct ctg gac aag ctg ctc atc ctg cac	787
Ile Asp Pro Ile Met Val Lys Ala Leu Asp Lys Leu Leu Ile Leu His	
215 220 225	
gct gac cac gag cag aac tgc tcc acc tcc acc gtt cgt atg atc ggt	835
Ala Asp His Glu Gln Asn Cys Ser Thr Ser Thr Val Arg Met Ile Gly	
230 235 240 245	
tcc gca cag gcc aac atg ttt gtc tcc atc gct ggt ggc atc aac gct	883
Ser Ala Gln Ala Asn Met Phe Val Ser Ile Ala Gly Gly Ile Asn Ala	
250 255 260	
ctg tcc ggc cca ctg cac ggt ggc gca aac cag gct gtt ctg gag atg	931
Leu Ser Gly Pro Leu His Gly Gly Ala Asn Gln Ala Val Leu Glu Met	
265 270 275	
ctc gaa gac atc aag agc aac cac ggt ggc gac gca acc gag ttc atg	979
Leu Glu Asp Ile Lys Ser Asn His Gly Gly Asp Ala Thr Glu Phe Met	
280 285 290	
aac aag gtc aag aac aag gaa gac ggc gtc cgc ctc atg ggc ttc gga	1027
Asn Lys Val Lys Asn Lys Glu Asp Gly Val Arg Leu Met Gly Phe Gly	
295 300 305	
cac cgc gtt tac aag aac tac gat cca cgt gca gca atc gtc aag gag	1075
His Arg Val Tyr Lys Asn Tyr Asp Pro Arg Ala Ala Ile Val Lys Glu	
310 315 320 325	
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Thr Ala His Glu Ile Leu Glu His Leu Gly Gly Asp Asp Leu Leu Asp	
330 335 340	
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Leu Ala Ile Lys Leu Glu Glu Ile Ala Leu Ala Asp Asp Tyr Phe Ile	
345 350 355	
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Ser Arg Lys Leu Tyr Pro Asn Val Asp Phe Tyr Thr Gly Leu Ile Tyr	
360 365 370	
cgc gca atg ggc ttc cca act gac ttc ttc acc gta ttg ttc gca atc	1267
Arg Ala Met Gly Phe Pro Thr Asp Phe Phe Thr Val Leu Phe Ala Ile	
375 380 385	
ggt cgt ctg cca gga tgg atc gct cac tac cgc gag cag ctc ggt gca	1315
Gly Arg Leu Pro Gly Trp Ile Ala His Tyr Arg Glu Gln Leu Gly Ala	
390 395 400 405	
gca ggc aac aag atc aac cgc cca cgc cag gtc tac acc ggc aac gaa	1363
Ala Gly Asn Lys Ile Asn Arg Pro Arg Gln Val Tyr Thr Gly Asn Glu	
410 415 420	
tcc cgc aag ttg gtt cct cgc gag gag cgc taaatttagc ggatgattct	1413
Ser Arg Lys Leu Val Pro Arg Glu Glu Arg	
425 430	
cgt	1416

774

Ala Thr Glu Phe Met Asn Lys Val Lys Asn Lys Glu Asp Gly Val Arg
 290 295 300

Leu Met Gly Phe Gly His Arg Val Tyr Lys Asn Tyr Asp Pro Arg Ala
 305 310 315 320

Ala Ile Val Lys Glu Thr Ala His Glu Ile Leu Glu His Leu Gly Gly
 325 330 335

Asp Asp Leu Leu Asp Leu Ala Ile Lys Leu Glu Glu Ile Ala Leu Ala
 340 345 350

Asp Asp Tyr Phe Ile Ser Arg Lys Leu Tyr Pro Asn Val Asp Phe Tyr
 355 360 365

Thr Gly Leu Ile Tyr Arg Ala Met Gly Phe Pro Thr Asp Phe Phe Thr
 370 375 380

Val Leu Phe Ala Ile Gly Arg Leu Pro Gly Trp Ile Ala His Tyr Arg
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 <223> RXA02621

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 Met Ser Glu Leu Ile
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tgt gga cca gct att ctc ttc gca cca gct gga cgt gct gag atc att 163
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 10 15 20

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 Gly Ala Gly Glu Val Asp Arg Glu Val Ala Tyr Arg Asn Ile Arg Glu
 40 45 50

tcg ggg ttg gat cct aaa cga acc att gtg aga acc gta ggg ccg agc 307
 Ser Gly Leu Asp Pro Lys Arg Thr Ile Val Arg Thr Val Gly Pro Ser
 55 60 65

gat cca cac ttt ttg gct gac gtg gag atg gtg aag tcc acg gat ttc	355
Asp Pro His Phe Leu Ala Asp Val Glu Met Val Lys Ser Thr Asp Phe	
70 75 80 85	
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Thr Leu Val Met Val Pro Lys Leu Leu Gly Ser Val Pro Glu Glu Leu	
90 95 100	
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Asp Gly Leu Asn Ile Ile Ala Met Ile Glu Thr Pro Gln Ala Ala Thr	
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Ser Ile Pro Gln Ile Ala Ala Asp Pro Lys Val Val Gly Met Phe Trp	
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Gly Ala Glu Asp Leu Thr His Leu Leu Gly Gly Thr His Ser Arg Phe	
135 140 145	
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Leu Gly Asp Glu Ser Asn Glu Gly Ser Tyr Arg Asp Thr Met Arg Leu	
150 155 160 165	
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Thr Arg Ala Leu Met His Leu His Ala Ala Asn Gly Lys Phe Thr	
170 175 180	
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Ile Asp Ala Ile His Ala Asp Phe His Asp Glu Glu Gly Leu Tyr Leu	
185 190 195	
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Glu Ala Val Asp Ala Ala Arg Thr Gly Phe Ala Gly Thr Ala Cys Ile	
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cac ccc aag cag atc gag att gtt cgg aga gcc tat cgg cca gag gct	787
His Pro Lys Gln Ile Glu Ile Val Arg Arg Ala Tyr Arg Pro Glu Ala	
215 220 225	
aac cag ttg gag tgg gcg aag aaa gtg gtg gag gaa gca gaa aac cat	835
Asn Gln Leu Glu Trp Ala Lys Lys Val Val Glu Glu Ala Glu Asn His	
230 235 240 245	
cca ggt gcg ttc aaa ctg gat ggt cag atg att gat gct ccg ttg att	883
Pro Gly Ala Phe Lys Leu Asp Gly Gln Met Ile Asp Ala Pro Leu Ile	
250 255 260	
tcg cag gcg cgg atg gtt att tcg cgt cag cct gct tgattagttc	929
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<211> 273

<212> PRT

<213> Corynebacterium glutamicum

<400> 548

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 35 40 45

Arg Asn Ile Arg Glu Ser Gly Leu Asp Pro Lys Arg Thr Ile Val Arg
 50 55 60

Thr Val Gly Pro Ser Asp Pro His Phe Leu Ala Asp Val Glu Met Val
 65 70 75 80

Lys Ser Thr Asp Phe Thr Leu Val Met Val Pro Lys Leu Leu Gly Ser
 85 90 95

Val Pro Glu Glu Leu Asp Gly Leu Asn Ile Ile Ala Met Ile Glu Thr
 100 105 110

Pro Gln Ala Ala Thr Ser Ile Pro Gln Ile Ala Ala Asp Pro Lys Val
 115 120 125

Val Gly Met Phe Trp Gly Ala Glu Asp Leu Thr His Leu Leu Gly Gly
 130 135 140

Thr His Ser Arg Phe Leu Gly Asp Glu Ser Asn Glu Gly Ser Tyr Arg
 145 150 155 160

Asp Thr Met Arg Leu Thr Arg Ala Leu Met His Leu His Ala Ala Ala
 165 170 175

Asn Gly Lys Phe Thr Ile Asp Ala Ile His Ala Asp Phe His Asp Glu
 180 185 190

Glu Gly Leu Tyr Leu Glu Ala Val Asp Ala Ala Arg Thr Gly Phe Ala
 195 200 205

Gly Thr Ala Cys Ile His Pro Lys Gln Ile Glu Ile Val Arg Arg Ala
 210 215 220

Tyr Arg Pro Glu Ala Asn Gln Leu Glu Trp Ala Lys Lys Val Val Glu
 225 230 235 240

Glu Ala Glu Asn His Pro Gly Ala Phe Lys Leu Asp Gly Gln Met Ile
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Asp Ala Pro Leu Ile Ser Gln Ala Arg Met Val Ile Ser Arg Gln Pro
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<212> DNA

<213> *Corynebacterium glutamicum*

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<222> (101)..(2314)

<223> RXN00519

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Pro Val Val Glu Ala Phe Ala Ala Thr Ala Gly Ile Glu Val Glu Thr
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cgg gac att tca ctc gct gga cgc atc ctc gcc cag ttc cca gag cgc 259
Arg Asp Ile Ser Leu Ala Gly Arg Ile Leu Ala Gln Phe Pro Glu Arg
                        40                        45                        50

ctc acc gaa gat cag aag gta ggc aac gca ctc gca gaa ctc ggc gag 307
Leu Thr Glu Asp Gln Lys Val Gly Asn Ala Leu Ala Glu Leu Gly Glu
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ctt gct aag act cct gaa gca aac atc att aag ctt cca aac atc tcc 355
Leu Ala Lys Thr Pro Glu Ala Asn Ile Ile Lys Leu Pro Asn Ile Ser
                        70                        75                        80                        85

gct tct gtt cca cag ctc aag gct gct att aag gaa ctg cag gac cag 403
Ala Ser Val Pro Gln Leu Lys Ala Ala Ile Lys Glu Leu Gln Asp Gln
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Gly Tyr Asp Ile Pro Glu Leu Pro Asp Asn Ala Thr Thr Asp Glu Glu
                        105                        110                        115

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Lys Asp Ile Leu Ala Arg Tyr Asn Ala Val Lys Gly Ser Ala Val Asn
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cca gtg ctg cgt gaa ggc aac tct gac cgc cgc gca cca atc gct gtc 547
Pro Val Leu Arg Glu Gly Asn Ser Asp Arg Arg Ala Pro Ile Ala Val
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gat tcc aag acc aac gtt gca acc atg gat gca aac gac ttc cgc cac 643
Asp Ser Lys Thr Asn Val Ala Thr Met Asp Ala Asn Asp Phe Arg His
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aac gag aag tcc atc atc ctc gac gct gct gat gaa gtt cag atc aag 691
Asn Glu Lys Ser Ile Ile Leu Asp Ala Ala Asp Glu Val Gln Ile Lys
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cac atc gca gct gac ggc acc gag acc atc ctc aag gac agc ctc aag 739

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Leu Leu Glu Gly Glu Val Leu Asp Gly Thr Val Leu Ser Ala Lys Ala	
215 220 225	
ctg gac gca ttc ctt ctc gag cag gtc gct cgc gca aag gca gaa ggt	835
Leu Asp Ala Phe Leu Leu Glu Gln Val Ala Arg Ala Lys Ala Glu Gly	
230 235 240 245	
atc ctc ttc tcc gca cac ctg aag gcc acc atg atg aag gtc tcc gac	883
Ile Leu Phe Ser Ala His Leu Lys Ala Thr Met Met Lys Val Ser Asp	
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cca atc atc ttc ggc cac gtt gtg cgc gct tac ttc gca gac gtt ttc	931
Pro Ile Ile Phe Gly His Val Val Arg Ala Tyr Phe Ala Asp Val Phe	
265 270 275	
gca cag tac ggt gag cag ctg ctc gca gct ggc ctc aac ggc gaa aac	979
Ala Gln Tyr Gly Glu Gln Leu Leu Ala Ala Gly Leu Asn Gly Glu Asn	
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ggc ctc gct gca atc ctc tcc ggc ttg gag tcc ctg gac aac ggc gaa	1027
Gly Leu Ala Ala Ile Leu Ser Gly Leu Glu Ser Leu Asp Asn Gly Glu	
295 300 305	
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Glu Ile Lys Ala Ala Phe Glu Lys Gly Leu Glu Asp Gly Pro Asp Leu	
310 315 320 325	
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Ala Met Val Asn Ser Ala Arg Gly Ile Thr Asn Leu His Val Pro Ser	
330 335 340	
gat gtc atc gtg gac gct tcc atg cca gca atg att cgt acc tcc ggc	1171
Asp Val Ile Val Asp Ala Ser Met Pro Ala Met Ile Arg Thr Ser Gly	
345 350 355	
cac atg tgg aac aaa gac gac cag gag cag gac acc ctg gca atc atc	1219
His Met Trp Asn Lys Asp Asp Gln Glu Gln Asp Thr Leu Ala Ile Ile	
360 365 370	
cca gac tcc tcc tac gct ggc gtc tac cag acc gtt atc gaa gac tgc	1267
Pro Asp Ser Ser Tyr Ala Gly Val Tyr Gln Thr Val Ile Glu Asp Cys	
375 380 385	
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Arg Lys Asn Gly Ala Phe Asp Pro Thr Thr Met Gly Thr Val Pro Asn	
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Val Gly Leu Met Ala Gln Lys Ala Glu Tyr Gly Ser His Asp Lys	
410 415 420	
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Thr Phe Arg Ile Glu Ala Asp Gly Val Val Gln Val Val Ser Ser Asn	
425 430 435	
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Gly Asp Val Leu Ile Glu His Asp Val Glu Ala Asn Asp Ile Trp Arg	

440	445	450	
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cca gag cgc gca cac gac cgc aac ctg gct tcc ctc gtt gag aag tac Pro Glu Arg Ala His Asp Arg Asn Leu Ala Ser Leu Val Glu Lys Tyr 490 495 500			1603
ctg gct gac cac gac acc gag ggc ctg gac atc cag atc ctc tcc cct Leu Ala Asp His Asp Thr Glu Gly Leu Asp Ile Gln Ile Leu Ser Pro 505 510 515			1651
gtt gag gca acc cag ctc tcc atc gac cgc atc cgc cgt ggc gag gac Val Glu Ala Thr Gln Leu Ser Ile Asp Arg Ile Arg Arg Gly Glu Asp 520 525 530			1699
acc atc tct gtc acc ggt aac gtt ctg cgt gac tac aac acc gac ctc Thr Ile Ser Val Thr Gly Asn Val Leu Arg Asp Tyr Asn Thr Asp Leu 535 540 545			1747
ttc cca atc ctg gag ctg ggc acc tct gca aag atg ctg tct gtc gtt Phe Pro Ile Leu Glu Leu Gly Thr Ser Ala Lys Met Leu Ser Val Val 550 555 560 565			1795
cct ttg atg gct ggc ggc gga ctg ttc gag acc ggt gct ggt gga tct Pro Leu Met Ala Gly Gly Gly Leu Phe Glu Thr Gly Ala Gly Gly Ser 570 575 580			1843
gct cct aag cac gtc cag cag gtt cag gaa gaa aac cac ctg cgt tgg Ala Pro Lys His Val Gln Gln Val Gln Glu Glu Asn His Leu Arg Trp 585 590 595			1891
gat tcc ctc ggt gag ttc ctc gca ctg gct gag tcc ttc cgc cac gag Asp Ser Leu Gly Glu Phe Leu Ala Leu Ala Glu Ser Phe Arg His Glu 600 605 610			1939
ctc aac aac aac ggc aac acc aag gcc ggc gtt ctg gct gac gct ctg Leu Asn Asn Asn Gly Asn Thr Lys Ala Gly Val Leu Ala Asp Ala Leu 615 620 625			1987
gac aag gca act gag aag ctg ctg aac gaa gag aag tcc cca tcc cgc Asp Lys Ala Thr Glu Lys Leu Leu Asn Glu Glu Lys Ser Pro Ser Arg 630 635 640 645			2035
aag gtt ggc gag atc gac aac cgt ggc tcc cac ttc tgg ctg acc aag Lys Val Gly Glu Ile Asp Asn Arg Gly Ser His Phe Trp Leu Thr Lys 650 655 660			2083
ttc tgg gct gac gag ctc gct gct cag acc gag gac gca gat ctg gct Phe Trp Ala Asp Glu Leu Ala Ala Gln Thr Glu Asp Ala Asp Leu Ala 665 670 675			2131
gct acc ttc gca cca gtc gca gaa gca ctg aac aca ggc gct gca gac Ala Thr Phe Ala Pro Val Ala Glu Ala Leu Asn Thr Gly Ala Ala Asp 680 685 690			2179

atc gat gct gca ctg ctc gca gtt cag ggt gga gca act gac ctt ggt 2227
 Ile Asp Ala Ala Leu Leu Ala Val Gln Gly Gly Ala Thr Asp L u Gly
 695 700 705

ggc tac tac tcc cct aac gag gag aag ctc acc aac atc atg cgc cca 2275
 Gly Tyr Tyr Ser Pro Asn Glu Glu Lys Leu Thr Asn Ile Met Arg Pro
 710 715 720 725

gtc gca cag ttc aac gag atc gtt gac gca ctg aag aag taaagtctct 2324
 Val Ala Gln Phe Asn Glu Ile Val Asp Ala Leu Lys Lys
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tcacaaaaag cgc 2337

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 35 40 45

Gln Phe Pro Glu Arg Leu Thr Glu Asp Gln Lys Val Gly Asn Ala Leu
 50 55 60

Ala Glu Leu Gly Glu Leu Ala Lys Thr Pro Glu Ala Asn Ile Ile Lys
 65 70 75 80

Leu Pro Asn Ile Ser Ala Ser Val Pro Gln Leu Lys Ala Ala Ile Lys
 85 90 95

Glu Leu Gln Asp Gln Gly Tyr Asp Ile Pro Glu Leu Pro Asp Asn Ala
 100 105 110

Thr Thr Asp Glu Glu Lys Asp Ile Leu Ala Arg Tyr Asn Ala Val Lys
 115 120 125

Gly Ser Ala Val Asn Pro Val Leu Arg Glu Gly Asn Ser Asp Arg Arg
 130 135 140

Ala Pro Ile Ala Val Lys Asn Phe Val Lys Lys Phe Pro His Arg Met
 145 150 155 160

Gly Glu Trp Ser Ala Asp Ser Lys Thr Asn Val Ala Thr Met Asp Ala
 165 170 175

Asn Asp Phe Arg His Asn Glu Lys Ser Ile Ile Leu Asp Ala Ala Asp
 180 185 190

Glu Val Gln Ile Lys His Ile Ala Ala Asp Gly Thr Glu Thr Ile Leu
 195 200 205

Lys Asp Ser Leu Lys Leu Leu Glu Gly Glu Val Leu Asp Gly Thr Val
 210 215 220
 Leu Ser Ala Lys Ala Leu Asp Ala Phe Leu Leu Glu Gln Val Ala Arg
 225 230 235 240
 Ala Lys Ala Glu Gly Ile Leu Phe Ser Ala His Leu Lys Ala Thr Met
 245 250 255
 Met Lys Val Ser Asp Pro Ile Ile Phe Gly His Val Val Arg Ala Tyr
 260 265 270
 Phe Ala Asp Val Phe Ala Gln Tyr Gly Glu Gln Leu Leu Ala Ala Gly
 275 280 285
 Leu Asn Gly Glu Asn Gly Leu Ala Ala Ile Leu Ser Gly Leu Glu Ser
 290 295 300
 Leu Asp Asn Gly Glu Glu Ile Lys Ala Ala Phe Glu Lys Gly Leu Glu
 305 310 315 320
 Asp Gly Pro Asp Leu Ala Met Val Asn Ser Ala Arg Gly Ile Thr Asn
 325 330 335
 Leu His Val Pro Ser Asp Val Ile Val Asp Ala Ser Met Pro Ala Met
 340 345 350
 Ile Arg Thr Ser Gly His Met Trp Asn Lys Asp Asp Gln Glu Gln Asp
 355 360 365
 Thr Leu Ala Ile Ile Pro Asp Ser Ser Tyr Ala Gly Val Tyr Gln Thr
 370 375 380
 Val Ile Glu Asp Cys Arg Lys Asn Gly Ala Phe Asp Pro Thr Thr Met
 385 390 395 400
 Gly Thr Val Pro Asn Val Gly Leu Met Ala Gln Lys Ala Glu Glu Tyr
 405 410 415
 Gly Ser His Asp Lys Thr Phe Arg Ile Glu Ala Asp Gly Val Val Gln
 420 425 430
 Val Val Ser Ser Asn Gly Asp Val Leu Ile Glu His Asp Val Glu Ala
 435 440 445
 Asn Asp Ile Trp Arg Ala Cys Gln Val Lys Asp Ala Pro Ile Gln Asp
 450 455 460
 Trp Val Lys Leu Ala Val Thr Arg Ser Arg Leu Ser Gly Met Pro Ala
 465 470 475 480
 Val Phe Trp Leu Asp Pro Glu Arg Ala His Asp Arg Asn Leu Ala Ser
 485 490 495
 Leu Val Glu Lys Tyr Leu Ala Asp His Asp Thr Glu Gly Leu Asp Ile
 500 505 510
 Gln Ile Leu Ser Pro Val Glu Ala Thr Gln Leu Ser Ile Asp Arg Ile
 515 520 525
 Arg Arg Gly Glu Asp Thr Ile Ser Val Thr Gly Asn Val Leu Arg Asp

530 535 540

Tyr Asn Thr Asp Leu Phe Pro Ile Leu Glu Leu Gly Thr Ser Ala Lys
545 550 555 560

Met Leu Ser Val Val Pro Leu Met Ala Gly Gly Gly Leu Phe Glu Thr
 565 570 575

Gly Ala Gly Gly Ser Ala Pro Lys His Val Gln Gln Val Gln Glu Glu
 580 585 590

Asn His Leu Arg Trp Asp Ser Leu Gly Glu Phe Leu Ala Leu Ala Glu
 595 600 605

Ser Phe Arg His Glu Leu Asn Asn Asn Gly Asn Thr Lys Ala Gly Val
 610 615 620

Leu Ala Asp Ala Leu Asp Lys Ala Thr Glu Lys Leu Leu Asn Glu Glu
625 630 635 640

Lys Ser Pro Ser Arg Lys Val Gly Glu Ile Asp Asn Arg Gly Ser His
 645 650 655

Phe Trp Leu Thr Lys Phe Trp Ala Asp Glu Leu Ala Ala Gln Thr Glu
 660 665 670

Asp Ala Asp Leu Ala Ala Thr Phe Ala Pro Val Ala Glu Ala Leu Asn
 675 680 685

Thr Gly Ala Ala Asp Ile Asp Ala Ala Leu Leu Ala Val Gln Gly Gly
690 695 700

Ala Thr Asp Leu Gly Gly Tyr Tyr Ser Pro Asn Glu Glu Lys Leu Thr
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Asn Ile Met Arg Pro Val Ala Gln Phe Asn Glu Ile Val Asp Ala Leu
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Lys Lys

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<211> 1059

<212> DNA

<213> Corynebacterium glutamicum

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<222> (1)..(1059)

<223> FRXA00521

<400> 551

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acc gag acc atc ctc aag gac agc ctc aag ctt ctt gaa ggc gaa gtt 96
Thr Glu Thr Ile Leu Lys Asp Ser Leu Lys Leu Leu Glu Gly Glu Val
 20 25 30

cta gac gga acc gtt ctg tcc gca aag gca ctg gac gca ttc ctt ctc	144
Leu Asp Gly Thr Val Leu Ser Ala Lys Ala Leu Asp Ala Phe Leu Leu	
35 40 45	
gag cag gtc gct cgc gca aag gca gaa ggt atc ctc ttc tcc gca cac	192
Glu Gln Val Ala Arg Ala Lys Ala Glu Gly Ile Leu Phe Ser Ala His	
50 55 60	
ctg aag gcc acc atg atg aag gtc tcc gac cca atc atc ttc ggc cac	240
Leu Lys Ala Thr Met Met Lys Val Ser Asp Pro Ile Ile Phe Gly His	
65 70 75 80	
gtt gtg cgc gct tac ttc gca gac gtt ttc gca cag tac ggt gag cag	288
Val Val Arg Ala Tyr Phe Ala Asp Val Phe Ala Gln Tyr Gly Glu Gln	
85 90 95	
ctg ctc gca gct ggc ctc aac ggc gaa aac ggc ctc gct gca atc ctc	336
Leu Leu Ala Ala Gly Leu Asn Gly Glu Asn Gly Leu Ala Ala Ile Leu	
100 105 110	
tcc ggc ttg gag tcc ctg gac aac ggc gaa gaa atc aag gct gca ttc	384
Ser Gly Leu Glu Ser Leu Asp Asn Gly Glu Glu Ile Lys Ala Ala Phe	
115 120 125	
gag aag ggc ttg gaa gac ggc cca gac ctg gcc atg gtt aac tcc gct	432
Glu Lys Gly Leu Glu Asp Gly Pro Asp Leu Ala Met Val Asn Ser Ala	
130 135 140	
cgc ggc atc acc aac ctg cat gtc cct tcc gat gtc atc gtg gac gct	480
Arg Gly Ile Thr Asn Leu His Val Pro Ser Asp Val Ile Val Asp Ala	
145 150 155 160	
tcc atg cca gca atg att cgt acc tcc ggc cac atg tgg aac aaa gac	528
Ser Met Pro Ala Met Ile Arg Thr Ser Gly His Met Trp Asn Lys Asp	
165 170 175	
gac cag gag cag gac acc ctg gca atc atc cca gac tcc tcc tac gct	576
Asp Gln Glu Gln Asp Thr Leu Ala Ile Ile Pro Asp Ser Ser Tyr Ala	
180 185 190	
ggc gtc tac cag acc gtt atc gaa gac tgc cgc aag aac ggc gca ttc	624
Gly Val Tyr Gln Thr Val Ile Glu Asp Cys Arg Lys Asn Gly Ala Phe	
195 200 205	
gat cca acc acc atg ggt acc gtc cct aac gtt ggt ctg atg gct cag	672
Asp Pro Thr Thr Met Gly Thr Val Pro Asn Val Gly Leu Met Ala Gln	
210 215 220	
aag gct gaa gag tac ggc tcc cat gac aag acc ttc cgc atc gaa gca	720
Lys Ala Glu Glu Tyr Gly Ser His Asp Lys Thr Phe Arg Ile Glu Ala	
225 230 235 240	
gac ggt gtg gtt cag gtt gtt tcc tcc aac ggc gac gtt ctc atc gag	768
Asp Gly Val Val Gln Val Val Ser Ser Asn Gly Asp Val Leu Ile Glu	
245 250 255	
cac gac gtt gag gca aat gac atc tgg cgt gca tgc cag gtc aag gat	816
His Asp Val Glu Ala Asn Asp Ile Trp Arg Ala Cys Gln Val Lys Asp	
260 265 270	
gcc cca atc cag gat tgg gta aag ctt gct gtc acc cgc tcc cgt ctc	864

Ala Pro Ile Gln Asp Trp Val Lys Leu Ala Val Thr Arg Ser Arg Leu
 275 280 285

tcc gga atg cct gca gtg ttc tgg ttg gat cca gag cgc gca cac gac 912
 Ser Gly Met Pro Ala Val Phe Trp Leu Asp Pro Glu Arg Ala His Asp
 290 295 300

cgc aac ctg gct tcc ctc gtt gag aag tac ctg gct gac cac gac acc 960
 Arg Asn Leu Ala Ser Leu Val Glu Lys Tyr Leu Ala Asp His Asp Thr
 305 310 315 320

gag ggc ctg gac atc cag atc ctc tac cct gtt gag gca acc cag ctc 1008
 Glu Gly Leu Asp Ile Gln Ile Leu Tyr Pro Val Glu Ala Thr Gln Leu
 325 330 335

tcc atc gac cgc atc cgc cgt ggc gag gac acc atc tct gtc acc ggt 1056
 Ser Ile Asp Arg Ile Arg Arg Gly Glu Asp Thr Ile Ser Val Thr Gly
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aac 1059
 Asn

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 <213> Corynebacterium glutamicum

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Leu Asp Gly Thr Val Leu Ser Ala Lys Ala Leu Asp Ala Phe Leu Leu
 35 40 45

Glu Gln Val Ala Arg Ala Lys Ala Glu Gly Ile Leu Phe Ser Ala His
 50 55 60

Leu Lys Ala Thr Met Met Lys Val Ser Asp Pro Ile Ile Phe Gly His
 65 70 75 80

Val Val Arg Ala Tyr Phe Ala Asp Val Phe Ala Gln Tyr Gly Glu Gln
 85 90 95

Leu Leu Ala Ala Gly Leu Asn Gly Glu Asn Gly Leu Ala Ala Ile Leu
 100 105 110

Ser Gly Leu Glu Ser Leu Asp Asn Gly Glu Glu Ile Lys Ala Ala Phe
 115 120 125

Glu Lys Gly Leu Glu Asp Gly Pro Asp Leu Ala Met Val Asn Ser Ala
 130 135 140

Arg Gly Ile Thr Asn Leu His Val Pro Ser Asp Val Ile Val Asp Ala
 145 150 155 160

Ser Met Pro Ala Met Ile Arg Thr Ser Gly His Met Trp Asn Lys Asp

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Asp	Gln	Glu	Gln	Asp	Thr	Leu	Ala	Ile	Ile	Pro	Asp	Ser	Ser	Tyr	Ala				
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Gly	Val	Tyr	Gln	Thr	Val	Ile	Glu	Asp	Cys	Arg	Lys	Asn	Gly	Ala	Phe				
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Asp	Pro	Thr	Thr	Met	Gly	Thr	Val	Pro	Asn	Val	Gly	Leu	Met	Ala	Gln				
	210					215					220								
Lys	Ala	Glu	Glu	Tyr	Gly	Ser	His	Asp	Lys	Thr	Phe	Arg	Ile	Glu	Ala				
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Asp	Gly	Val	Val	Gln	Val	Val	Ser	Ser	Asn	Gly	Asp	Val	Leu	Ile	Glu				
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His	Asp	Val	Glu	Ala	Asn	Asp	Ile	Trp	Arg	Ala	Cys	Gln	Val	Lys	Asp				
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Ala	Pro	Ile	Gln	Asp	Trp	Val	Lys	Leu	Ala	Val	Thr	Arg	Ser	Arg	Leu				
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Ser	Gly	Met	Pro	Ala	Val	Phe	Trp	Leu	Asp	Pro	Glu	Arg	Ala	His	Asp				
	290					295					300								
Arg	Asn	Leu	Ala	Ser	Leu	Val	Glu	Lys	Tyr	Leu	Ala	Asp	His	Asp	Thr				
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Glu	Gly	Leu	Asp	Ile	Gln	Ile	Leu	Tyr	Pro	Val	Glu	Ala	Thr	Gln	Leu				
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 <222> (1)..(1671)
 <223> RXN02209

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gac	cgc	atc	ctt	ctc	tcc	gag	gca	aag	gag	cag	ttc	cgt	aag	gat	ctg	96
Asp	Arg	Ile	Leu	Leu	Ser	Glu	Ala	Lys	Glu	Gln	Phe	Arg	Lys	Asp	Leu	
			20					25					30			
cca	acc	tac	acc	gac	gac	gct	gtt	tcc	gta	gac	acc	tcc	atc	cct	gca	144
Pro	Thr	Tyr	Thr	Asp	Asp	Ala	Val	Ser	Val	Asp	Thr	Ser	Ile	Pro	Ala	
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acc cgc atg gtt aac gaa ggt ggc gga cag cct gaa ggc ggc gtc gaa	192
Thr Arg Met Val Asn Glu Gly Gly Gly Gln Pro Glu Gly Gly Val Glu	
50 55 60	
gct gac aac tac aac gct tcc tgg gct ggc tcc ggc gag tcc ttg gct	240
Ala Asp Asn Tyr Asn Ala Ser Trp Ala Gly Ser Gly Glu Ser Leu Ala	
65 70 75 80	
act ggc gca gaa gga cgt cct tcc aag cca gtc acc gtt gca tcc cca	288
Thr Gly Ala Glu Gly Arg Pro Ser Lys Pro Val Thr Val Ala Ser Pro	
85 90 95	
cag ggt ggc gag tac acc atc gac cac ggc atg gtt gca att gca tcc	336
Gln Gly Gly Glu Tyr Thr Ile Asp His Gly Met Val Ala Ile Ala Ser	
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atc acc tct tgc acc aac acc tct aac cca tcc gtg atg atc ggc gct	384
Ile Thr Ser Cys Thr Asn Thr Ser Asn Pro Ser Val Met Ile Gly Ala	
115 120 125	
ggc ctg atc gca cgt aag gca gca gaa aag ggc ctc aag tcc aag cct	432
Gly Leu Ile Ala Arg Lys Ala Ala Glu Lys Gly Leu Lys Ser Lys Pro	
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tgg gtt aag acc atc tgt gca cca ggt tcc cag gtt gtc gac ggc tac	480
Trp Val Lys Thr Ile Cys Ala Pro Gly Ser Gln Val Val Asp Gly Tyr	
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Tyr Gln Arg Ala Asp Leu Trp Lys Asp Leu Glu Ala Met Gly Phe Tyr	
165 170 175	
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Leu Ser Gly Phe Gly Cys Thr Thr Cys Ile Gly Asn Ser Gly Pro Leu	
180 185 190	
cca gag gaa atc tcc gct gcg atc aac gag cac gac ctg acc gca acc	624
Pro Glu Glu Ile Ser Ala Ala Ile Asn Glu His Asp Leu Thr Ala Thr	
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gca gtt ttg tcc ggt aac cgt aac ttc gag gga cgt atc tcc cct gac	672
Ala Val Leu Ser Gly Asn Arg Asn Phe Glu Gly Arg Ile Ser Pro Asp	
210 215 220	
gtt aag atg aac tac ctg gca tcc cca atc atg gtc att gct tac gca	720
Val Lys Met Asn Tyr Leu Ala Ser Pro Ile Met Val Ile Ala Tyr Ala	
225 230 235 240	
atc gct ggc acc atg gac ttc gac ttc gag aac gaa gct ctt gga cag	768
Ile Ala Gly Thr Met Asp Phe Asp Phe Glu Asn Glu Ala Leu Gly Gln	
245 250 255	
gac cag gac ggc aac gac gtc ttc ctg aag gac atc tgg cct tcc acc	816
Asp Gln Asp Gly Asn Asp Val Phe Leu Lys Asp Ile Trp Pro Ser Thr	
260 265 270	
gag gaa atc gaa gac acc atc cag cag gca atc tcc cgt gag ctt tac	864
Glu Glu Ile Glu Asp Thr Ile Gln Gln Ala Ile Ser Arg Glu Leu Tyr	
275 280 285	

gaa gct gac tac gca gat gtc ttc aag ggt gac aag cag tgg cag gaa	912
Glu Ala Asp Tyr Ala Asp Val Phe Lys Gly Asp Lys Gln Trp Gln Glu	
290 295 300	
ctc gat gtt cct acc ggt gac acc ttc gag tgg gac gag aac tcc acc	960
Leu Asp Val Pro Thr Gly Asp Thr Phe Glu Trp Asp Glu Asn Ser Thr	
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tac atc cgc aag gca cct tac ttc gac ggc atg cct gtc gag cca gtg	1008
Tyr Ile Arg Lys Ala Pro Tyr Phe Asp Gly Met Pro Val Glu Pro Val	
325 330 335	
gca gtc acc gac atc cag ggc gca cgc gtt ctg gct aag ctc ggc gac	1056
Ala Val Thr Asp Ile Gln Gly Ala Arg Val Leu Ala Lys Leu Gly Asp	
340 345 350	
tct gtc acc acc gac cac atc tcc cct gct tcc tcc att aag cca ggt	1104
Ser Val Thr Thr Asp His Ile Ser Pro Ala Ser Ser Ile Lys Pro Gly	
355 360 365	
acc cct gca gct cag tac ttg gat gag cac ggt gtg gaa cgc cac gac	1152
Thr Pro Ala Ala Gln Tyr Leu Asp Glu His Gly Val Glu Arg His Asp	
370 375 380	
tac aac tcc ctg ggt tcc agg cgt ggt aac cac gag gtc atg atg cgc	1200
Tyr Asn Ser Leu Gly Ser Arg Arg Gly Asn His Glu Val Met Met Arg	
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ggc acc ttc gcc aac atc cgc ctc cag aac cag ctg gtt gac atc gca	1248
Gly Thr Phe Ala Asn Ile Arg Leu Gln Asn Gln Leu Val Asp Ile Ala	
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ggt ggc tac acc cgc gac ttc acc cag gag ggt gct cca cag gcg ttc	1296
Gly Gly Tyr Thr Arg Asp Phe Thr Gln Glu Gly Ala Pro Gln Ala Phe	
420 425 430	
atc tac gac gct tcc gtc aac tac aag gct gct ggc att ccg ctg gtc	1344
Ile Tyr Asp Ala Ser Val Asn Tyr Lys Ala Ala Gly Ile Pro Leu Val	
435 440 445	
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Val Leu Gly Gly Lys Glu Tyr Gly Thr Gly Ser Ser Arg Asp Trp Ala	
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gct aag ggc act aac ctg ctc gga att cgc gca gtt atc acc gag tcc	1440
Ala Lys Gly Thr Asn Leu Leu Gly Ile Arg Ala Val Ile Thr Glu Ser	
465 470 475 480	
ttc gag cgt att cac cgc tcc aac ctc atc ggt atg ggc gtt gtc cca	1488
Phe Glu Arg Ile His Arg Ser Asn Leu Ile Gly Met Gly Val Val Pro	
485 490 495	
ctg cag ttc cct gca ggc gaa tcc cac gag tcc ctg ggc ctt gac ggc	1536
Leu Gln Phe Pro Ala Gly Glu Ser His Glu Ser Leu Gly Leu Asp Gly	
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acc gag acc ttc gac atc acc gga ctg acc gca ctt aac gag ggc gag	1584
Thr Glu Thr Phe Asp Ile Thr Gly Leu Thr Ala Leu Asn Glu Gly Glu	
515 520 525	
act cct aag act gtc aag gtc acc gca acc aag gag aac ggc gac gtc	1632

Thr Pro Lys Thr Val Lys Val Thr Ala Thr Lys Glu Asn Gly Asp Val
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 gtc gag ttc gac gca att tgt ccg cat cga cac ccc agg tgaggctgac 1681
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tactaccgcc acg 1694

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<213> Corynebacterium glutamicum

<400> 554

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 35 40 45
 Thr Arg Met Val Asn Glu Gly Gly Gly Gln Pro Glu Gly Gly Val Glu
 50 55 60
 Ala Asp Asn Tyr Asn Ala Ser Trp Ala Gly Ser Gly Glu Ser Leu Ala
 65 70 75 80
 Thr Gly Ala Glu Gly Arg Pro Ser Lys Pro Val Thr Val Ala Ser Pro
 85 90 95
 Gln Gly Gly Glu Tyr Thr Ile Asp His Gly Met Val Ala Ile Ala Ser
 100 105 110
 Ile Thr Ser Cys Thr Asn Thr Ser Asn Pro Ser Val Met Ile Gly Ala
 115 120 125
 Gly Leu Ile Ala Arg Lys Ala Ala Glu Lys Gly Leu Lys Ser Lys Pro
 130 135 140
 Trp Val Lys Thr Ile Cys Ala Pro Gly Ser Gln Val Val Asp Gly Tyr
 145 150 155 160
 Tyr Gln Arg Ala Asp Leu Trp Lys Asp Leu Glu Ala Met Gly Phe Tyr
 165 170 175
 Leu Ser Gly Phe Gly Cys Thr Thr Cys Ile Gly Asn Ser Gly Pro Leu
 180 185 190
 Pro Glu Glu Ile Ser Ala Ala Ile Asn Glu His Asp Leu Thr Ala Thr
 195 200 205
 Ala Val Leu Ser Gly Asn Arg Asn Phe Glu Gly Arg Ile Ser Pro Asp
 210 215 220
 Val Lys Met Asn Tyr Leu Ala Ser Pro Ile Met Val Ile Ala Tyr Ala
 225 230 235 240

Ile Ala Gly Thr Met Asp Phe Asp Phe Glu Asn Glu Ala Leu Gly Gln
 245 250 255
 Asp Gln Asp Gly Asn Asp Val Phe Leu Lys Asp Ile Trp Pro Ser Thr
 260 265 270
 Glu Glu Ile Glu Asp Thr Ile Gln Gln Ala Ile Ser Arg Glu Leu Tyr
 275 280 285
 Glu Ala Asp Tyr Ala Asp Val Phe Lys Gly Asp Lys Gln Trp Gln Glu
 290 295 300
 Leu Asp Val Pro Thr Gly Asp Thr Phe Glu Trp Asp Glu Asn Ser Thr
 305 310 315 320
 Tyr Ile Arg Lys Ala Pro Tyr Phe Asp Gly Met Pro Val Glu Pro Val
 325 330 335
 Ala Val Thr Asp Ile Gln Gly Ala Arg Val Leu Ala Lys Leu Gly Asp
 340 345 350
 Ser Val Thr Thr Asp His Ile Ser Pro Ala Ser Ser Ile Lys Pro Gly
 355 360 365
 Thr Pro Ala Ala Gln Tyr Leu Asp Glu His Gly Val Glu Arg His Asp
 370 375 380
 Tyr Asn Ser Leu Gly Ser Arg Arg Gly Asn His Glu Val Met Met Arg
 385 390 395 400
 Gly Thr Phe Ala Asn Ile Arg Leu Gln Asn Gln Leu Val Asp Ile Ala
 405 410 415
 Gly Gly Tyr Thr Arg Asp Phe Thr Gln Glu Gly Ala Pro Gln Ala Phe
 420 425 430
 Ile Tyr Asp Ala Ser Val Asn Tyr Lys Ala Ala Gly Ile Pro Leu Val
 435 440 445
 Val Leu Gly Gly Lys Glu Tyr Gly Thr Gly Ser Ser Arg Asp Trp Ala
 450 455 460
 Ala Lys Gly Thr Asn Leu Leu Gly Ile Arg Ala Val Ile Thr Glu Ser
 465 470 475 480
 Phe Glu Arg Ile His Arg Ser Asn Leu Ile Gly Met Gly Val Val Pro
 485 490 495
 Leu Gln Phe Pro Ala Gly Glu Ser His Glu Ser Leu Gly Leu Asp Gly
 500 505 510
 Thr Glu Thr Phe Asp Ile Thr Gly Leu Thr Ala Leu Asn Glu Gly Glu
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 Val Glu Phe Asp Ala Ile Cys Pro His Arg His Pro Arg
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<220>
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 <222> (1)..(1659)
 <223> FRXA02209

<400> 555
 gtt gtt cct tcc atc gct ggc cct aag cgc cca cag gac cgc atc ctt 48
 Val Val Pro Ser Ile Ala Gly Pro Lys Arg Pro Gln Asp Arg Ile Leu
 1 5 10 15
 ctc tcc gag gca aag gag cag ttc cgt aag gat ctg cca acc tac acc 96
 Leu Ser Glu Ala Lys Glu Gln Phe Arg Lys Asp Leu Pro Thr Tyr Thr
 20 25 30
 gac gac gct gtt tcc gta gac acc tcc atc cct gca acc cgc atg gtt 144
 Asp Asp Ala Val Ser Val Asp Thr Ser Ile Pro Ala Thr Arg Met Val
 35 40 45
 aac gaa ggt ggc gga cag cct gaa ggc ggc gtc gaa gct gac aac tac 192
 Asn Glu Gly Gly Gly Gln Pro Glu Gly Gly Val Glu Ala Asp Asn Tyr
 50 55 60
 aac gct tcc tgg gct ggc tcc ggc gag tcc ttg gct act ggc gca gaa 240
 Asn Ala Ser Trp Ala Gly Ser Gly Glu Ser Leu Ala Thr Gly Ala Glu
 65 70 75 80
 gga cgt cct tcc aag cca gtc acc gtt gca tcc cca cag ggt ggc gag 288
 Gly Arg Pro Ser Lys Pro Val Thr Val Ala Ser Pro Gln Gly Gly Glu
 85 90 95
 tac acc atc gac cac ggc atg gtt gca att gca tcc atc acc tct tgc 336
 Tyr Thr Ile Asp His Gly Met Val Ala Ile Ala Ser Ile Thr Ser Cys
 100 105 110
 acc aac acc tct aac cca tcc gtg atg atc ggc gct ggc ctg atc gca 384
 Thr Asn Thr Ser Asn Pro Ser Val Met Ile Gly Ala Gly Leu Ile Ala
 115 120 125
 cgt aag gca gca gaa aag ggc ctc aag tcc aag cct tgg gtt aag acc 432
 Arg Lys Ala Ala Glu Lys Gly Leu Lys Ser Lys Pro Trp Val Lys Thr
 130 135 140
 atc tgt gca cca ggt tcc cag gtt gtc gac ggc tac tac cag cgc gca 480
 Ile Cys Ala Pro Gly Ser Gln Val Val Asp Gly Tyr Tyr Gln Arg Ala
 145 150 155 160
 gac ctc tgg aag gac ctt gag gcc atg ggc ttc tac ctc tcc ggc ttc 528
 Asp Leu Trp Lys Asp Leu Glu Ala Met Gly Phe Tyr Leu Ser Gly Phe
 165 170 175
 ggc tgc acc acc tgt att ggt aac tcc ggc cca ctg cca gag gaa atc 576
 Gly Cys Thr Thr Cys Ile Gly Asn Ser Gly Pro Leu Pro Glu Glu Ile
 180 185 190
 tcc gct gcg atc aac gag cac gac ctg acc gca acc gca gtt ttg tcc 624
 Ser Ala Ala Ile Asn Glu His Asp Leu Thr Ala Thr Ala Val Leu Ser

195	200	205	
ggt aac cgt aac ttc gag gga cgt atc tcc cct gac gtt aag atg aac Gly Asn Arg Asn Phe Glu Gly Arg Ile Ser Pro Asp Val Lys Met Asn 210 215 220			672
tac ctg gca tcc cca atc atg gtc att gct tac gca atc gct ggc acc Tyr Leu Ala Ser Pro Ile Met Val Ile Ala Tyr Ala Ile Ala Gly Thr 225 230 235 240			720
atg gac ttc gac ttc gag aac gaa gct ctt gga cag gac cag gac ggc Met Asp Phe Asp Phe Glu Asn Glu Ala Leu Gly Gln Asp Gln Asp Gly 245 250 255			768
aac gac gtc ttc ctg aag gac atc tgg cct tcc acc gag gaa atc gaa Asn Asp Val Phe Leu Lys Asp Ile Trp Pro Ser Thr Glu Glu Ile Glu 260 265 270			816
gac acc atc cag cag gca atc tcc cgt gag ctt tac gaa gct gac tac Asp Thr Ile Gln Gln Ala Ile Ser Arg Glu Leu Tyr Glu Ala Asp Tyr 275 280 285			864
gca gat gtc ttc aag ggt gac aag cag tgg cag gaa ctc gat gtt cct Ala Asp Val Phe Lys Gly Asp Lys Gln Trp Gln Glu Leu Asp Val Pro 290 295 300			912
acc ggt gac acc ttc gag tgg gac gag aac tcc acc tac atc cgc aag Thr Gly Asp Thr Phe Glu Trp Asp Glu Asn Ser Thr Tyr Ile Arg Lys 305 310 315 320			960
gca cct tac ttc gac ggc atg cct gtc gag cca gtg gca gtc acc gac Ala Pro Tyr Phe Asp Gly Met Pro Val Glu Pro Val Ala Val Thr Asp 325 330 335			1008
atc cag ggc gca cgc gtt ctg gct aag ctc ggc gac tct gtc acc acc Ile Gln Gly Ala Arg Val Leu Ala Lys Leu Gly Asp Ser Val Thr Thr 340 345 350			1056
gac cac atc tcc cct gct tcc tcc att aag cca ggt acc cct gca gct Asp His Ile Ser Pro Ala Ser Ser Ile Lys Pro Gly Thr Pro Ala Ala 355 360 365			1104
cag tac ttg gat gag cac ggt gtg gaa cgc cac gac tac aac tcc ctg Gln Tyr Leu Asp Glu His Gly Val Glu Arg His Asp Tyr Asn Ser Leu 370 375 380			1152
ggt tcc agg cgt ggt aac cac gag gtc atg atg cgc ggc acc ttc gcc Gly Ser Arg Arg Gly Asn His Glu Val Met Met Arg Gly Thr Phe Ala 385 390 395 400			1200
aac atc cgc ctc cag aac cag ctg gtt gac atc gca ggt ggc tac acc Asn Ile Arg Leu Gln Asn Gln Leu Val Asp Ile Ala Gly Gly Tyr Thr 405 410 415			1248
cgc gac ttc acc cag gag ggt gct cca cag gcg ttc atc tac gac gct Arg Asp Phe Thr Gln Glu Gly Ala Pro Gln Ala Phe Ile Tyr Asp Ala 420 425 430			1296
tcc gtc aac tac aag gct gct ggc att ccg ctg gtc gtc ttg ggc ggc Ser Val Asn Tyr Lys Ala Ala Gly Ile Pro Leu Val Val Leu Gly Gly 435 440 445			1344

aag gag tac ggc acc ggt tct tcc cgt gac tgg gca gct aag ggc act 1392
Lys Glu Tyr Gly Thr Gly Ser Ser Arg Asp Trp Ala Ala Lys Gly Thr
450 455 460

aac ctg ctc gga att cgc gca gtt atc acc gag tcc ttc gag cgt att 1440
Asn Leu Leu Gly Ile Arg Ala Val Ile Thr Glu Ser Phe Glu Arg Ile
465 470 475 480

cac cgc tcc aac ctc atc ggt atg ggc gtt gtc cca ctg cag ttc cct 1488
His Arg Ser Asn Leu Ile Gly Met Gly Val Val Pro Leu Gln Phe Pro
485 490 495

gca ggc gaa tcc cac gag tcc ctg ggc ctt gac ggc acc gag acc ttc 1536
Ala Gly Glu Ser His Glu Ser Leu Gly Leu Asp Gly Thr Glu Thr Phe
500 505 510

gac atc acc gga ctg acc gca ctt aac gag ggc gag act cct aag act 1584
Asp Ile Thr Gly Leu Thr Ala Leu Asn Glu Gly Glu Thr Pro Lys Thr
515 520 525

gtc aag gtc acc gca acc aag gag aac ggc gac gtc gtc gag ttc gac 1632
Val Lys Val Thr Ala Thr Lys Glu Asn Gly Asp Val Val Glu Phe Asp
530 535 540

gca att tgt ccg cat cga cac ccc agg tgaggctgac tactaccgcc 1679
Ala Ile Cys Pro His Arg His Pro Arg
545 550

acg 1682

<210> 556

<211> 553

<212> PRT

<213> Corynebacterium glutamicum

<400> 556

Val Val Pro Ser Ile Ala Gly Pro Lys Arg Pro Gln Asp Arg Ile Leu
1 5 10 15

Leu Ser Glu Ala Lys Glu Gln Phe Arg Lys Asp Leu Pro Thr Tyr Thr
20 25 30

Asp Asp Ala Val Ser Val Asp Thr Ser Ile Pro Ala Thr Arg Met Val
35 40 45

Asn Glu Gly Gly Gly Gln Pro Glu Gly Gly Val Glu Ala Asp Asn Tyr
50 55 60

Asn Ala Ser Trp Ala Gly Ser Gly Glu Ser Leu Ala Thr Gly Ala Glu
65 70 75 80

Gly Arg Pro Ser Lys Pro Val Thr Val Ala Ser Pro Gln Gly Gly Glu
85 90 95

Tyr Thr Ile Asp His Gly Met Val Ala Ile Ala Ser Ile Thr Ser Cys
100 105 110

Thr Asn Thr Ser Asn Pro Ser Val Met Ile Gly Ala Gly Leu Ile Ala
115 120 125

Arg Lys Ala Ala Glu Lys Gly Leu Lys Ser Lys Pro Trp Val Lys Thr
 130 135 140
 Ile Cys Ala Pro Gly Ser Gln Val Val Asp Gly Tyr Tyr Gln Arg Ala
 145 150 155 160
 Asp Leu Trp Lys Asp Leu Glu Ala Met Gly Phe Tyr Leu Ser Gly Phe
 165 170 175
 Gly Cys Thr Thr Cys Ile Gly Asn Ser Gly Pro Leu Pro Glu Glu Ile
 180 185 190
 Ser Ala Ala Ile Asn Glu His Asp Leu Thr Ala Thr Ala Val Leu Ser
 195 200 205
 Gly Asn Arg Asn Phe Glu Gly Arg Ile Ser Pro Asp Val Lys Met Asn
 210 215 220
 Tyr Leu Ala Ser Pro Ile Met Val Ile Ala Tyr Ala Ile Ala Gly Thr
 225 230 235 240
 Met Asp Phe Asp Phe Glu Asn Glu Ala Leu Gly Gln Asp Gln Asp Gly
 245 250 255
 Asn Asp Val Phe Leu Lys Asp Ile Trp Pro Ser Thr Glu Glu Ile Glu
 260 265 270
 Asp Thr Ile Gln Gln Ala Ile Ser Arg Glu Leu Tyr Glu Ala Asp Tyr
 275 280 285
 Ala Asp Val Phe Lys Gly Asp Lys Gln Trp Gln Glu Leu Asp Val Pro
 290 295 300
 Thr Gly Asp Thr Phe Glu Trp Asp Glu Asn Ser Thr Tyr Ile Arg Lys
 305 310 315 320
 Ala Pro Tyr Phe Asp Gly Met Pro Val Glu Pro Val Ala Val Thr Asp
 325 330 335
 Ile Gln Gly Ala Arg Val Leu Ala Lys Leu Gly Asp Ser Val Thr Thr
 340 345 350
 Asp His Ile Ser Pro Ala Ser Ser Ile Lys Pro Gly Thr Pro Ala Ala
 355 360 365
 Gln Tyr Leu Asp Glu His Gly Val Glu Arg His Asp Tyr Asn Ser Leu
 370 375 380
 Gly Ser Arg Arg Gly Asn His Glu Val Met Met Arg Gly Thr Phe Ala
 385 390 395 400
 Asn Ile Arg Leu Gln Asn Gln Leu Val Asp Ile Ala Gly Gly Tyr Thr
 405 410 415
 Arg Asp Phe Thr Gln Glu Gly Ala Pro Gln Ala Phe Ile Tyr Asp Ala
 420 425 430
 Ser Val Asn Tyr Lys Ala Ala Gly Ile Pro Leu Val Val Leu Gly Gly
 435 440 445

Lys Glu Tyr Gly Thr Gly Ser Ser Arg Asp Trp Ala Ala Lys Gly Thr
450 455 460

Asn Leu Leu Gly Ile Arg Ala Val Ile Thr Glu Ser Phe Glu Arg Ile
465 470 475 480

His Arg Ser Asn Leu Ile Gly Met Gly Val Val Pro Leu Gln Phe Pro
485 490 495

Ala Gly Glu Ser His Glu Ser Leu Gly Leu Asp Gly Thr Glu Thr Phe
500 505 510

Asp Ile Thr Gly Leu Thr Ala Leu Asn Glu Gly Glu Thr Pro Lys Thr
515 520 525

Val Lys Val Thr Ala Thr Lys Glu Asn Gly Asp Val Val Glu Phe Asp
530 535 540

Ala Ile Cys Pro His Arg His Pro Arg
545 550

<210> 557

<211> 874

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(874)

<223> RXN02213

<400> 557

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gcgaaatctc accctaaaaa agttagaatt ggagctcact gtg act gaa agc aag 115
Val Thr Glu Ser Lys
1 5

aac tcc ttc aat gct aag agc acc ctt gaa gtt ggc gac aag tcc tat 163
Asn Ser Phe Asn Ala Lys Ser Thr Leu Glu Val Gly Asp Lys Ser Tyr
10 15 20

gac tac ttc gcc ctc tct gca gtg cct ggc atg gag aag ctg ccg tac 211
Asp Tyr Phe Ala Leu Ser Ala Val Pro Gly Met Glu Lys Leu Pro Tyr
25 30 35

tcc ctc aag gtt ctc gga gag aac ctt ctt cgt acc gaa gac ggc gca 259
Ser Leu Lys Val Leu Gly Glu Asn Leu Leu Arg Thr Glu Asp Gly Ala
40 45 50

aac atc acc aac gag cac att gag gct atc gcc aac tgg gat gca tct 307
Asn Ile Thr Asn Glu His Ile Glu Ala Ile Ala Asn Trp Asp Ala Ser
55 60 65

tcc gat cca agc atc gaa atc cag ttc acc cca gcc cgt gtt ctc atg 355
Ser Asp Pro Ser Ile Glu Ile Gln Phe Thr Pro Ala Arg Val Leu Met
70 75 80 85

cag gac ttc acc ggt gtc cct tgt gta gtt gac ctc gca acc atg cgt 403
Gln Asp Phe Thr Gly Val Pro Cys Val Val Asp Leu Ala Thr Met Arg

90										95										100										
gag gca gtt gct gca ctc ggt ggc gac cct aac gac gtc aac cca ctg	451																													
Glu Ala Val Ala Ala Leu Gly Gly Asp Pro Asn Asp Val Asn Pro Leu																														
105 110 115																														
aac cca gcc gag atg gtc att gac cac tcc gtc atc gtg gag gct ttc	499																													
Asn Pro Ala Glu Met Val Ile Asp His Ser Val Ile Val Glu Ala Phe																														
120 125 130																														
ggc cgc cca gat gca ctg gct aag aac gtt gag atc gag tac gag cgc	547																													
Gly Arg Pro Asp Ala Leu Ala Lys Asn Val Glu Ile Glu Tyr Glu Arg																														
135 140 145																														
aac gag gag cgt tac cag ttc ctg cgt tgg ggt tcc gag tcc ttc tcc	595																													
Asn Glu Glu Arg Tyr Gln Phe Leu Arg Trp Gly Ser Glu Ser Phe Ser																														
150 155 160 165																														
aac ttc cgc gtt gtt cct cca gga acc ggt atc gtc cac cag gtc aac	643																													
Asn Phe Arg Val Val Pro Pro Gly Thr Gly Ile Val His Gln Val Asn																														
170 175 180																														
att gag tac ttg gct cgc gtc gtc ttc gac aac gag ggc ctt gca tac	691																													
Ile Glu Tyr Leu Ala Arg Val Val Phe Asp Asn Glu Gly Leu Ala Tyr																														
185 190 195																														
cca gat acc tgc atc ggt acc gac tcc cac acc acc atg gaa aac ggc	739																													
Pro Asp Thr Cys Ile Gly Thr Asp Ser His Thr Thr Met Glu Asn Gly																														
200 205 210																														
ctg ggc atc ctg ggc tgg ggc gtt ggt ggc att gag gct gaa gca gca	787																													
Leu Gly Ile Leu Gly Trp Gly Val Gly Gly Ile Glu Ala Glu Ala Ala																														
215 220 225																														
atg ctc ggc cag cca gtg tcc atg ctg atc cct cgc gtt gtt ggc ttc	835																													
Met Leu Gly Gln Pro Val Ser Met Leu Ile Pro Arg Val Val Gly Phe																														
230 235 240 245																														
aag ttg acc ggc gag atc cca gta ggc gtt acc gca act	874																													
Lys Leu Thr Gly Glu Ile Pro Val Gly Val Thr Ala Thr																														
250 255																														

<210> 558

<211> 258

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 558

Val Thr Glu Ser Lys Asn Ser Phe Asn Ala Lys Ser Thr Leu Glu Val
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Gly Asp Lys Ser Tyr Asp Tyr Phe Ala Leu Ser Ala Val Pro Gly Met
20 25 30

Glu Lys Leu Pro Tyr Ser Leu Lys Val Leu Gly Glu Asn Leu Leu Arg
35 40 45

Thr Glu Asp Gly Ala Asn Ile Thr Asn Glu His Ile Glu Ala Ile Ala
50 55 60

Asn Trp Asp Ala Ser Ser Asp Pro Ser Ile Glu Ile Gln Phe Thr Pro
 65 70 75 80
 Ala Arg Val Leu Met Gln Asp Phe Thr Gly Val Pro Cys Val Val Asp
 85 90 95
 Leu Ala Thr Met Arg Glu Ala Val Ala Ala Leu Gly Gly Asp Pro Asn
 100 105 110
 Asp Val Asn Pro Leu Asn Pro Ala Glu Met Val Ile Asp His Ser Val
 115 120 125
 Ile Val Glu Ala Phe Gly Arg Pro Asp Ala Leu Ala Lys Asn Val Glu
 130 135 140
 Ile Glu Tyr Glu Arg Asn Glu Glu Arg Tyr Gln Phe Leu Arg Trp Gly
 145 150 155 160
 Ser Glu Ser Phe Ser Asn Phe Arg Val Val Pro Pro Gly Thr Gly Ile
 165 170 175
 Val His Gln Val Asn Ile Glu Tyr Leu Ala Arg Val Val Phe Asp Asn
 180 185 190
 Glu Gly Leu Ala Tyr Pro Asp Thr Cys Ile Gly Thr Asp Ser His Thr
 195 200 205
 Thr Met Glu Asn Gly Leu Gly Ile Leu Gly Trp Gly Val Gly Gly Ile
 210 215 220
 Glu Ala Glu Ala Ala Met Leu Gly Gln Pro Val Ser Met Leu Ile Pro
 225 230 235 240
 Arg Val Val Gly Phe Lys Leu Thr Gly Glu Ile Pro Val Gly Val Thr
 245 250 255

Ala Thr

<210> 559
 <211> 817
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(817)
 <223> FRXA02213

<400> 559
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gcgaaatctc accctaaaaa agttagaatt ggagctcact gtg act gaa agc aag 115
 Val Thr Glu Ser Lys 5
 1

aac tcc ttc aat gct aag agc acc ctt gaa gtt ggc gac aag tcc tat 163
 Asn Ser Phe Asn Ala Lys Ser Thr Leu Glu Val Gly Asp Lys Ser Tyr 20
 10 15

gac tac ttc gcc ctc tct gca gtg cct ggc atg gag aag ctg ccg tac 211
 Asp Tyr Phe Ala Leu Ser Ala Val Pro Gly Met Glu Lys Leu Pro Tyr
 25 30 35

tcc ctc aag gtt ctc gga gag aac ctt ctt cgt acc gaa gac ggc gca 259
 Ser Leu Lys Val Leu Gly Glu Asn Leu Leu Arg Thr Glu Asp Gly Ala
 40 45 50

aac atc acc aac gag cac att gag gct atc gcc aac tgg gat gca tct 307
 Asn Ile Thr Asn Glu His Ile Glu Ala Ile Ala Asn Trp Asp Ala Ser
 55 60 65

tcc gat cca agc atc gaa atc cag ttc acc cca gcc cgt gtt ctc atg 355
 Ser Asp Pro Ser Ile Glu Ile Gln Phe Thr Pro Ala Arg Val Leu Met
 70 75 80 85

cag gac ttc acc ggt gtc cct tgt gta gtt gac ctc gca acc atg cgt 403
 Gln Asp Phe Thr Gly Val Pro Cys Val Val Asp Leu Ala Thr Met Arg
 90 95 100

gag gca gtt gct gca ctc ggt ggc gac cct aac gac gtc aac cca ctg 451
 Glu Ala Val Ala Ala Leu Gly Gly Asp Pro Asn Asp Val Asn Pro Leu
 105 110 115

aac cca gcc gag atg gtc att gac cac tcc gtc atc gtg gag gct ttc 499
 Asn Pro Ala Glu Met Val Ile Asp His Ser Val Ile Val Glu Ala Phe
 120 125 130

ggc cgc cca gat gca ctg gct aag aac gtt gag atc gag tac gag cgc 547
 Gly Arg Pro Asp Ala Leu Ala Lys Asn Val Glu Ile Glu Tyr Glu Arg
 135 140 145

aac gag gag cgt tac cag ttc ctg cgt tgg ggt tcc gag tcc ttc tcc 595
 Asn Glu Glu Arg Tyr Gln Phe Leu Arg Trp Gly Ser Glu Ser Phe Ser
 150 155 160 165

aac ttc cgc gtt gtt cct cca gga acc ggt atc gtc cac cag gtc aac 643
 Asn Phe Arg Val Val Pro Pro Gly Thr Gly Ile Val His Gln Val Asn
 170 175 180

att gag tac ttg gct cgc gtc gtc ttc gac aac gag ggc ctt gca tac 691
 Ile Glu Tyr Leu Ala Arg Val Val Phe Asp Asn Glu Gly Leu Ala Tyr
 185 190 195

cca gat acc tgc atc ggt acc gac tcc cac acc acc atg gaa aac ggc 739
 Pro Asp Thr Cys Ile Gly Thr Asp Ser His Thr Thr Met Glu Asn Gly
 200 205 210

ctg ggc atc ctg ggc tgg ggc gtt ggt ggc att gag gct gaa gca gca 787
 Leu Gly Ile Leu Gly Trp Gly Val Gly Gly Ile Glu Ala Glu Ala Ala
 215 220 225

atg ctc ggc cag cca gtg tcc atg ctg atc 817
 Met Leu Gly Gln Pro Val Ser Met Leu Ile
 230 235

<210> 560

<211> 239

<212> PRT

<213> Corynebacterium glutamicum

<400> 560

Val Thr Glu Ser Lys Asn Ser Phe Asn Ala Lys Ser Thr Leu Glu Val
 1 5 10 15
 Gly Asp Lys Ser Tyr Asp Tyr Phe Ala Leu Ser Ala Val Pro Gly Met
 20 25 30
 Glu Lys Leu Pro Tyr Ser Leu Lys Val Leu Gly Glu Asn Leu Leu Arg
 35 40 45
 Thr Glu Asp Gly Ala Asn Ile Thr Asn Glu His Ile Glu Ala Ile Ala
 50 55 60
 Asn Trp Asp Ala Ser Ser Asp Pro Ser Ile Glu Ile Gln Phe Thr Pro
 65 70 75 80
 Ala Arg Val Leu Met Gln Asp Phe Thr Gly Val Pro Cys Val Val Asp
 85 90 95
 Leu Ala Thr Met Arg Glu Ala Val Ala Ala Leu Gly Gly Asp Pro Asn
 100 105 110
 Asp Val Asn Pro Leu Asn Pro Ala Glu Met Val Ile Asp His Ser Val
 115 120 125
 Ile Val Glu Ala Phe Gly Arg Pro Asp Ala Leu Ala Lys Asn Val Glu
 130 135 140
 Ile Glu Tyr Glu Arg Asn Glu Glu Arg Tyr Gln Phe Leu Arg Trp Gly
 145 150 155 160
 Ser Glu Ser Phe Ser Asn Phe Arg Val Val Pro Pro Gly Thr Gly Ile
 165 170 175
 Val His Gln Val Asn Ile Glu Tyr Leu Ala Arg Val Val Phe Asp Asn
 180 185 190
 Glu Gly Leu Ala Tyr Pro Asp Thr Cys Ile Gly Thr Asp Ser His Thr
 195 200 205
 Thr Met Glu Asn Gly Leu Gly Ile Leu Gly Trp Gly Val Gly Gly Ile
 210 215 220
 Glu Ala Glu Ala Ala Met Leu Gly Gln Pro Val Ser Met Leu Ile
 225 230 235

<210> 561

<211> 2891

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (1)..(2868)

<223> RXA02056

<400> 561

cgc cac tct gtt cca cgt cta acc aag ggc cag ggc acc atc atc ggt
 Arg His Ser Val Pro Arg Leu Thr Lys Gly Gln Gly Thr Ile Ile Gly

48

1	5	10	15	
gtc ggt tcc atg gat tac cca gca gag ttc cag ggc gct tca gaa gac				96
Val Gly Ser Met Asp Tyr Pro Ala Glu Phe Gln Gly Ala Ser Glu Asp	20	25	30	
cgc ctt gca gag ctc ggc gtt ggc aaa ctt gtc acc atc acc tcc acc				144
Arg Leu Ala Glu Leu Gly Val Gly Lys Leu Val Thr Ile Thr Ser Thr	35	40	45	
tac gat cac cgc gtg atc cag ggt gct gtg tcc ggt gaa ttc ctg cgc				192
Tyr Asp His Arg Val Ile Gln Gly Ala Val Ser Gly Glu Phe Leu Arg	50	55	60	
acc atg tct cgc ctg ctc acc gat gat tcc ttc tgg gat gag atc ttc				240
Thr Met Ser Arg Leu Leu Thr Asp Asp Ser Phe Trp Asp Glu Ile Phe	65	70	75	80
gac gca atg aac gtt cct tac acc cca atg cgt tgg gca cag gac gtt				288
Asp Ala Met Asn Val Pro Tyr Thr Pro Met Arg Trp Ala Gln Asp Val	85	90	95	
cca aac acc ggt gtt gat aag aac acc cgc gtc atg cag ctc att gag				336
Pro Asn Thr Gly Val Asp Lys Asn Thr Arg Val Met Gln Leu Ile Glu	100	105	110	
gca tac cgc tcc cgt gga cac ctc atc gct gac acc aac cca ctt tca				384
Ala Tyr Arg Ser Arg Gly His Leu Ile Ala Asp Thr Asn Pro Leu Ser	115	120	125	
tgg gtt cag cct ggc atg cca gtt cca gac cac cgc gac ctc gac atc				432
Trp Val Gln Pro Gly Met Pro Val Pro Asp His Arg Asp Leu Asp Ile	130	135	140	
gag acc cac aac ctg acc atc tgg gat ctg gac cgt acc ttc aac gtc				480
Glu Thr His Asn Leu Thr Ile Trp Asp Leu Asp Arg Thr Phe Asn Val	145	150	155	160
ggt ggc ttc ggc ggc aag gag acc atg acc ctg cgc gag gta ctg tcc				528
Gly Gly Phe Gly Gly Lys Glu Thr Met Thr Leu Arg Glu Val Leu Ser	165	170	175	
cgc ctc cgc gct gcg tac acc ctc aag gtc ggc tcc gaa tac acc cac				576
Arg Leu Arg Ala Ala Tyr Thr Leu Lys Val Gly Ser Glu Tyr Thr His	180	185	190	
atc ctg gac cgc gac gag cgc acc tgg ctg cag gac cgc ctc gag gcc				624
Ile Leu Asp Arg Asp Glu Arg Thr Trp Leu Gln Asp Arg Leu Glu Ala	195	200	205	
gga atg cca aag cca acc cag gca gag cag aag tac atc ctg cag aag				672
Gly Met Pro Lys Pro Thr Gln Ala Glu Gln Lys Tyr Ile Leu Gln Lys	210	215	220	
ctg aac gcc gcg gag gct ttc gag aac ttc ctg cag acc aag tac gtc				720
Leu Asn Ala Ala Glu Ala Phe Glu Asn Phe Leu Gln Thr Lys Tyr Val	225	230	235	240
ggc cag aag cgc ttc tcc ctc gaa ggt gca gaa gca ctt atc cca ctg				768
Gly Gln Lys Arg Phe Ser Leu Glu Gly Ala Glu Ala Leu Ile Pro Leu	245	250	255	

atg gac tcc gcc atc gac acc gcc gca ggc caa ggc ctc gac gaa gtt	816
Met Asp Ser Ala Ile Asp Thr Ala Ala Gly Gln Gly Leu Asp Glu Val	
260 265 270	
gtc atc ggt atg cca cac cgt ggt cgc ctc aac gtg ctg ttc aac atc	864
Val Ile Gly Met Pro His Arg Gly Arg Leu Asn Val Leu Phe Asn Ile	
275 280 285	
gtg ggc aag cca ctg gca tcc atc ttc aac gag ttt gaa ggc caa atg	912
Val Gly Lys Pro Leu Ala Ser Ile Phe Asn Glu Phe Glu Gly Gln Met	
290 295 300	
gag cag ggc cag atc ggt ggc tcc ggt gac gtg aag tac cac ctc ggt	960
Glu Gln Gly Gln Ile Gly Gly Ser Gly Asp Val Lys Tyr His Leu Gly	
305 310 315 320	
tcc gaa ggc cag cac ctg cag atg ttc ggc gac ggc gag atc aag gtc	1008
Ser Glu Gly Gln His Leu Gln Met Phe Gly Asp Gly Glu Ile Lys Val	
325 330 335	
tcc ctg act gct aac ccg tcc cac ctg gaa gct gtt aac cca gcg atg	1056
Ser Leu Thr Ala Asn Pro Ser His Leu Glu Ala Val Asn Pro Ala Met	
340 345 350	
gaa ggt att gtc cgc gca aag cag gac tac ctg gac aag ggc gta gac	1104
Glu Gly Ile Val Arg Ala Lys Gln Asp Tyr Leu Asp Lys Gly Val Asp	
355 360 365	
ggc aag act gtt gtg cca ctg ctg ctc cac ggt gac gct gca ttc gca	1152
Gly Lys Thr Val Val Pro Leu Leu Leu His Gly Asp Ala Ala Phe Ala	
370 375 380	
ggc ctg ggc atc gtg cca gaa acc atc aac ctg gct aag ctg cgt ggc	1200
Gly Leu Gly Ile Val Pro Glu Thr Ile Asn Leu Ala Lys Leu Arg Gly	
385 390 395 400	
tac gac gtc ggc ggc acc atc cac atc gtg gtg aac aac cag atc ggc	1248
Tyr Asp Val Gly Gly Thr Ile His Ile Val Val Asn Asn Gln Ile Gly	
405 410 415	
ttc acc acc acc cca gac tcc agc cgc tcc atg cac tac gca acc gac	1296
Phe Thr Thr Thr Pro Asp Ser Ser Arg Ser Met His Tyr Ala Thr Asp	
420 425 430	
tac gcc aag gca ttc ggc tgc cca gtc ttc cac gtc aac ggc gac gac	1344
Tyr Ala Lys Ala Phe Gly Cys Pro Val Phe His Val Asn Gly Asp Asp	
435 440 445	
cca gag gca gtt gtc tgg gtt ggc cag ctg gcc acc gag tac cgt cgt	1392
Pro Glu Ala Val Val Trp Val Gly Gln Leu Ala Thr Glu Tyr Arg Arg	
450 455 460	
cgc ttc ggc aag gac gtc ttc atc gac ctc gtc tgc tac cgc ctc cgc	1440
Arg Phe Gly Lys Asp Val Phe Ile Asp Leu Val Cys Tyr Arg Leu Arg	
465 470 475 480	
ggc cac aac gaa gct gat gat cct tcc atg acc cag cca aag atg tat	1488
Gly His Asn Glu Ala Asp Asp Pro Ser Met Thr Gln Pro Lys Met Tyr	
485 490 495	

gag ctc atc acc ggc cgc gag acc gtt cgt gct cag tac acc gaa gac	1536
Glu Leu Ile Thr Gly Arg Glu Thr Val Arg Ala Gln Tyr Thr Glu Asp	
500 505 510	
ctg ctc gga cgt gga gac ctc tcc aac gaa gat gca gaa gca gtc gtc	1584
Leu Leu Gly Arg Gly Asp Leu Ser Asn Glu Asp Ala Glu Ala Val Val	
515 520 525	
cgc gac ttc cac gac cag atg gaa tct gtg ttc aac gaa gtc aag gaa	1632
Arg Asp Phe His Asp Gln Met Glu Ser Val Phe Asn Glu Val Lys Glu	
530 535 540	
ggc ggc aag aag cag gct gag gca cag acc ggc atc acc ggc tcc cag	1680
Gly Gly Lys Lys Gln Ala Glu Ala Gln Thr Gly Ile Thr Gly Ser Gln	
545 550 555 560	
aag ctt cca cac ggc ctt gag acc aac atc tcc cgt gaa gag ctc ctg	1728
Lys Leu Pro His Gly Leu Glu Thr Asn Ile Ser Arg Glu Glu Leu Leu	
565 570 575	
gaa ctg gga cag gct ttc gcc aac acc cca gaa ggc ttc aac tac cac	1776
Glu Leu Gly Gln Ala Phe Ala Asn Thr Pro Glu Gly Phe Asn Tyr His	
580 585 590	
cca cgt gtg gct ccc gtt gct aag aag cgc gtc tcc tct gtc acc gaa	1824
Pro Arg Val Ala Pro Val Ala Lys Lys Arg Val Ser Ser Val Thr Glu	
595 600 605	
ggt ggc atc gac tgg gca tgg ggc gag ctc ctc gcc ttc ggt tcc ctg	1872
Gly Gly Ile Asp Trp Ala Trp Gly Glu Leu Leu Ala Phe Gly Ser Leu	
610 615 620	
gct aac tcc ggc cgc ttg gtt cgc ctt gca ggt gaa gat tcc cgc cgc	1920
Ala Asn Ser Gly Arg Leu Val Arg Leu Ala Gly Glu Asp Ser Arg Arg	
625 630 635 640	
ggt acc ttc acc cag cgc cac gca gtt gcc atc gac cca gcg acc gct	1968
Gly Thr Phe Thr Gln Arg His Ala Val Ala Ile Asp Pro Ala Thr Ala	
645 650 655	
gaa gag ttc aac cca ctc cac gag ctt gca cag tcc aag ggc aac aac	2016
Glu Glu Phe Asn Pro Leu His Glu Leu Ala Gln Ser Lys Gly Asn Asn	
660 665 670	
ggt aag ttc ctg gtc tac aac tcc gca ctg acc gag tac gca ggc atg	2064
Gly Lys Phe Leu Val Tyr Asn Ser Ala Leu Thr Glu Tyr Ala Gly Met	
675 680 685	
ggc ttc gag tac ggc tac tcc gta gga aac gaa gac tcc atc gtt gca	2112
Gly Phe Glu Tyr Gly Tyr Ser Val Gly Asn Glu Asp Ser Ile Val Ala	
690 695 700	
tgg gaa gca cag ttc ggc gac ttc gcc aac ggc gct cag acc atc atc	2160
Trp Glu Ala Gln Phe Gly Asp Phe Ala Asn Gly Ala Gln Thr Ile Ile	
705 710 715 720	
gat gag tac gtc tcc tca ggc gaa gct aag tgg ggc cag acc tcc aag	2208
Asp Glu Tyr Val Ser Ser Gly Glu Ala Lys Trp Gly Gln Thr Ser Lys	
725 730 735	
ctg atc ctt ctg ctg cct cac ggc tac gaa ggc cag ggc cca gac cac	2256

Leu Ile Leu Leu Leu Pro His Gly Tyr Glu Gly Gln Gly Pro Asp His
 740 745 750
 tct tcc gca cgt atc gag cgc ttc ctg cag ctg tgc gct gag ggt tcc 2304
 Ser Ser Ala Arg Ile Glu Arg Phe Leu Gln Leu Cys Ala Glu Gly Ser
 755 760 765
 atg act gtt gct cag cca tcc acc cca gca aac cac ttc cac cta ctg 2352
 Met Thr Val Ala Gln Pro Ser Thr Pro Ala Asn His Phe His Leu Leu
 770 775 780
 cgt cgt cac gct ctg tcc gac ctg aag cgt cca ctg gtt atc ttc acc 2400
 Arg Arg His Ala Leu Ser Asp Leu Lys Arg Pro Leu Val Ile Phe Thr
 785 790 795 800
 ccg aag tcc atg ctg cgt aac aag gct gct gcc tcc gca cca gaa gac 2448
 Pro Lys Ser Met Leu Arg Asn Lys Ala Ala Ala Ser Ala Pro Glu Asp
 805 810 815
 ttc act gag gtc acc aag ttc cag tcc gtg atc aac gat cca aac gtt 2496
 Phe Thr Glu Val Thr Lys Phe Gln Ser Val Ile Asn Asp Pro Asn Val
 820 825 830
 gca gat gca gcc aag gtg aag aag gtc atg ctg gtc tcc ggc aag ctg 2544
 Ala Asp Ala Ala Lys Val Lys Lys Val Met Leu Val Ser Gly Lys Leu
 835 840 845
 tac tac gaa ttg gca aag cgc aag gag aag gac gga cgc gac gac atc 2592
 Tyr Tyr Glu Leu Ala Lys Arg Lys Glu Lys Asp Gly Arg Asp Asp Ile
 850 855 860
 gcg atc gtt cgt atc gaa atg ctc cac cca att ccg ttc aac cgc atc 2640
 Ala Ile Val Arg Ile Glu Met Leu His Pro Ile Pro Phe Asn Arg Ile
 865 870 875 880
 tcc gag gct ctt gcc ggc tac cct aac gct gag gaa gtc ctc ttc gtt 2688
 Ser Glu Ala Leu Ala Gly Tyr Pro Asn Ala Glu Glu Val Leu Phe Val
 885 890 895
 cag gat gag cca gca aac cag ggc cca tgg ccg ttc tac cag gag cac 2736
 Gln Asp Glu Pro Ala Asn Gln Gly Pro Trp Pro Phe Tyr Gln Glu His
 900 905 910
 ctc cca gag ctg atc ccg aac atg cca aag atg cgc cgc gtt tcc cgc 2784
 Leu Pro Glu Leu Ile Pro Asn Met Pro Lys Met Arg Arg Val Ser Arg
 915 920 925
 cgc gct cag tcc tcc acc gca act ggt gtt gcc aag gtg cac cag ctg 2832
 Arg Ala Gln Ser Ser Thr Ala Thr Gly Val Ala Lys Val His Gln Leu
 930 935 940
 gag gag aag cag ctt atc gac gag gct ttc gag gct taagtcttta 2878
 Glu Glu Lys Gln Leu Ile Asp Glu Ala Phe Glu Ala
 945 950 955
 tagtcctgca cta 2891

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 <212> PRT

<213> Corynebacterium glutamicum

<400> 562

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 Val Gly Ser Met Asp Tyr Pro Ala Glu Phe Gln Gly Ala Ser Glu Asp
 20 25 30
 Arg Leu Ala Glu Leu Gly Val Gly Lys Leu Val Thr Ile Thr Ser Thr
 35 40 45
 Tyr Asp His Arg Val Ile Gln Gly Ala Val Ser Gly Glu Phe Leu Arg
 50 55 60
 Thr Met Ser Arg Leu Leu Thr Asp Asp Ser Phe Trp Asp Glu Ile Phe
 65 70 75 80
 Asp Ala Met Asn Val Pro Tyr Thr Pro Met Arg Trp Ala Gln Asp Val
 85 90 95
 Pro Asn Thr Gly Val Asp Lys Asn Thr Arg Val Met Gln Leu Ile Glu
 100 105 110
 Ala Tyr Arg Ser Arg Gly His Leu Ile Ala Asp Thr Asn Pro Leu Ser
 115 120 125
 Trp Val Gln Pro Gly Met Pro Val Pro Asp His Arg Asp Leu Asp Ile
 130 135 140
 Glu Thr His Asn Leu Thr Ile Trp Asp Leu Asp Arg Thr Phe Asn Val
 145 150 155 160
 Gly Gly Phe Gly Gly Lys Glu Thr Met Thr Leu Arg Glu Val Leu Ser
 165 170 175
 Arg Leu Arg Ala Ala Tyr Thr Leu Lys Val Gly Ser Glu Tyr Thr His
 180 185 190
 Ile Leu Asp Arg Asp Glu Arg Thr Trp Leu Gln Asp Arg Leu Glu Ala
 195 200 205
 Gly Met Pro Lys Pro Thr Gln Ala Glu Gln Lys Tyr Ile Leu Gln Lys
 210 215 220
 Leu Asn Ala Ala Glu Ala Phe Glu Asn Phe Leu Gln Thr Lys Tyr Val
 225 230 235 240
 Gly Gln Lys Arg Phe Ser Leu Glu Gly Ala Glu Ala Leu Ile Pro Leu
 245 250 255
 Met Asp Ser Ala Ile Asp Thr Ala Ala Gly Gln Gly Leu Asp Glu Val
 260 265 270
 Val Ile Gly Met Pro His Arg Gly Arg Leu Asn Val Leu Phe Asn Ile
 275 280 285
 Val Gly Lys Pro Leu Ala Ser Ile Phe Asn Glu Phe Glu Gly Gln Met
 290 295 300
 Glu Gln Gly Gln Ile Gly Gly Ser Gly Asp Val Lys Tyr His Leu Gly

305	310	315	320
Ser Glu Gly Gln His Leu Gln Met Phe Gly Asp Gly Glu Ile Lys Val	325	330	335
Ser Leu Thr Ala Asn Pro Ser His Leu Glu Ala Val Asn Pro Ala Met	340	345	350
Glu Gly Ile Val Arg Ala Lys Gln Asp Tyr Leu Asp Lys Gly Val Asp	355	360	365
Gly Lys Thr Val Val Pro Leu Leu Leu His Gly Asp Ala Ala Phe Ala	370	375	380
Gly Leu Gly Ile Val Pro Glu Thr Ile Asn Leu Ala Lys Leu Arg Gly	385	390	395
Tyr Asp Val Gly Gly Thr Ile His Ile Val Val Asn Asn Gln Ile Gly	405	410	415
Phe Thr Thr Thr Pro Asp Ser Ser Arg Ser Met His Tyr Ala Thr Asp	420	425	430
Tyr Ala Lys Ala Phe Gly Cys Pro Val Phe His Val Asn Gly Asp Asp	435	440	445
Pro Glu Ala Val Val Trp Val Gly Gln Leu Ala Thr Glu Tyr Arg Arg	450	455	460
Arg Phe Gly Lys Asp Val Phe Ile Asp Leu Val Cys Tyr Arg Leu Arg	465	470	475
Gly His Asn Glu Ala Asp Asp Pro Ser Met Thr Gln Pro Lys Met Tyr	485	490	495
Glu Leu Ile Thr Gly Arg Glu Thr Val Arg Ala Gln Tyr Thr Glu Asp	500	505	510
Leu Leu Gly Arg Gly Asp Leu Ser Asn Glu Asp Ala Glu Ala Val Val	515	520	525
Arg Asp Phe His Asp Gln Met Glu Ser Val Phe Asn Glu Val Lys Glu	530	535	540
Gly Gly Lys Lys Gln Ala Glu Ala Gln Thr Gly Ile Thr Gly Ser Gln	545	550	555
Lys Leu Pro His Gly Leu Glu Thr Asn Ile Ser Arg Glu Glu Leu Leu	565	570	575
Glu Leu Gly Gln Ala Phe Ala Asn Thr Pro Glu Gly Phe Asn Tyr His	580	585	590
Pro Arg Val Ala Pro Val Ala Lys Lys Arg Val Ser Ser Val Thr Glu	595	600	605
Gly Gly Ile Asp Trp Ala Trp Gly Glu Leu Leu Ala Phe Gly Ser Leu	610	615	620
Ala Asn Ser Gly Arg Leu Val Arg Leu Ala Gly Glu Asp Ser Arg Arg	625	630	635
			640

Gly Thr Phe Thr Gln Arg His Ala Val Ala Ile Asp Pro Ala Thr Ala
 645 650 655
 Glu Glu Phe Asn Pro Leu His Glu Leu Ala Gln Ser Lys Gly Asn Asn
 660 665 670
 Gly Lys Phe Leu Val Tyr Asn Ser Ala Leu Thr Glu Tyr Ala Gly Met
 675 680 685
 Gly Phe Glu Tyr Gly Tyr Ser Val Gly Asn Glu Asp Ser Ile Val Ala
 690 695 700
 Trp Glu Ala Gln Phe Gly Asp Phe Ala Asn Gly Ala Gln Thr Ile Ile
 705 710 715 720
 Asp Glu Tyr Val Ser Ser Gly Glu Ala Lys Trp Gly Gln Thr Ser Lys
 725 730 735
 Leu Ile Leu Leu Leu Pro His Gly Tyr Glu Gly Gln Gly Pro Asp His
 740 745 750
 Ser Ser Ala Arg Ile Glu Arg Phe Leu Gln Leu Cys Ala Glu Gly Ser
 755 760 765
 Met Thr Val Ala Gln Pro Ser Thr Pro Ala Asn His Phe His Leu Leu
 770 775 780
 Arg Arg His Ala Leu Ser Asp Leu Lys Arg Pro Leu Val Ile Phe Thr
 785 790 795 800
 Pro Lys Ser Met Leu Arg Asn Lys Ala Ala Ala Ser Ala Pro Glu Asp
 805 810 815
 Phe Thr Glu Val Thr Lys Phe Gln Ser Val Ile Asn Asp Pro Asn Val
 820 825 830
 Ala Asp Ala Ala Lys Val Lys Lys Val Met Leu Val Ser Gly Lys Leu
 835 840 845
 Tyr Tyr Glu Leu Ala Lys Arg Lys Glu Lys Asp Gly Arg Asp Asp Ile
 850 855 860
 Ala Ile Val Arg Ile Glu Met Leu His Pro Ile Pro Phe Asn Arg Ile
 865 870 875 880
 Ser Glu Ala Leu Ala Gly Tyr Pro Asn Ala Glu Glu Val Leu Phe Val
 885 890 895
 Gln Asp Glu Pro Ala Asn Gln Gly Pro Trp Pro Phe Tyr Gln Glu His
 900 905 910
 Leu Pro Glu Leu Ile Pro Asn Met Pro Lys Met Arg Arg Val Ser Arg
 915 920 925
 Arg Ala Gln Ser Ser Thr Ala Thr Gly Val Ala Lys Val His Gln Leu
 930 935 940
 Glu Glu Lys Gln Leu Ile Asp Glu Ala Phe Glu Ala
 945 950 955

<210> 563
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 <212> DNA
 <213> Corynebacterium glutamicum

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 <222> (1)..(1494)
 <223> RXA01745

<400> 563
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 Ile Leu Ala Asp Glu Asp Asp Thr Val Asp Val Gly Ala Val Ile Ala
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 cgc atc ggt gac gca aac gca gct gca gca cct gcc gaa gag gaa gca 96
 Arg Ile Gly Asp Ala Asn Ala Ala Ala Pro Ala Glu Glu Glu Ala
 20 25 30
 gct cct gcc gaa gag gaa gaa cca gtt aag gaa gag cca aag aag gag 144
 Ala Pro Ala Glu Glu Glu Glu Pro Val Lys Glu Glu Pro Lys Lys Glu
 35 40 45
 gca gct cct gaa gct cca gca gca act ggc gcc gca acc gat gtg gaa 192
 Ala Ala Pro Glu Ala Pro Ala Ala Thr Gly Ala Ala Thr Asp Val Glu
 50 55 60
 atg cca gaa ctc ggc gaa tcc gtc acc gaa ggc acc att acc cag tgg 240
 Met Pro Glu Leu Gly Glu Ser Val Thr Glu Gly Thr Ile Thr Gln Trp
 65 70 75 80
 ctc aag gct gtc ggc gac acc gtc gaa gta gac gaa cca ctt ctt gag 288
 Leu Lys Ala Val Gly Asp Thr Val Glu Val Asp Glu Pro Leu Leu Glu
 85 90 95
 gtc tcc acc gac aag gtc gac acc gaa atc cca tcc cca gta gca ggc 336
 Val Ser Thr Asp Lys Val Asp Thr Glu Ile Pro Ser Pro Val Ala Gly
 100 105 110
 acc atc gtg gag atc ctt gca gac gaa gac gac acc gtc gac gtc ggc 384
 Thr Ile Val Glu Ile Leu Ala Asp Glu Asp Asp Thr Val Asp Val Gly
 115 120 125
 gca gtc atc gcc cgc atc ggt gac gca aac gca gct gca gca cct gcc 432
 Ala Val Ile Ala Arg Ile Gly Asp Ala Asn Ala Ala Ala Pro Ala
 130 135 140
 gaa gag gaa gca gct cct gcc gaa gag gag gaa cca gtt aag gaa gag 480
 Glu Glu Glu Ala Ala Pro Ala Glu Glu Glu Glu Pro Val Lys Glu Glu
 145 150 155 160
 cca aag aag gaa gag ccc aag aag gaa gag ccc aag aag gaa gca gct 528
 Pro Lys Lys Glu Glu Pro Lys Lys Glu Glu Pro Lys Lys Glu Ala Ala
 165 170 175
 act aca cct gct gcg gca tcc gca act gtg tcc gct tct ggc gac aac 576
 Thr Thr Pro Ala Ala Ala Ser Ala Thr Val Ser Ala Ser Gly Asp Asn
 180 185 190
 gtt cca tac gtc acc cca ctg gtg cgc aag ctt gct gaa aag cac ggc 624

Val	Pro	Tyr	Val	Thr	Pro	Leu	Val	Arg	Lys	Leu	Ala	Glu	Lys	His	Gly		
	195						200					205					
gtt	gac	ttg	aac	acc	gtg	acc	ggt	acc	ggt	atc	ggt	ggc	cgt	atc	cgc	672	
Val	Asp	Leu	Asn	Thr	Val	Thr	Gly	Thr	Gly	Ile	Gly	Gly	Arg	Ile	Arg		
	210					215					220						
aag	cag	gat	gtt	ttg	gct	gct	gcg	aac	ggc	gag	gct	gca	cct	gct	gag	720	
Lys	Gln	Asp	Val	Leu	Ala	Ala	Ala	Asn	Gly	Glu	Ala	Ala	Pro	Ala	Glu		
	225				230				235						240		
gct	gct	gct	cct	gtt	tcc	gct	tgg	tcc	act	aag	tct	gtt	gac	cct	gag	768	
Ala	Ala	Ala	Pro	Val	Ser	Ala	Trp	Ser	Thr	Lys	Ser	Val	Asp	Pro	Glu		
				245				250						255			
aag	gct	aag	ctc	cgt	ggt	acc	act	cag	aag	gtc	aac	cgc	atc	cgt	gag	816	
Lys	Ala	Lys	Leu	Arg	Gly	Thr	Thr	Gln	Lys	Val	Asn	Arg	Ile	Arg	Glu		
			260					265					270				
atc	acc	gcg	atg	aag	acc	gtc	gag	gct	ctg	cag	att	tct	gct	cag	ctc	864	
Ile	Thr	Ala	Met	Lys	Thr	Val	Glu	Ala	Leu	Gln	Ile	Ser	Ala	Gln	Leu		
		275					280					285					
acc	cag	ctg	cac	gag	gtc	gat	atg	act	cgc	gtt	gct	gag	ctg	cgt	aag	912	
Thr	Gln	Leu	His	Glu	Val	Asp	Met	Thr	Arg	Val	Ala	Glu	Leu	Arg	Lys		
		290				295					300						
aag	aac	aag	ccc	gcg	ttc	atc	gag	aag	cac	ggt	gtg	aac	ctc	act	tac	960	
Lys	Asn	Lys	Pro	Ala	Phe	Ile	Glu	Lys	His	Gly	Val	Asn	Leu	Thr	Tyr		
	305				310					315					320		
ctg	cca	ttc	ttc	gtg	aag	gca	gtt	gtc	gag	gct	ttg	gtt	tcc	cat	cca	1008	
Leu	Pro	Phe	Phe	Val	Lys	Ala	Val	Val	Glu	Ala	Leu	Val	Ser	His	Pro		
				325				330						335			
aac	gtc	aac	gcg	tct	ttc	aac	gcg	aag	acc	aag	gag	atg	acc	tac	cac	1056	
Asn	Val	Asn	Ala	Ser	Phe	Asn	Ala	Lys	Thr	Lys	Glu	Met	Thr	Tyr	His		
			340					345					350				
tcc	tcc	gtt	aac	ctc	tcc	atc	gct	gtt	gat	acc	cca	gct	ggt	ctg	ttg	1104	
Ser	Ser	Val	Asn	Leu	Ser	Ile	Ala	Val	Asp	Thr	Pro	Ala	Gly	Leu	Leu		
		355					360					365					
acc	cca	gtc	att	cac	gat	gct	cag	gat	ctc	tcc	atc	cca	gag	atc	gca	1152	
Thr	Pro	Val	Ile	His	Asp	Ala	Gln	Asp	Leu	Ser	Ile	Pro	Glu	Ile	Ala		
		370				375					380						
aag	gca	att	gtt	gac	ctg	gct	gat	cgt	tca	cgc	aac	aac	aag	ctg	aag	1200	
Lys	Ala	Ile	Val	Asp	Leu	Ala	Asp	Arg	Ser	Arg	Asn	Asn	Lys	Leu	Lys		
	385				390				395						400		
cca	aac	gat	ctg	tcc	ggt	ggc	acc	ttc	acc	atc	acc	aac	att	ggt	tct	1248	
Pro	Asn	Asp	Leu	Ser	Gly	Gly	Thr	Phe	Thr	Ile	Thr	Asn	Ile	Gly	Ser		
				405				410						415			
gaa	ggc	gca	ctg	tct	gat	acc	cca	atc	ctg	gtt	cca	cca	cag	gct	ggc	1296	
Glu	Gly	Ala	Leu	Ser	Asp	Thr	Pro	Ile	Leu	Val	Pro	Pro	Gln	Ala	Gly		
			420					425					430				
atc	ttg	ggc	acc	ggc	gcg	atc	gtg	aag	cgt	cca	gtt	gtc	atc	acc	gag	1344	
Ile	Leu	Gly	Thr	Gly	Ala	Ile	Val	Lys	Arg	Pro	Val	Val	Ile	Thr	Glu		

435	440	445	
gat gga att gat tcc atc gcg atc cgt cag atg gtc ttc cta cca ctg			1392
Asp Gly Ile Asp Ser Ile Ala Ile Arg Gln Met Val Phe Leu Pro Leu			
450	455	460	
acc tac gac cac cag gtt gta gat ggc gca gat gct ggt cgc ttc ctg			1440
Thr Tyr Asp His Gln Val Val Asp Gly Ala Asp Ala Gly Arg Phe Leu			
465	470	475	480
acc acc atc aag gac cgc ctt gag acc gct aac ttc gaa ggc gat ctg			1488
Thr Thr Ile Lys Asp Arg Leu Glu Thr Ala Asn Phe Glu Gly Asp Leu			
485	490	495	
cag ctc taagatctct gcaagttaaa acc			1517
Gln Leu			

<210> 564

<211> 498

<212> PRT

<213> Corynebacterium glutamicum

<400> 564

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Arg Ile Gly Asp Ala Asn Ala Ala Ala Pro Ala Glu Glu Glu Ala			
20	25	30	
Ala Pro Ala Glu Glu Glu Glu Pro Val Lys Glu Glu Pro Lys Lys Glu			
35	40	45	
Ala Ala Pro Glu Ala Pro Ala Ala Thr Gly Ala Ala Thr Asp Val Glu			
50	55	60	
Met Pro Glu Leu Gly Glu Ser Val Thr Glu Gly Thr Ile Thr Gln Trp			
65	70	75	80
Leu Lys Ala Val Gly Asp Thr Val Glu Val Asp Glu Pro Leu Leu Glu			
85	90	95	
Val Ser Thr Asp Lys Val Asp Thr Glu Ile Pro Ser Pro Val Ala Gly			
100	105	110	
Thr Ile Val Glu Ile Leu Ala Asp Glu Asp Asp Thr Val Asp Val Gly			
115	120	125	
Ala Val Ile Ala Arg Ile Gly Asp Ala Asn Ala Ala Ala Pro Ala			
130	135	140	
Glu Glu Glu Ala Ala Pro Ala Glu Glu Glu Glu Pro Val Lys Glu Glu			
145	150	155	160
Pro Lys Lys Glu Glu Pro Lys Lys Glu Glu Pro Lys Lys Glu Ala Ala			
165	170	175	
Thr Thr Pro Ala Ala Ala Ser Ala Thr Val Ser Ala Ser Gly Asp Asn			
180	185	190	

Val Pro Tyr Val Thr Pro Leu Val Arg Lys Leu Ala Glu Lys His Gly
 195 200 205
 Val Asp Leu Asn Thr Val Thr Gly Thr Gly Ile Gly Gly Arg Ile Arg
 210 215 220
 Lys Gln Asp Val Leu Ala Ala Ala Asn Gly Glu Ala Ala Pro Ala Glu
 225 230 235 240
 Ala Ala Ala Pro Val Ser Ala Trp Ser Thr Lys Ser Val Asp Pro Glu
 245 250 255
 Lys Ala Lys Leu Arg Gly Thr Thr Gln Lys Val Asn Arg Ile Arg Glu
 260 265 270
 Ile Thr Ala Met Lys Thr Val Glu Ala Leu Gln Ile Ser Ala Gln Leu
 275 280 285
 Thr Gln Leu His Glu Val Asp Met Thr Arg Val Ala Glu Leu Arg Lys
 290 295 300
 Lys Asn Lys Pro Ala Phe Ile Glu Lys His Gly Val Asn Leu Thr Tyr
 305 310 315 320
 Leu Pro Phe Phe Val Lys Ala Val Val Glu Ala Leu Val Ser His Pro
 325 330 335
 Asn Val Asn Ala Ser Phe Asn Ala Lys Thr Lys Glu Met Thr Tyr His
 340 345 350
 Ser Ser Val Asn Leu Ser Ile Ala Val Asp Thr Pro Ala Gly Leu Leu
 355 360 365
 Thr Pro Val Ile His Asp Ala Gln Asp Leu Ser Ile Pro Glu Ile Ala
 370 375 380
 Lys Ala Ile Val Asp Leu Ala Asp Arg Ser Arg Asn Asn Lys Leu Lys
 385 390 395 400
 Pro Asn Asp Leu Ser Gly Gly Thr Phe Thr Ile Thr Asn Ile Gly Ser
 405 410 415
 Glu Gly Ala Leu Ser Asp Thr Pro Ile Leu Val Pro Pro Gln Ala Gly
 420 425 430
 Ile Leu Gly Thr Gly Ala Ile Val Lys Arg Pro Val Val Ile Thr Glu
 435 440 445
 Asp Gly Ile Asp Ser Ile Ala Ile Arg Gln Met Val Phe Leu Pro Leu
 450 455 460
 Thr Tyr Asp His Gln Val Val Asp Gly Ala Asp Ala Gly Arg Phe Leu
 465 470 475 480
 Thr Thr Ile Lys Asp Arg Leu Glu Thr Ala Asn Phe Glu Gly Asp Leu
 485 490 495
 Gln Leu

[illegible]

ggc ggt gac cca atc atc ggt aca acc cat atc gac gct ctg gag gcc 691
 Gly Gly Asp Pro Ile Ile Gly Thr Thr His Ile Asp Ala Leu Glu Ala
 185 190 195

 ttt gaa gct gat cct gag acc aag gca atc gtc atg atc ggt gag atc 739
 Phe Glu Ala Asp Pro Glu Thr Lys Ala Ile Val Met Ile Gly Glu Ile
 200 205 210

 ggt gga gat gca gag gaa cgc gct gct gac ttc att tct aag cac gtg 787
 Gly Gly Asp Ala Glu Glu Arg Ala Ala Asp Phe Ile Ser Lys His Val
 215 220 225

 aca aaa cca gtt gtg ggt tac gtg gca ggc ttt acc gcc cct gaa gga 835
 Thr Lys Pro Val Val Gly Tyr Val Ala Gly Phe Thr Ala Pro Glu Gly
 230 235 240 245

 aag acc atg ggg cat gct ggc gcc atc gtg aca ggt tca gaa ggc act 883
 Lys Thr Met Gly His Ala Gly Ala Ile Val Thr Gly Ser Glu Gly Thr
 250 255 260

 gcg cga gca aag aag cat gca ttg gag gcc gtg ggt gtt cgc gtg gga 931
 Ala Arg Ala Lys Lys His Ala Leu Glu Ala Val Gly Val Arg Val Gly
 265 270 275

 aca act ccg agt gaa acc gcg aag ctt atg cgt gag gta gtt gca gct 979
 Thr Thr Pro Ser Glu Thr Ala Lys Leu Met Arg Glu Val Val Ala Ala
 280 285 290

 ttg taactaacag gccacagatc tta 1005
 Leu

<210> 566
 <211> 294
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 566
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 Thr Gly Ser Glu Gly Ser Glu His Ala Arg Arg Ile Leu Ala Ser Gly
 20 25 30

 Ala Lys Leu Val Gly Gly Thr Asn Pro Arg Lys Ala Gly Gln Thr Ile
 35 40 45

 Leu Ile Asn Asp Thr Glu Leu Pro Val Phe Gly Thr Val Lys Glu Ala
 50 55 60

 Met Glu Glu Thr Gly Ala Asp Val Thr Val Ile Phe Val Pro Pro Ala
 65 70 75 80

 Phe Ala Lys Ala Ala Ile Ile Glu Ala Ile Asp Ala His Ile Pro Leu
 85 90 95

 Cys Val Ile Ile Thr Glu Gly Ile Pro Val Arg Asp Ala Ser Glu Ala
 100 105 110

 Trp Ala Tyr Ala Lys Lys Val Gly His Thr Arg Ile Ile Gly Pro Asn

115	120	125
Cys Pro Gly Ile Ile Thr 130	Pro Gly Glu Ser Leu 135	Ala Gly Ile Thr Pro 140
Ala Asn Ile Ala Gly Ser 145	Gly Pro Ile Gly Leu 150	Ile Ser Lys Ser Gly 155
Thr Leu Thr Tyr 165	Gln Met Met Tyr Glu 165	Leu Ser Asp Ile Gly 170
Thr Ala Ile Gly Ile Gly 180	Gly Gly Asp Pro Ile 185	Ile Gly Thr Thr His 190
Asp Ala Leu Glu Ala Phe 195	Glu Ala Asp Pro Glu 200	Thr Lys Ala Ile Val 205
Met Ile Gly Glu Ile Gly 210	Gly Gly Asp Ala Glu 215	Glu Arg Ala Ala Asp 220
Ile Ser Lys His Val Thr 225	Lys Pro Val Val Gly 230	Tyr Val Ala Gly Phe 235
Thr Ala Pro Glu Gly Lys 245	Thr Met Gly His Ala 250	Gly Ala Ile Val Thr 255
Gly Ser Glu Gly Thr Ala 260	Arg Ala Lys Lys His 265	Ala Leu Glu Ala Val 270
Gly Val Arg Val Gly Thr 275	Thr Thr Pro Ser Glu 280	Thr Ala Lys Leu Met 285
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 <213> Corynebacterium glutamicum

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 <222> (101)..(1372)
 <223> RXA00783

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 Leu Lys His Leu Leu
 1 5
 tta cgg gaa gac ttt gtt aaa gac gca gaa ggc tct aag cat ggg ccg 163
 Leu Arg Glu Asp Phe Val Lys Asp Ala Glu Gly Ser Lys His Gly Pro
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 gaa atg gaa ttg gca gtg gat ctt ttt gaa tac caa gca cgg gac ctc 211
 Glu Met Glu Leu Ala Val Asp Leu Phe Glu Tyr Gln Ala Arg Asp Leu
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ttt gaa acc cat ggt gtg cca gtg ttg aag gga att gtg gca tca aca	259
Phe Glu Thr His Gly Val Pro Val Leu Lys Gly Ile Val Ala Ser Thr	
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cca gag gcg gcg agg aaa gcg gct gag gaa atc ggc gga ctg acc gtc	307
Pro Glu Ala Ala Arg Lys Ala Ala Glu Glu Ile Gly Gly Leu Thr Val	
55 60 65	
gtc aag gct cag gtc aag gtg ggc gga cgt ggc aag gcg ggt ggc gtc	355
Val Lys Ala Gln Val Lys Val Gly Gly Arg Gly Lys Ala Gly Gly Val	
70 75 80 85	
cgt gtg gca ccg acg tcg gct cag gct ttt gat gct gcg gat gcg att	403
Arg Val Ala Pro Thr Ser Ala Gln Ala Phe Asp Ala Ala Asp Ala Ile	
90 95 100	
ctc ggc atg gat atc aaa gga cac act gtt aat cag gtg atg gtg gcg	451
Leu Gly Met Asp Ile Lys Gly His Thr Val Asn Gln Val Met Val Ala	
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cag ggc gct gac att gct gag gaa tac tat ttc tcc att ttg ttg gat	499
Gln Gly Ala Asp Ile Ala Glu Glu Tyr Tyr Phe Ser Ile Leu Leu Asp	
120 125 130	
cgc gcg aat cgt tcg tat ctg gct atg tgc tct gtt gaa ggt ggc atg	547
Arg Ala Asn Arg Ser Tyr Leu Ala Met Cys Ser Val Glu Gly Gly Met	
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gag atc gag atc ctg gcg aag gaa aag cct gaa gct ttg gca aag gtg	595
Glu Ile Glu Ile Leu Ala Lys Glu Lys Pro Glu Ala Leu Ala Lys Val	
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Glu Val Asp Pro Leu Thr Gly Ile Asp Glu Asp Lys Ala Arg Glu Ile	
170 175 180	
gtc act gct gct ggc ttt gaa act gag gtg gca gag aaa gtc att ccg	691
Val Thr Ala Ala Gly Phe Glu Thr Glu Val Ala Glu Lys Val Ile Pro	
185 190 195	
gtg ctg atc aag atc tgg cag gtg tat tac gaa gag gaa gca aca ctc	739
Val Leu Ile Lys Ile Trp Gln Val Tyr Tyr Glu Glu Glu Ala Thr Leu	
200 205 210	
gtt gag gtg aac ccg ttg gtg ctc acg gat gac ggc gat gtg att gcg	787
Val Glu Val Asn Pro Leu Val Leu Thr Asp Asp Gly Asp Val Ile Ala	
215 220 225	
ctt gat ggc aag atc acg ctg gat gat aac gct gat ttc cgc cat gat	835
Leu Asp Gly Lys Ile Thr Leu Asp Asp Asn Ala Asp Phe Arg His Asp	
230 235 240 245	
aac cgt ggt gcg ttg gct gaa tct gcc ggt ggc ttg gac att ttg gaa	883
Asn Arg Gly Ala Leu Ala Glu Ser Ala Gly Gly Leu Asp Ile Leu Glu	
250 255 260	
ctg aag gcc aag aag aat gat ctg aac tac gtg aaa ctt gat ggc tct	931
Leu Lys Ala Lys Lys Asn Asp Leu Asn Tyr Val Lys Leu Asp Gly Ser	
265 270 275	
gtg ggc atc att ggc aat ggt gca ggt ttg gtg atg tcc acg ttg gat	979

Val Gly Ile Ile Gly Asn Gly Ala Gly Leu Val Met Ser Thr Leu Asp
 280 285 290
 atc gtg gct gca gct ggt gaa cgc cat ggt ggg cag cgc ccc gcg aac 1027
 Ile Val Ala Ala Ala Gly Glu Arg His Gly Gly Gln Arg Pro Ala Asn
 295 300 305
 ttc cta gac att ggt ggc gga gca tca gct gaa tcg atg gct gct ggt 1075
 Phe Leu Asp Ile Gly Gly Gly Ala Ser Ala Glu Ser Met Ala Ala Gly
 310 315 320 325
 ctc gat gtg atc ctt ggg gat agc cag gta cgc agt gtg ttt gtg aat 1123
 Leu Asp Val Ile Leu Gly Asp Ser Gln Val Arg Ser Val Phe Val Asn
 330 335 340
 gtg ttt ggt ggc atc acc gcg tgt gat gtg gtg gca aag gga atc gtt 1171
 Val Phe Gly Gly Ile Thr Ala Cys Asp Val Val Ala Lys Gly Ile Val
 345 350 355
 gga gct ttg gat gtg ctc ggc gat caa gca acg aag cct ctt gtg gtg 1219
 Gly Ala Leu Asp Val Leu Gly Asp Gln Ala Thr Lys Pro Leu Val Val
 360 365 370
 cgc ctt gat ggc aac aac gtg gtg gaa ggc aga cga atc ctc gcg gaa 1267
 Arg Leu Asp Gly Asn Asn Val Val Glu Gly Arg Arg Ile Leu Ala Glu
 375 380 385
 tat aac cac cct ttg gtc acc gtt gtg gag ggt atg gat gca gcg gct 1315
 Tyr Asn His Pro Leu Val Thr Val Val Glu Gly Met Asp Ala Ala Ala
 390 395 400 405
 gat cac gct gcc cat ttg gcc aat ctt gcc cag cac ggc cag ttc gca 1363
 Asp His Ala Ala His Leu Ala Asn Leu Ala Gln His Gly Gln Phe Ala
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 Thr Ala Asn

<210> 568

<211> 424

<212> PRT

<213> Corynebacterium glutamicum

<400> 568

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 20 25 30
 Gln Ala Arg Asp Leu Phe Glu Thr His Gly Val Pro Val Leu Lys Gly
 35 40 45
 Ile Val Ala Ser Thr Pro Glu Ala Ala Arg Lys Ala Ala Glu Glu Ile
 50 55 60
 Gly Gly Leu Thr Val Val Lys Ala Gln Val Lys Val Gly Gly Arg Gly
 65 70 75 80

Lys Ala Gly Gly Val Arg Val Ala Pro Thr Ser Ala Gln Ala Phe Asp
 85 90 95
 Ala Ala Asp Ala Ile Leu Gly Met Asp Ile Lys Gly His Thr Val Asn
 100 105 110
 Gln Val Met Val Ala Gln Gly Ala Asp Ile Ala Glu Glu Tyr Tyr Phe
 115 120 125
 Ser Ile Leu Leu Asp Arg Ala Asn Arg Ser Tyr Leu Ala Met Cys Ser
 130 135 140
 Val Glu Gly Gly Met Glu Ile Glu Ile Leu Ala Lys Glu Lys Pro Glu
 145 150 155 160
 Ala Leu Ala Lys Val Glu Val Asp Pro Leu Thr Gly Ile Asp Glu Asp
 165 170 175
 Lys Ala Arg Glu Ile Val Thr Ala Ala Gly Phe Glu Thr Glu Val Ala
 180 185 190
 Glu Lys Val Ile Pro Val Leu Ile Lys Ile Trp Gln Val Tyr Tyr Glu
 195 200 205
 Glu Glu Ala Thr Leu Val Glu Val Asn Pro Leu Val Leu Thr Asp Asp
 210 215 220
 Gly Asp Val Ile Ala Leu Asp Gly Lys Ile Thr Leu Asp Asp Asn Ala
 225 230 235 240
 Asp Phe Arg His Asp Asn Arg Gly Ala Leu Ala Glu Ser Ala Gly Gly
 245 250 255
 Leu Asp Ile Leu Glu Leu Lys Ala Lys Lys Asn Asp Leu Asn Tyr Val
 260 265 270
 Lys Leu Asp Gly Ser Val Gly Ile Ile Gly Asn Gly Ala Gly Leu Val
 275 280 285
 Met Ser Thr Leu Asp Ile Val Ala Ala Ala Gly Glu Arg His Gly Gly
 290 295 300
 Gln Arg Pro Ala Asn Phe Leu Asp Ile Gly Gly Gly Ala Ser Ala Glu
 305 310 315 320
 Ser Met Ala Ala Gly Leu Asp Val Ile Leu Gly Asp Ser Gln Val Arg
 325 330 335
 Ser Val Phe Val Asn Val Phe Gly Gly Ile Thr Ala Cys Asp Val Val
 340 345 350
 Ala Lys Gly Ile Val Gly Ala Leu Asp Val Leu Gly Asp Gln Ala Thr
 355 360 365
 Lys Pro Leu Val Val Arg Leu Asp Gly Asn Asn Val Val Glu Gly Arg
 370 375 380
 Arg Ile Leu Ala Glu Tyr Asn His Pro Leu Val Thr Val Val Glu Gly
 385 390 395 400
 Met Asp Ala Ala Ala Asp His Ala Ala His Leu Ala Asn Leu Ala Gln

405

410

415

His Gly Gln Phe Ala Thr Ala Asn
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<210> 569

<211> 1623

<212> DNA

<213> Corynebacterium glutamicum

<220>

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<222> (101)..(1600)

<223> RXN01695

<400> 569

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Met Ser Asp Ser Pro
1 5

aag aac gca ccg agg att acc gat gag gca gat gta gtt ctc att ggt 163
Lys Asn Ala Pro Arg Ile Thr Asp Glu Ala Asp Val Val Leu Ile Gly
10 15 20

gcc ggt atc atg agc tcc acg ctg ggt gca atg ctg cgt cag ctg gag 211
Ala Gly Ile Met Ser Ser Thr Leu Gly Ala Met Leu Arg Gln Leu Glu
25 30 35

cca agc tgg act cag atc gtc ttc gag cgt ttg gat gga ccg gca caa 259
Pro Ser Trp Thr Gln Ile Val Phe Glu Arg Leu Asp Gly Pro Ala Gln
40 45 50

gag tcg tcc tcc ccg tgg aac aat gca gga acc ggc cac tct gct cta 307
Glu Ser Ser Ser Pro Trp Asn Asn Ala Gly Thr Gly His Ser Ala Leu
55 60 65

tgc gag ctg aac tac acc cca gag gtt aag ggc aag gtt gaa att gcc 355
Cys Glu Leu Asn Tyr Thr Pro Glu Val Lys Gly Lys Val Glu Ile Ala
70 75 80 85

aag gct gta gga atc aac gag aag ttc cag gtt tcc cgt cag ttc tgg 403
Lys Ala Val Gly Ile Asn Glu Lys Phe Gln Val Ser Arg Gln Phe Trp
90 95 100

tct cac ctc gtt gaa gag gga gtg ctg tct gat cct aag gaa ttc atc 451
Ser His Leu Val Glu Glu Gly Val Leu Ser Asp Pro Lys Glu Phe Ile
105 110 115

aac cct gtt cct cac gta tct ttc ggc cag ggc gca gat cag gtt gca 499
Asn Pro Val Pro His Val Ser Phe Gly Gln Gly Ala Asp Gln Val Ala
120 125 130

tac atc aag gct cgc tac gaa gct ttg aag gat cac cca ctc ttc cag 547
Tyr Ile Lys Ala Arg Tyr Glu Ala Leu Lys Asp His Pro Leu Phe Gln
135 140 145

ggc atg acc tac gct gac gat gaa gct acc ttc acc gag aag ctg cct 595
Gly Met Thr Tyr Ala Asp Asp Glu Ala Thr Phe Thr Glu Lys Leu Pro

150	155	160	165	
ttg atg gca aag ggc cgt gac ttc tct gat cca gta gca atc tct tgg				643
Leu Met Ala Lys Gly Arg Asp Phe Ser Asp Pro Val Ala Ile Ser Trp				
170		175	180	
atc gat gaa ggc acc gac atc aac tac ggt gct cag acc aag cag tac				691
Ile Asp Glu Gly Thr Asp Ile Asn Tyr Gly Ala Gln Thr Lys Gln Tyr				
185		190	195	
ctg gat gca gct gaa gtt gaa ggc act gaa atc cgc tat ggc cac gaa				739
Leu Asp Ala Ala Glu Val Glu Gly Thr Glu Ile Arg Tyr Gly His Glu				
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gtc aag agc atc aag gct gat ggc gca aag tgg atc gtg acc gtc aag				787
Val Lys Ser Ile Lys Ala Asp Gly Ala Lys Trp Ile Val Thr Val Lys				
215		220	225	
aac gta cac act ggc gac acc aag acc atc aag gca aac ttc gtg ttc				835
Asn Val His Thr Gly Asp Thr Lys Thr Ile Lys Ala Asn Phe Val Phe				
230		235	240	245
gtc ggc gca ggc gga tac gca ctg gat ctg ctt cgc agc gca ggc atc				883
Val Gly Ala Gly Gly Tyr Ala Leu Asp Leu Leu Arg Ser Ala Gly Ile				
250		255	260	
cca cag gtc aag ggc ttc gct gga ttc cca gta tcc ggc ctg tgg ctt				931
Pro Gln Val Lys Gly Phe Ala Gly Phe Pro Val Ser Gly Leu Trp Leu				
265		270	275	
cgt tgc acc aac gag gaa ctg atc gag cag cac gca gcc aag gta tat				979
Arg Cys Thr Asn Glu Glu Leu Ile Glu Gln His Ala Ala Lys Val Tyr				
280		285	290	
ggc aag gca tct gtt ggc gct cct cca atg tct gtt cct cac ctt gac				1027
Gly Lys Ala Ser Val Gly Ala Pro Pro Met Ser Val Pro His Leu Asp				
295		300	305	
acc cgc gtt atc gag ggt gaa aag ggt ctg ctc ttt gga cct tac ggt				1075
Thr Arg Val Ile Glu Gly Glu Lys Gly Leu Leu Phe Gly Pro Tyr Gly				
310		315	320	325
ggc tgg acc cct aag ttc ttg aag gaa ggc tcc tac ctg gac ctg ttc				1123
Gly Trp Thr Pro Lys Phe Leu Lys Glu Gly Ser Tyr Leu Asp Leu Phe				
330		335	340	
aag tcc atc cgc cca gac aac att cct tcc tac ctt ggc gtt gct gct				1171
Lys Ser Ile Arg Pro Asp Asn Ile Pro Ser Tyr Leu Gly Val Ala Ala				
345		350	355	
cag gaa ttt gat ctg acc aag tac ctt gtc act gaa gtt ctc aag gac				1219
Gln Glu Phe Asp Leu Thr Lys Tyr Leu Val Thr Glu Val Leu Lys Asp				
360		365	370	
cag gac aag cgt atg gat gct ctt cgc gag tac atg cca gag gca caa				1267
Gln Asp Lys Arg Met Asp Ala Leu Arg Glu Tyr Met Pro Glu Ala Gln				
375		380	385	
aac ggc gat tgg gag acc atc gtt gcc gga cag cgt gtt cag gtt att				1315
Asn Gly Asp Trp Glu Thr Ile Val Ala Gly Gln Arg Val Gln Val Ile				
390		395	400	405

aag cct gca gga ttc cct aag ttc ggt tcc ctg gaa ttc ggc acc acc 1363
Lys Pro Ala Gly Phe Pro Lys Phe Gly Ser Leu Glu Phe Gly Thr Thr
410 415 420

ttg atc aac aac tcc gaa ggc acc atc gcc gga ttg ctc ggt gct tcc 1411
Leu Ile Asn Asn Ser Glu Gly Thr Ile Ala Gly Leu Leu Gly Ala Ser
425 430 435

cct gga gca tcc atc gca cct tcc gca atg atc gag ctg ctt gag cgt 1459
Pro Gly Ala Ser Ile Ala Pro Ser Ala Met Ile Glu Leu Leu Glu Arg
440 445 450

tgc ttc ggt gac cgc atg atc gag tgg ggc gac aag ctg aag gac atg 1507
Cys Phe Gly Asp Arg Met Ile Glu Trp Gly Asp Lys Leu Lys Asp Met
455 460 465

atc cct tcc tac ggc aag aag ctt gct tcc gag cca gca ctg ttt gag 1555
Ile Pro Ser Tyr Gly Lys Lys Leu Ala Ser Glu Pro Ala Leu Phe Glu
470 475 480 485

cag cag tgg gca cgc acc cag aag acc ctg aag ctt gag gaa gcc 1600
Gln Gln Trp Ala Arg Thr Gln Lys Thr Leu Lys Leu Glu Glu Ala
490 495 500

taaattcttct aactgctttc ttt 1623

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<212> PRT
<213> Corynebacterium glutamicum

<400> 570
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35 40 45
Asp Gly Pro Ala Gln Glu Ser Ser Ser Pro Trp Asn Asn Ala Gly Thr
50 55 60
Gly His Ser Ala Leu Cys Glu Leu Asn Tyr Thr Pro Glu Val Lys Gly
65 70 75 80
Lys Val Glu Ile Ala Lys Ala Val Gly Ile Asn Glu Lys Phe Gln Val
85 90 95
Ser Arg Gln Phe Trp Ser His Leu Val Glu Glu Gly Val Leu Ser Asp
100 105 110
Pro Lys Glu Phe Ile Asn Pro Val Pro His Val Ser Phe Gly Gln Gly
115 120 125
Ala Asp Gln Val Ala Tyr Ile Lys Ala Arg Tyr Glu Ala Leu Lys Asp
130 135 140

His Pro Leu Phe Gln Gly Met Thr Tyr Ala Asp Asp Glu Ala Thr Phe
 145 150 155 160
 Thr Glu Lys Leu Pro Leu Met Ala Lys Gly Arg Asp Phe Ser Asp Pro
 165 170 175
 Val Ala Ile Ser Trp Ile Asp Glu Gly Thr Asp Ile Asn Tyr Gly Ala
 180 185 190
 Gln Thr Lys Gln Tyr Leu Asp Ala Ala Glu Val Glu Gly Thr Glu Ile
 195 200 205
 Arg Tyr Gly His Glu Val Lys Ser Ile Lys Ala Asp Gly Ala Lys Trp
 210 215 220
 Ile Val Thr Val Lys Asn Val His Thr Gly Asp Thr Lys Thr Ile Lys
 225 230 235 240
 Ala Asn Phe Val Phe Val Gly Ala Gly Gly Tyr Ala Leu Asp Leu Leu
 245 250 255
 Arg Ser Ala Gly Ile Pro Gln Val Lys Gly Phe Ala Gly Phe Pro Val
 260 265 270
 Ser Gly Leu Trp Leu Arg Cys Thr Asn Glu Glu Leu Ile Glu Gln His
 275 280 285
 Ala Ala Lys Val Tyr Gly Lys Ala Ser Val Gly Ala Pro Pro Met Ser
 290 295 300
 Val Pro His Leu Asp Thr Arg Val Ile Glu Gly Glu Lys Gly Leu Leu
 305 310 315 320
 Phe Gly Pro Tyr Gly Gly Trp Thr Pro Lys Phe Leu Lys Glu Gly Ser
 325 330 335
 Tyr Leu Asp Leu Phe Lys Ser Ile Arg Pro Asp Asn Ile Pro Ser Tyr
 340 345 350
 Leu Gly Val Ala Ala Gln Glu Phe Asp Leu Thr Lys Tyr Leu Val Thr
 355 360 365
 Glu Val Leu Lys Asp Gln Asp Lys Arg Met Asp Ala Leu Arg Glu Tyr
 370 375 380
 Met Pro Glu Ala Gln Asn Gly Asp Trp Glu Thr Ile Val Ala Gly Gln
 385 390 395 400
 Arg Val Gln Val Ile Lys Pro Ala Gly Phe Pro Lys Phe Gly Ser Leu
 405 410 415
 Glu Phe Gly Thr Thr Leu Ile Asn Asn Ser Glu Gly Thr Ile Ala Gly
 420 425 430
 Leu Leu Gly Ala Ser Pro Gly Ala Ser Ile Ala Pro Ser Ala Met Ile
 435 440 445
 Glu Leu Leu Glu Arg Cys Phe Gly Asp Arg Met Ile Glu Trp Gly Asp
 450 455 460
 Lys Leu Lys Asp Met Ile Pro Ser Tyr Gly Lys Lys Leu Ala Ser Glu

465 470 475 480

Pro Ala Leu Phe Glu Gln Gln Trp Ala Arg Thr Gln Lys Thr Leu Lys
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Leu Glu Glu Ala
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<213> Corynebacterium glutamicum
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<223> FRXA01615
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aag aac gca ccg agg att acc gat gag gca gat gta gtt ctc att ggt															163
Lys	Asn	Ala	Pro	Arg	Ile	Thr	Asp	Glu	Ala	Asp	Val	Val	Leu	Ile	Gly
				10					15					20	
gcc ggt atc atg agc tcc acg ctg ggt gca atg ctg cgt cag ctg gag															211
Ala	Gly	Ile	Met	Ser	Ser	Thr	Leu	Gly	Ala	Met	Leu	Arg	Gln	Leu	Glu
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cca agc tgg act cag atc gtc ttc gag cgt ttg gat gga ccg gca caa															259
Pro	Ser	Trp	Thr	Gln	Ile	Val	Phe	Glu	Arg	Leu	Asp	Gly	Pro	Ala	Gln
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gag tcg tcc tcc ccg tgg aac aat gca gga acc ggc cac tct gct cta															307
Glu	Ser	Ser	Ser	Pro	Trp	Asn	Asn	Ala	Gly	Thr	Gly	His	Ser	Ala	Leu
	55					60					65				
tgc gag ctg aac tac acc cca gag gtt aag ggc aag gtt gaa att gcc															355
Cys	Glu	Leu	Asn	Tyr	Thr	Pro	Glu	Val	Lys	Gly	Lys	Val	Glu	Ile	Ala
70					75					80				85	
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Lys	Ala	Val	Gly	Ile	Asn	Glu	Lys	Phe	Gln	Val	Ser	Arg	Gln	Phe	Trp
				90					95					100	
tct cac ctc gtt gaa gag gga gtg ctg tct gat cct aag gaa ttc atc															451
Ser	His	Leu	Val	Glu	Glu	Gly	Val	Leu	Ser	Asp	Pro	Lys	Glu	Phe	Ile
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aac cct gtt cct cac gta tct ttc ggc cag ggc gca gat cag gtt gca															499
Asn	Pro	Val	Pro	His	Val	Ser	Phe	Gly	Gln	Gly	Ala	Asp	Gln	Val	Ala
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135					140						145				

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 Gly Met Thr Tyr Ala Asp Asp Glu Ala Thr Phe Thr Glu Lys Leu Pro
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 Leu Met Ala Lys Gly Arg Asp Phe Ser Asp Pro Val Ala Ile Ser Trp
 170 175 180

atc gat gaa ggc acc gac atc aac tac ggt gct cag acc aag cag tac 691
 Ile Asp Glu Gly Thr Asp Ile Asn Tyr Gly Ala Gln Thr Lys Gln Tyr
 185 190 195

ctg gat gca gct gaa gtt gaa ggc act gaa atc cgc tat ggc cac gaa 739
 Leu Asp Ala Ala Glu Val Glu Gly Thr Glu Ile Arg Tyr Gly His Glu
 200 205 210

gtc aag agc atc aag gct gat ggc gca aag tgg atc gtg acc gtc aag 787
 Val Lys Ser Ile Lys Ala Asp Gly Ala Lys Trp Ile Val Thr Val Lys
 215 220 225

aac gta cac act ggc gac acc aag acc atc aag gca aac ttc gtg ttc 835
 Asn Val His Thr Gly Asp Thr Lys Thr Ile Lys Ala Asn Phe Val Phe
 230 235 240 245

gtc ggc gca ggc gga tac gca ctg gat ctg ctt cgc agc gca ggc atc 883
 Val Gly Ala Gly Gly Tyr Ala Leu Asp Leu Leu Arg Ser Ala Gly Ile
 250 255 260

cca cag gtc aag ggc ttc gct gga ttc cca gta tcc ggc ctg tgg ctt 931
 Pro Gln Val Lys Gly Phe Ala Gly Phe Pro Val Ser Gly Leu Trp Leu
 265 270 275

cgt tgc acc aac gag gaa ctg atc gag cag cac gca gcc aag gta tat 979
 Arg Cys Thr Asn Glu Glu Leu Ile Glu Gln His Ala Ala Lys Val Tyr
 280 285 290

ggc aag gca tct gtt ggc gct cct cca atg tct gtt cct cac ctt gac 1027
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 295 300 305

acc cgc gtt atc 1039
 Thr Arg Val Ile
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<210> 572
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 <212> PRT
 <213> Corynebacterium glutamicum

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 35 40 45

Asp Gly Pro Ala Gln Glu Ser Ser Ser Pro Trp Asn Asn Ala Gly Thr
 50 55 60
 Gly His Ser Ala Leu Cys Glu Leu Asn Tyr Thr Pro Glu Val Lys Gly
 65 70 75 80
 Lys Val Glu Ile Ala Lys Ala Val Gly Ile Asn Glu Lys Phe Gln Val
 85 90 95
 Ser Arg Gln Phe Trp Ser His Leu Val Glu Glu Gly Val Leu Ser Asp
 100 105 110
 Pro Lys Glu Phe Ile Asn Pro Val Pro His Val Ser Phe Gly Gln Gly
 115 120 125
 Ala Asp Gln Val Ala Tyr Ile Lys Ala Arg Tyr Glu Ala Leu Lys Asp
 130 135 140
 His Pro Leu Phe Gln Gly Met Thr Tyr Ala Asp Asp Glu Ala Thr Phe
 145 150 155 160
 Thr Glu Lys Leu Pro Leu Met Ala Lys Gly Arg Asp Phe Ser Asp Pro
 165 170 175
 Val Ala Ile Ser Trp Ile Asp Glu Gly Thr Asp Ile Asn Tyr Gly Ala
 180 185 190
 Gln Thr Lys Gln Tyr Leu Asp Ala Ala Glu Val Glu Gly Thr Glu Ile
 195 200 205
 Arg Tyr Gly His Glu Val Lys Ser Ile Lys Ala Asp Gly Ala Lys Trp
 210 215 220
 Ile Val Thr Val Lys Asn Val His Thr Gly Asp Thr Lys Thr Ile Lys
 225 230 235 240
 Ala Asn Phe Val Phe Val Gly Ala Gly Gly Tyr Ala Leu Asp Leu Leu
 245 250 255
 Arg Ser Ala Gly Ile Pro Gln Val Lys Gly Phe Ala Gly Phe Pro Val
 260 265 270
 Ser Gly Leu Trp Leu Arg Cys Thr Asn Glu Glu Leu Ile Glu Gln His
 275 280 285
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 Val Pro His Leu Asp Thr Arg Val Ile
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<210> 573

<211> 233

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (1)..(210)

<223> FRXA01695

<400> 573

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 1             5             10             15

atg atc gag ctg ctt gag cgt tgc ttc ggt gac cgc atg atc gag tgg 96
Met Ile Glu Leu Leu Glu Arg Cys Phe Gly Asp Arg Met Ile Glu Trp
          20             25             30

ggc gac aag ctg aag gac atg atc cct tcc tac ggc aag aag ctt gct 144
Gly Asp Lys Leu Lys Asp Met Ile Pro Ser Tyr Gly Lys Lys Leu Ala
          35             40             45

tcc gag cca gca ctg ttt gag cag cag tgg gca cgc acc cag aag acc 192
Ser Glu Pro Ala Leu Phe Glu Gln Gln Trp Ala Arg Thr Gln Lys Thr
          50             55             60

ctg aag ctt gag gaa gcc taaatcttct aactgctttc ttt 233
Leu Lys Leu Glu Glu Ala
 65             70

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<210> 574

<211> 70

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 574

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Ala Gly Leu Leu Gly Ala Ser Pro Gly Ala Ser Ile Ala Pro Ser Ala
 1             5             10             15

Met Ile Glu Leu Leu Glu Arg Cys Phe Gly Asp Arg Met Ile Glu Trp
          20             25             30

Gly Asp Lys Leu Lys Asp Met Ile Pro Ser Tyr Gly Lys Lys Leu Ala
          35             40             45

Ser Glu Pro Ala Leu Phe Glu Gln Gln Trp Ala Arg Thr Gln Lys Thr
          50             55             60

Leu Lys Leu Glu Glu Ala
 65             70

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<210> 575

<211> 1063

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(1063)

<223> RXA00290

<400> 575

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gagcttcccc caaaaacacc gattaacaag gctaaatgat atg acc atc gac ctg 115
Met Thr Ile Asp Leu
          1             5

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cag cgt tcc acc caa aac ctc acc cat gag gaa atc ttc gag gca cac	163
Gln Arg Ser Thr Gln Asn Leu Thr His Glu Glu Ile Phe Glu Ala His	
10 15 20	
gag ggc gga aag ctc tcc att agt tcc act cgt ccg ctc cgc gac atg	211
Glu Gly Gly Lys Leu Ser Ile Ser Ser Thr Arg Pro Leu Arg Asp Met	
25 30 35	
cgc gat ctt tcc ctt gct tac acc cct ggt gtt gct cag gtt tgt gaa	259
Arg Asp Leu Ser Leu Ala Tyr Thr Pro Gly Val Ala Gln Val Cys Glu	
40 45 50	
gca atc aag gaa gat cca gag gtt gcg cgc acc cac acg ggc att gga	307
Ala Ile Lys Glu Asp Pro Glu Val Ala Arg Thr His Thr Gly Ile Gly	
55 60 65	
aac acc gtc gcg gtt att tcc gac ggc acc gct gtt ctt ggc ctt ggc	355
Asn Thr Val Ala Val Ile Ser Asp Gly Thr Ala Val Leu Gly Leu Gly	
70 75 80 85	
gat atc gga cct cag gcc tcc ctt ccc gtc atg gag ggc aag gct cag	403
Asp Ile Gly Pro Gln Ala Ser Leu Pro Val Met Glu Gly Lys Ala Gln	
90 95 100	
ctg ttt agc tct ttc gct ggc ctg aag gct atc cct atc gtt ttg gac	451
Leu Phe Ser Ser Phe Ala Gly Leu Lys Ala Ile Pro Ile Val Leu Asp	
105 110 115	
gtt cac gat gtt gac gct ttg gtt gag acc atc gca gcc atc gcg cct	499
Val His Asp Val Asp Ala Leu Val Glu Thr Ile Ala Ala Ile Ala Pro	
120 125 130	
tct ttc ggt gct atc aac ttg gag gac atc tcc gct cct cgt tgc ttc	547
Ser Phe Gly Ala Ile Asn Leu Glu Asp Ile Ser Ala Pro Arg Cys Phe	
135 140 145	
gag gtg gag cgc cgc ctc atc gag cgt ctc gat att cca gtt atg cac	595
Glu Val Glu Arg Arg Leu Ile Glu Arg Leu Asp Ile Pro Val Met His	
150 155 160 165	
gat gac cag cac ggc acc gct gtg gtt atc ctc gct gcg ctg cgc aac	643
Asp Asp Gln His Gly Thr Ala Val Val Ile Leu Ala Ala Leu Arg Asn	
170 175 180	
tcc ctg aag ctg ctg gat cgc aag atc gaa gac ctc aag att gtt att	691
Ser Leu Lys Leu Leu Asp Arg Lys Ile Glu Asp Leu Lys Ile Val Ile	
185 190 195	
tcc ggc gca ggc gca gcg ggc gtt gca gct gta gat atg ctg acc aac	739
Ser Gly Ala Gly Ala Ala Gly Val Ala Ala Val Asp Met Leu Thr Asn	
200 205 210	
gct gga gca acc gac atc gtg gtt ctt gat tcc cga ggc atc atc cac	787
Ala Gly Ala Thr Asp Ile Val Val Leu Asp Ser Arg Gly Ile Ile His	
215 220 225	
gac agc cgt gag gat ctt tcc cca gtt aag gct gct ctt gca gag aag	835
Asp Ser Arg Glu Asp Leu Ser Pro Val Lys Ala Ala Leu Ala Glu Lys	
230 235 240 245	

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<400> 576
Met Thr Ile Asp Leu Gln Arg Ser Thr Gln Asn Leu Thr His Glu Glu
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Ile Phe Glu Ala His Glu Gly Gly Lys Leu Ser Ile Ser Ser Thr Arg
      20             25             30
Pro Leu Arg Asp Met Arg Asp Leu Ser Leu Ala Tyr Thr Pro Gly Val
      35             40             45
Ala Gln Val Cys Glu Ala Ile Lys Glu Asp Pro Glu Val Ala Arg Thr
      50             55             60
His Thr Gly Ile Gly Asn Thr Val Ala Val Ile Ser Asp Gly Thr Ala
  65             70             75             80
Val Leu Gly Leu Gly Asp Ile Gly Pro Gln Ala Ser Leu Pro Val Met
      85             90             95
Glu Gly Lys Ala Gln Leu Phe Ser Ser Phe Ala Gly Leu Lys Ala Ile
      100            105            110
Pro Ile Val Leu Asp Val His Asp Val Asp Ala Leu Val Glu Thr Ile
      115            120            125
Ala Ala Ile Ala Pro Ser Phe Gly Ala Ile Asn Leu Glu Asp Ile Ser
      130            135            140
Ala Pro Arg Cys Phe Glu Val Glu Arg Arg Leu Ile Glu Arg Leu Asp
  145            150            155            160
Ile Pro Val Met His Asp Asp Gln His Gly Thr Ala Val Val Ile Leu
      165            170            175
Ala Ala Leu Arg Asn Ser Leu Lys Leu Leu Asp Arg Lys Ile Glu Asp

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180	185	190
Leu Lys Ile Val Ile Ser Gly Ala Gly Ala Ala Gly Val Ala Ala Val 195 200 205		
Asp Met Leu Thr Asn Ala Gly Ala Thr Asp Ile Val Val Leu Asp Ser 210 215 220		
Arg Gly Ile Ile His Asp Ser Arg Glu Asp Leu Ser Pro Val Lys Ala 225 230 235 240		
Ala Leu Ala Glu Lys Thr Asn Pro Arg Gly Ile Ser Gly Gly Ile Asn 245 250 255		
Glu Ala Phe Thr Gly Ala Asp Leu Phe Ile Gly Val Ser Gly Gly Asn 260 265 270		
Ile Gly Glu Asp Ala Leu Lys Leu Met Ala Pro Glu Pro Ile Leu Phe 275 280 285		
Thr Leu Ala Asn Pro Thr Pro Glu Ile Asp Pro Glu Leu Ser Gln Lys 290 295 300		
Tyr Gly Ala Ile Val Ala Thr Gly Pro Val Leu Thr Cys Leu Thr Arg 305 310 315 320		
Ser		

<210> 577
 <211> 1347
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1324)
 <223> RXN01048

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 gagcttcccg caaaaacacc gattaacaag gctaaatgat atg acc atc gac ctg 115
 Met Thr Ile Asp Leu
 1 5
 cag cgt tcc acc caa aac ctc acc cat gag gaa atc ttc gag gca cac 163
 Gln Arg Ser Thr Gln Asn Leu Thr His Glu Glu Ile Phe Glu Ala His
 10 15 20
 gag ggc gga aag ctc tcc att agt tcc act cgt ccg ctc cgc gac atg 211
 Glu Gly Gly Lys Leu Ser Ile Ser Thr Arg Pro Leu Arg Asp Met
 25 30 35
 cgc gat ctt tcc ctt gct tac acc cct ggt gtt gct cag gtt tgt gaa 259
 Arg Asp Leu Ser Leu Ala Tyr Thr Pro Gly Val Ala Gln Val Cys Glu
 40 45 50
 gca atc aag gaa gat cca gag gtt gcg cgc acc cac acg ggc att gga 307
 Ala Ile Lys Glu Asp Pro Glu Val Ala Arg Thr His Thr Gly Ile Gly

55	60	65	
aac acc gtc gcg gtt att tcc gac ggc acc gct gtt ctt ggc ctt ggc			355
Asn Thr Val Ala Val Ile Ser Asp Gly Thr Ala Val Leu Gly Leu Gly			
70	75	80	85
gat atc gga cct cag gcc tcc ctt ccc gtc atg gag ggc aag gct cag			403
Asp Ile Gly Pro Gln Ala Ser Leu Pro Val Met Glu Gly Lys Ala Gln			
	90	95	100
ctg ttt agc tct ttc gct ggc ctg aag gct atc cct atc gtt ttg gac			451
Leu Phe Ser Ser Phe Ala Gly Leu Lys Ala Ile Pro Ile Val Leu Asp			
	105	110	115
gtt cac gat gtt gac gct ttg gtt gag acc atc gca gcc atc gcg cct			499
Val His Asp Val Asp Ala Leu Val Glu Thr Ile Ala Ala Ile Ala Pro			
	120	125	130
tct ttc ggt gct atc aac ttg gag gac atc tcc gct cct cgt tgc ttc			547
Ser Phe Gly Ala Ile Asn Leu Glu Asp Ile Ser Ala Pro Arg Cys Phe			
	135	140	145
gag gtg gag cgc cgc ctc atc gag cgt ctc gat att cca gtt atg cac			595
Glu Val Glu Arg Arg Leu Ile Glu Arg Leu Asp Ile Pro Val Met His			
	150	155	160
gat gac cag cac ggc acc gct gtg gtt atc ctc gct gcg ctg cgc aac			643
Asp Asp Gln His Gly Thr Ala Val Val Ile Leu Ala Ala Leu Arg Asn			
	170	175	180
tcc ctg aag ctg ctg gat cgc aag atc gaa gac ctc aag att gtt att			691
Ser Leu Lys Leu Leu Asp Arg Lys Ile Glu Asp Leu Lys Ile Val Ile			
	185	190	195
tcc ggc gca ggc gca gcg ggc gtt gca gct gta gat atg ctg acc aac			739
Ser Gly Ala Gly Ala Ala Gly Val Ala Ala Val Asp Met Leu Thr Asn			
	200	205	210
gct gga gca acc gac atc gtg gtt ctt gat tcc cga ggc atc atc cac			787
Ala Gly Ala Thr Asp Ile Val Val Leu Asp Ser Arg Gly Ile Ile His			
	215	220	225
gac agc cgt gag gat ctt tcc cca gtt aag gct gct ctt gca gag aag			835
Asp Ser Arg Glu Asp Leu Ser Pro Val Lys Ala Ala Leu Ala Glu Lys			
	230	235	240
acc aac cct cgt ggc atc agc ggt ggc atc aat gag gct ttc acc ggc			883
Thr Asn Pro Arg Gly Ile Ser Gly Gly Ile Asn Glu Ala Phe Thr Gly			
	250	255	260
gcg gac ctg ttc att ggc gtg tcc ggc ggc aac atc ggc gag gac gct			931
Ala Asp Leu Phe Ile Gly Val Ser Gly Gly Asn Ile Gly Glu Asp Ala			
	265	270	275
ctc aaa ctc atg gcc ccg gag cca atc ctg ttc acc ctg gcg aac cca			979
Leu Lys Leu Met Ala Pro Glu Pro Ile Leu Phe Thr Leu Ala Asn Pro			
	280	285	290
acc cca gag atc gat cct gag ctg tct cag aag tac ggc gcc atc gtc			1027
Thr Pro Glu Ile Asp Pro Glu Leu Ser Gln Lys Tyr Gly Ala Ile Val			
	295	300	305

gcg acc ggg cgc tct gac ctg cct aac cag atc aac aac gtg ctg gcg 1075
 Ala Thr Gly Arg Ser Asp Leu Pro Asn Gln Ile Asn Asn Val Leu Ala
 310 315 320 325

ttc cca gga att ttc gcc ggc gct ctc gca gcc aag gct aag aag atc 1123
 Phe Pro Gly Ile Phe Ala Gly Ala Leu Ala Ala Lys Ala Lys Lys Ile
 330 335 340

acc ccc gag atg aag ctc gcc gct cag agg caa tcg cag aca tcg cag 1171
 Thr Pro Glu Met Lys Leu Ala Ala Gln Arg Gln Ser Gln Thr Ser Gln
 345 350 355

ctg agg acc tcg agg tcg gcc gca tcg tgc cta ccg ccc tgg atc ccc 1219
 Leu Arg Thr Ser Arg Ser Ala Ala Ser Cys Leu Pro Pro Trp Ile Pro
 360 365 370

gcg ttg ccc caa cag tca agg cag ctg tcc agg ccg tcg cca aag cgc 1267
 Ala Leu Pro Gln Gln Ser Arg Gln Leu Ser Arg Pro Ser Pro Lys Arg
 375 380 385

aaa acg ctt aaa aat ttg ctt atc gac gcc tcc ctc ccc gtc gag gcg 1315
 Lys Thr Leu Lys Asn Leu Leu Ile Asp Ala Ser Leu Pro Val Glu Ala
 390 395 400 405

cca ata ttt taagagcaaa cttgaggccc aca 1347
 Pro Ile Phe

<210> 578
 <211> 408
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 578
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 1 5 10 15

Ile Phe Glu Ala His Glu Gly Gly Lys Leu Ser Ile Ser Ser Thr Arg
 20 25 30

Pro Leu Arg Asp Met Arg Asp Leu Ser Leu Ala Tyr Thr Pro Gly Val
 35 40 45

Ala Gln Val Cys Glu Ala Ile Lys Glu Asp Pro Glu Val Ala Arg Thr
 50 55 60

His Thr Gly Ile Gly Asn Thr Val Ala Val Ile Ser Asp Gly Thr Ala
 65 70 75 80

Val Leu Gly Leu Gly Asp Ile Gly Pro Gln Ala Ser Leu Pro Val Met
 85 90 95

Glu Gly Lys Ala Gln Leu Phe Ser Ser Phe Ala Gly Leu Lys Ala Ile
 100 105 110

Pro Ile Val Leu Asp Val His Asp Val Asp Ala Leu Val Glu Thr Ile
 115 120 125

Ala Ala Ile Ala Pro Ser Phe Gly Ala Ile Asn Leu Glu Asp Ile Ser

130	135	140
Ala Pro Arg Cys Phe Glu Val Glu Arg Arg Leu Ile Glu Arg Leu Asp 145 150 155 160		
Ile Pro Val Met His Asp Asp Gln His Gly Thr Ala Val Val Ile Leu 165 170 175		
Ala Ala Leu Arg Asn Ser Leu Lys Leu Leu Asp Arg Lys Ile Glu Asp 180 185 190		
Leu Lys Ile Val Ile Ser Gly Ala Gly Ala Ala Gly Val Ala Ala Val 195 200 205		
Asp Met Leu Thr Asn Ala Gly Ala Thr Asp Ile Val Val Leu Asp Ser 210 215 220		
Arg Gly Ile Ile His Asp Ser Arg Glu Asp Leu Ser Pro Val Lys Ala 225 230 235 240		
Ala Leu Ala Glu Lys Thr Asn Pro Arg Gly Ile Ser Gly Gly Ile Asn 245 250 255		
Glu Ala Phe Thr Gly Ala Asp Leu Phe Ile Gly Val Ser Gly Gly Asn 260 265 270		
Ile Gly Glu Asp Ala Leu Lys Leu Met Ala Pro Glu Pro Ile Leu Phe 275 280 285		
Thr Leu Ala Asn Pro Thr Pro Glu Ile Asp Pro Glu Leu Ser Gln Lys 290 295 300		
Tyr Gly Ala Ile Val Ala Thr Gly Arg Ser Asp Leu Pro Asn Gln Ile 305 310 315 320		
Asn Asn Val Leu Ala Phe Pro Gly Ile Phe Ala Gly Ala Leu Ala Ala 325 330 335		
Lys Ala Lys Lys Ile Thr Pro Glu Met Lys Leu Ala Ala Gln Arg Gln 340 345 350		
Ser Gln Thr Ser Gln Leu Arg Thr Ser Arg Ser Ala Ala Ser Cys Leu 355 360 365		
Pro Pro Trp Ile Pro Ala Leu Pro Gln Gln Ser Arg Gln Leu Ser Arg 370 375 380		
Pro Ser Pro Lys Arg Lys Thr Leu Lys Asn Leu Leu Ile Asp Ala Ser 385 390 395 400		
Leu Pro Val Glu Ala Pro Ile Phe 405		

<210> 579

<211> 311

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

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Ser Gly Ala Gly Ala Ala Gly Val Ala Ala Val Asp Met Leu Thr Asn			
200	205	210	
gct gga gca acc gac atc gtg gtt ctt gat tcc cga ggc atc atc cac			787
Ala Gly Ala Thr Asp Ile Val Val Leu Asp Ser Arg Gly Ile Ile His			
215	220	225	
gac agc cgt gag gat ctt tcc cca gtt aag gct gct ctt gca gag aag			835
Asp Ser Arg Glu Asp Leu Ser Pro Val Lys Ala Ala Leu Ala Glu Lys			
230	235	240	245
acc aac cct cgt ggc atc agc ggt ggc atc aat gag gct ttc acc ggc			883
Thr Asn Pro Arg Gly Ile Ser Gly Gly Ile Asn Glu Ala Phe Thr Gly			
250	255	260	
gcg gac ctg ttc att ggc gtg tcc ggc ggc aac atc ggc gag gac gct			931
Ala Asp Leu Phe Ile Gly Val Ser Gly Gly Asn Ile Gly Glu Asp Ala			
265	270	275	
ctc aaa ctc atg gcc ccg gag cca atc ctg ttc acc ctg gcg aac cca			979
Leu Lys Leu Met Ala Pro Glu Pro Ile Leu Phe Thr Leu Ala Asn Pro			
280	285	290	
acc cca gag atc gat cct gag ctg tct cag aag tac ggc gcc atc gtc			1027
Thr Pro Glu Ile Asp Pro Glu Leu Ser Gln Lys Tyr Gly Ala Ile Val			
295	300	305	
gcg acc ggg ccg gtc ttg acc tgc cta acc aga tca			1063
Ala Thr Gly Pro Val Leu Thr Cys Leu Thr Arg Ser			
310	315	320	

<210> 582

<211> 321

<212> PRT

<213> Corynebacterium glutamicum

<400> 582

Met	Thr	Ile	Asp	Leu	Gln	Arg	Ser	Thr	Gln	Asn	Leu	Thr	His	Glu	Glu
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Ile	Phe	Glu	Ala	His	Glu	Gly	Gly	Lys	Leu	Ser	Ile	Ser	Ser	Thr	Arg
		20						25						30	

Pro	Leu	Arg	Asp	Met	Arg	Asp	Leu	Ser	Leu	Ala	Tyr	Thr	Pro	Gly	Val
		35					40					45			

Ala	Gln	Val	Cys	Glu	Ala	Ile	Lys	Glu	Asp	Pro	Glu	Val	Ala	Arg	Thr
		50				55				60					

His	Thr	Gly	Ile	Gly	Asn	Thr	Val	Ala	Val	Ile	Ser	Asp	Gly	Thr	Ala
	65				70					75					80

Val	Leu	Gly	Leu	Gly	Asp	Ile	Gly	Pro	Gln	Ala	Ser	Leu	Pro	Val	Met
				85					90					95	

Glu	Gly	Lys	Ala	Gln	Leu	Phe	Ser	Ser	Phe	Ala	Gly	Leu	Lys	Ala	Ile
			100					105					110		

<222> (1)..(288)

<223> FRXA01048

<400> 579

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cgc tct gac ttg cct aac cag atc aac aac gtg ctg gcg ttc cca gga      48
Arg Ser Asp Leu Pro Asn Gln Ile Asn Asn Val Leu Ala Phe Pro Gly
  1              5              10              15

att ttc gcc ggc gct ctc gca gcc aag gct aag aag atc acc ccc gag      96
Ile Phe Ala Gly Ala Leu Ala Ala Lys Ala Lys Lys Ile Thr Pro Glu
              20              25              30

atg aag ctc gcc gct cag agg caa tcg cag aca tcg cag ctg agg acc     144
Met Lys Leu Ala Ala Gln Arg Gln Ser Gln Thr Ser Gln Leu Arg Thr
              35              40              45

tcg agg tcg gcc gca tcg tgc cta ccg ccc tgg atc ccc gcg ttg ccc     192
Ser Arg Ser Ala Ala Ser Cys Leu Pro Pro Trp Ile Pro Ala Leu Pro
              50              55              60

caa cag tca agg cag ctg tcc agg ccg tcg cca aag cgc aaa acg ctt     240
Gln Gln Ser Arg Gln Leu Ser Arg Pro Ser Pro Lys Arg Lys Thr Leu
              65              70              75              80

aaa aat ttg ctt atc gac gcc tcc ctc ccc gtc gag gcg cca ata ttt     288
Lys Asn Leu Leu Ile Asp Ala Ser Leu Pro Val Glu Ala Pro Ile Phe
              85              90              95

taagagcaaa cttgaggccc aca                                           311

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<210> 580

<211> 96

<212> PRT

<213> Corynebacterium glutamicum

<400> 580

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Arg Ser Asp Leu Pro Asn Gln Ile Asn Asn Val Leu Ala Phe Pro Gly
  1              5              10              15

Ile Phe Ala Gly Ala Leu Ala Ala Lys Ala Lys Lys Ile Thr Pro Glu
              20              25              30

Met Lys Leu Ala Ala Gln Arg Gln Ser Gln Thr Ser Gln Leu Arg Thr
              35              40              45

Ser Arg Ser Ala Ala Ser Cys Leu Pro Pro Trp Ile Pro Ala Leu Pro
              50              55              60

Gln Gln Ser Arg Gln Leu Ser Arg Pro Ser Pro Lys Arg Lys Thr Leu
              65              70              75              80

Lys Asn Leu Leu Ile Asp Ala Ser Leu Pro Val Glu Ala Pro Ile Phe
              85              90              95

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<210> 581

<211> 1063

Pro Ile Val Leu Asp Val His Asp Val Asp Ala Leu Val Glu Thr Ile
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 Ala Ala Ile Ala Pro Ser Phe Gly Ala Ile Asn Leu Glu Asp Ile Ser
 130 135 140
 Ala Pro Arg Cys Phe Glu Val Glu Arg Arg Leu Ile Glu Arg Leu Asp
 145 150 155 160
 Ile Pro Val Met His Asp Asp Gln His Gly Thr Ala Val Val Ile Leu
 165 170 175
 Ala Ala Leu Arg Asn Ser Leu Lys Leu Leu Asp Arg Lys Ile Glu Asp
 180 185 190
 Leu Lys Ile Val Ile Ser Gly Ala Gly Ala Ala Gly Val Ala Ala Val
 195 200 205
 Asp Met Leu Thr Asn Ala Gly Ala Thr Asp Ile Val Val Leu Asp Ser
 210 215 220
 Arg Gly Ile Ile His Asp Ser Arg Glu Asp Leu Ser Pro Val Lys Ala
 225 230 235 240
 Ala Leu Ala Glu Lys Thr Asn Pro Arg Gly Ile Ser Gly Gly Ile Asn
 245 250 255
 Glu Ala Phe Thr Gly Ala Asp Leu Phe Ile Gly Val Ser Gly Gly Asn
 260 265 270
 Ile Gly Glu Asp Ala Leu Lys Leu Met Ala Pro Glu Pro Ile Leu Phe
 275 280 285
 Thr Leu Ala Asn Pro Thr Pro Glu Ile Asp Pro Glu Leu Ser Gln Lys
 290 295 300
 Tyr Gly Ala Ile Val Ala Thr Gly Pro Val Leu Thr Cys Leu Thr Arg
 305 310 315 320
 Ser

<210> 583
 <211> 582
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (1)..(582)
 <223> RXN03101

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 Ile Leu Ala Asp Glu Asp Asp Thr Val Asp Val Gly Ala Val Ile Ala
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 cgc atc ggt gac gca aac gca gct gca gca cct gcc gaa gag gaa gca 96
 Arg Ile Gly Asp Ala Asn Ala Ala Ala Pro Ala Glu Glu Glu Ala

20										25										30										
gct cct gcc gaa gag gaa gaa cca gtt aag gaa gag cca aag aag gag	144																													
Ala Pro Ala Glu Glu Glu Glu Pro Val Lys Glu Glu Pro Lys Lys Glu																														
35 40 45																														
gca gct cct gaa gct cca gca gca act ggc gcc gca acc gat gtg gaa	192																													
Ala Ala Pro Glu Ala Pro Ala Ala Thr Gly Ala Ala Thr Asp Val Glu																														
50 55 60																														
atg cca gaa ctc ggc gaa tcc gtc acc gaa ggc acc att acc cag tgg	240																													
Met Pro Glu Leu Gly Glu Ser Val Thr Glu Gly Thr Ile Thr Gln Trp																														
65 70 75 80																														
ctc aag gct gtc ggc gac acc gtc gaa gta gac gaa cca ctt ctt gag	288																													
Leu Lys Ala Val Gly Asp Thr Val Glu Val Asp Glu Pro Leu Leu Glu																														
85 90 95																														
gtc tcc acc gac aag gtc gac acc gaa atc cca tcc cca gta gca ggc	336																													
Val Ser Thr Asp Lys Val Asp Thr Glu Ile Pro Ser Pro Val Ala Gly																														
100 105 110																														
acc atc gtg gag atc ctt gca gac gaa gac gac acc gtc gac gtc ggc	384																													
Thr Ile Val Glu Ile Leu Ala Asp Glu Asp Asp Thr Val Asp Val Gly																														
115 120 125																														
gca gtc atc gcc cgc atc ggt gac gca aac gca gct gca gca cct gcc	432																													
Ala Val Ile Ala Arg Ile Gly Asp Ala Asn Ala Ala Ala Pro Ala																														
130 135 140																														
gaa gag gaa gca gct cct gcc gaa gag gag gaa cca gtt aag gaa gag	480																													
Glu Glu Glu Ala Ala Pro Ala Glu Glu Glu Glu Pro Val Lys Glu Glu																														
145 150 155 160																														
cca aag aag gaa gag ccc aag aag gaa gag ccc aag aag gaa gca gct	528																													
Pro Lys Lys Glu Glu Pro Lys Lys Glu Glu Pro Lys Lys Glu Ala Ala																														
165 170 175																														
act aca cct gct gcg gca tcc gca act gtg tcc gct tct ggc gac aac	576																													
Thr Thr Pro Ala Ala Ala Ser Ala Thr Val Ser Ala Ser Gly Asp Asn																														
180 185 190																														
ggt cca	582																													
Val Pro																														

<210> 584

<211> 194

<212> PRT

<213> Corynebacterium glutamicum

<400> 584

Ile	Leu	Ala	Asp	Glu	Asp	Asp	Thr	Val	Asp	Val	Gly	Ala	Val	Ile	Ala
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Arg	Ile	Gly	Asp	Ala	Asn	Ala	Ala	Ala	Ala	Pro	Ala	Glu	Glu	Glu	Ala
			20				25					30			

Ala	Pro	Ala	Glu	Glu	Glu	Glu	Pro	Val	Lys	Glu	Glu	Pro	Lys	Lys	Glu
		35					40					45			

Ala Ala Pro Glu Ala Pro Ala Ala Thr Gly Ala Ala Thr Asp Val Glu
 50 55 60

Met Pro Glu Leu Gly Glu Ser Val Thr Glu Gly Thr Ile Thr Gln Trp
 65 70 75 80

Leu Lys Ala Val Gly Asp Thr Val Glu Val Asp Glu Pro Leu Leu Glu
 85 90 95

Val Ser Thr Asp Lys Val Asp Thr Glu Ile Pro Ser Pro Val Ala Gly
 100 105 110

Thr Ile Val Glu Ile Leu Ala Asp Glu Asp Asp Thr Val Asp Val Gly
 115 120 125

Ala Val Ile Ala Arg Ile Gly Asp Ala Asn Ala Ala Ala Pro Ala
 130 135 140

Glu Glu Glu Ala Ala Pro Ala Glu Glu Glu Glu Pro Val Lys Glu Glu
 145 150 155 160

Pro Lys Lys Glu Glu Pro Lys Lys Glu Glu Pro Lys Lys Glu Ala Ala
 165 170 175

Thr Thr Pro Ala Ala Ala Ser Ala Thr Val Ser Ala Ser Gly Asp Asn
 180 185 190

Val Pro

<210> 585
 <211> 540
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(517)
 <223> RXN02046

<400> 585
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aaattattaa catccgacgc aacgcttcag gagagtcctc atg aaa gag aca ctg 115
 Met Lys Glu Thr Leu
 1 5

acc acc ggt tta acc cac caa atg acc tac ata gtg cca gca aac cgc 163
 Thr Thr Gly Leu Thr His Gln Met Thr Tyr Ile Val Pro Ala Asn Arg
 10 15 20

aca gtt ccg cat ctg ctt ccc gaa gca gca gaa ttt gaa acc atg cca 211
 Thr Val Pro His Leu Leu Pro Glu Ala Ala Glu Phe Glu Thr Met Pro
 25 30 35

gat gtc ctg gcc act gga tat atg gtc ggc atc atc gag tgg gcc tgc 259
 Asp Val Leu Ala Thr Gly Tyr Met Val Gly Ile Ile Glu Trp Ala Cys
 40 45 50

atg gaa ctt ctg cgt ccc cat ttg gac gac ggt gaa atc tcg ctg ggc 307
 Met Glu Leu Leu Arg Pro His Leu Asp Asp Gly Glu Ile Ser Leu Gly
 55 60 65
 act cat gtg aac ttc tcc cac gca gct cca acg gtt cct gga tcc acg 355
 Thr His Val Asn Phe Ser His Ala Ala Pro Thr Val Pro Gly Ser Thr
 70 75 80 85
 gtc acc atc gat gtt gag gtg aca gag atc aac cgt cgt gca gtt acc 403
 Val Thr Ile Asp Val Glu Val Thr Glu Ile Asn Arg Arg Ala Val Thr
 90 95 100
 ttc aac atc act gca gct gat gag ttc gcc acc atc agc acc ggc acc 451
 Phe Asn Ile Thr Ala Ala Asp Glu Phe Ala Thr Ile Ser Thr Gly Thr
 105 110 115
 cac cag cgc ggt gtg gtt aac cgt gag aag ttt gtc tcc cgt ctg cct 499
 His Gln Arg Gly Val Val Asn Arg Glu Lys Phe Val Ser Arg Leu Pro
 120 125 130
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 Glu Ala Pro Lys Glu Asn
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<210> 586
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 <212> PRT
 <213> Corynebacterium glutamicum

<400> 586
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 Val Pro Ala Asn Arg Thr Val Pro His Leu Leu Pro Glu Ala Ala Glu
 20 25 30
 Phe Glu Thr Met Pro Asp Val Leu Ala Thr Gly Tyr Met Val Gly Ile
 35 40 45
 Ile Glu Trp Ala Cys Met Glu Leu Leu Arg Pro His Leu Asp Asp Gly
 50 55 60
 Glu Ile Ser Leu Gly Thr His Val Asn Phe Ser His Ala Ala Pro Thr
 65 70 75 80
 Val Pro Gly Ser Thr Val Thr Ile Asp Val Glu Val Thr Glu Ile Asn
 85 90 95
 Arg Arg Ala Val Thr Phe Asn Ile Thr Ala Ala Asp Glu Phe Ala Thr
 100 105 110
 Ile Ser Thr Gly Thr His Gln Arg Gly Val Val Asn Arg Glu Lys Phe
 115 120 125
 Val Ser Arg Leu Pro Glu Ala Pro Lys Glu Asn
 130 135

<210> 587
 <211> 1683

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1660)

<223> RXN00389

<400> 587

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tctggcgcag gttcctaccg ccttcagttg aggtgaaagc atg atc acc gca acc 115
                                   Met Ile Thr Ala Thr
                                   1 5

gca ctg cat ggg tgt tca ctg att gat ggc gag tgg gtc gct gga aaa 163
Ala Leu His Gly Cys Ser Leu Ile Asp Gly Glu Trp Val Ala Gly Lys
                                   10 15 20

aat ggt gag att aca gga ttc gat ccg cgc acc aat gcg agt ctg aac 211
Asn Gly Glu Ile Thr Gly Phe Asp Pro Arg Thr Asn Ala Ser Leu Asn
                                   25 30 35

cct tcc tac tct tta gca aac agc gca cag ctg cgc gcc gcc aca aca 259
Pro Ser Tyr Ser Leu Ala Asn Ser Ala Gln Leu Arg Ala Ala Thr Thr
                                   40 45 50

tcg gcg aag cga gct ttt gaa agc tac cga ctc act act cca gag gtt 307
Ser Ala Lys Arg Ala Phe Glu Ser Tyr Arg Leu Thr Thr Pro Glu Val
                                   55 60 65

aga gca gat ttc ctg gat tcc atc gct gac aac atc gat gcg cta tcc 355
Arg Ala Asp Phe Leu Asp Ser Ile Ala Asp Asn Ile Asp Ala Leu Ser
                                   70 75 80 85

ggc gag atc gtg caa cgg gcg agc ctg gag aca ggt ttg gga act acc 403
Gly Glu Ile Val Gln Arg Ala Ser Leu Glu Thr Gly Leu Gly Thr Thr
                                   90 95 100

cga ctc aca ggc gaa gta gcc cgc acc agc aac cag ctc cgc ctg ttt 451
Arg Leu Thr Gly Glu Val Ala Arg Thr Ser Asn Gln Leu Arg Leu Phe
                                   105 110 115

gca gaa acc gtg aga agc gga cag ttc cac cga gta cgc att gaa cga 499
Ala Glu Thr Val Arg Ser Gly Gln Phe His Arg Val Arg Ile Glu Arg
                                   120 125 130

gga ccg cgg att gat ctt cgc cag cgt cag gtt ccg ttg gga cca gtc 547
Gly Pro Arg Ile Asp Leu Arg Gln Arg Gln Val Pro Leu Gly Pro Val
                                   135 140 145

gcg gta ttc ggg gca agc aac ttc ccc gtc gct ttc tct act gct ggt 595
Ala Val Phe Gly Ala Ser Asn Phe Pro Val Ala Phe Ser Thr Ala Gly
                                   150 155 160 165

ggc gat aca gca tca gcg ttg gct gca ggc tgc cct gtg gtt ttt aag 643
Gly Asp Thr Ala Ser Ala Leu Ala Ala Gly Cys Pro Val Val Phe Lys
                                   170 175 180

gcg cat aat gcg cac cct gga aca gct gag ctc gtc ggg caa gcg gtg 691
Ala His Asn Ala His Pro Gly Thr Ala Glu Leu Val Gly Gln Ala Val

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185					190					195					
cgg gga gcc gtc gaa aag cat gag ttt gat gct ggt gtg ttt aac ctt	739														
Arg Gly Ala Val Glu Lys His Glu Phe Asp Ala Gly Val Phe Asn Leu															
200	205					210									
gtc tac ggc cgt ggc gtg gaa att ggc cag gag ctg gct gcg gat ccg	787														
Val Tyr Gly Arg Gly Val Glu Ile Gly Gln Glu Leu Ala Ala Asp Pro															
215	220					225									
aat atc acg gca atc ggt ttt acc ggt tca cgc cag ggt ggt ttg gca	835														
Asn Ile Thr Ala Ile Gly Phe Thr Gly Ser Arg Gln Gly Gly Leu Ala															
230	235					240					245				
ctg tca cag act gcg ttt agc cgc cca gtt ccc gtt cca gtc ttt gca	883														
Leu Ser Gln Thr Ala Phe Ser Arg Pro Val Pro Val Pro Val Phe Ala															
250	255					260									
gaa atg agt gcc acc aac cct gtg ttc gtc ttc ccc ggc gcg ctg gcg	931														
Glu Met Ser Ala Thr Asn Pro Val Phe Val Phe Pro Gly Ala Leu Ala															
265	270					275									
gat ttg gat gca tcg agt tcc ttg gct gag gcg ttt acc gct tcc gtc	979														
Asp Leu Asp Ala Ser Ser Ser Leu Ala Glu Ala Phe Thr Ala Ser Val															
280	285					290									
acc ggc agt tcc ggg caa ttg tgc acc aag cct ggc ctc gtt ttc atc	1027														
Thr Gly Ser Ser Gly Gln Leu Cys Thr Lys Pro Gly Leu Val Phe Ile															
295	300					305									
ccg cgc ggt gtt gtt ggt gat gct ttt gtg gcg ctc gta gca gcc aaa	1075														
Pro Arg Gly Val Val Gly Asp Ala Phe Val Ala Leu Val Ala Ala Lys															
310	315					320					325				
ttt aaa gaa acc acg ggt caa acg atg ctc acg caa ggc atc gct cag	1123														
Phe Lys Glu Thr Thr Gly Gln Thr Met Leu Thr Gln Gly Ile Ala Gln															
330	335					340									
gca tgg cag cgc gga gtc gac aac ctt gca gca cag cca agt gta aaa	1171														
Ala Trp Gln Arg Gly Val Asp Asn Leu Ala Ala Gln Pro Ser Val Lys															
345	350					355									
atc ctc gcc caa ggc acc ccc gga gat gga gag aac gcg ccg ggc ccg	1219														
Ile Leu Ala Gln Gly Thr Pro Gly Asp Gly Glu Asn Ala Pro Gly Pro															
360	365					370									
gtg gtg ttt gaa agt gat gtg cag gcg ttg cta aat aat gtg gtg ttg	1267														
Val Val Phe Glu Ser Asp Val Gln Ala Leu Leu Asn Asn Val Val Leu															
375	380					385									
cag gaa gaa atc ttc ggt gcg gca tcg ctg gtg gtg cgt tat gat tcc	1315														
Gln Glu Glu Ile Phe Gly Ala Ala Ser Leu Val Val Arg Tyr Asp Ser															
390	395					400					405				
ccg gat caa ctc cac caa gta gcc aat tca ctc gag gga caa tta aca	1363														
Pro Asp Gln Leu His Gln Val Ala Asn Ser Leu Glu Gly Gln Leu Thr															
410	415					420									
gcc acg atc cac gca tcc cag gat gat ttc cag gaa gtc tcg aaa ctt	1411														
Ala Thr Ile His Ala Ser Gln Asp Phe Gln Glu Val Ser Lys Leu															
425	430					435									

atc ccc ctc ttg gag gat ctc gcg ggc cgt gtt ctt tac ggc ggc tgg 1459
 Ile Pro Leu Leu Glu Asp Leu Ala Gly Arg Val Leu Tyr Gly Gly Trp
 440 445 450

cca acg ggt gtg gaa gtt ggg cac acg gtt atc cat gga ggc cct tat 1507
 Pro Thr Gly Val Glu Val Gly His Thr Val Ile His Gly Gly Pro Tyr
 455 460 465

ccg gcg acc tca aat gcg cag tcg aca agt gtt gga acc ctg gca atc 1555
 Pro Ala Thr Ser Asn Ala Gln Ser Thr Ser Val Gly Thr Leu Ala Ile
 470 475 480 485

gag aga ttt atg cgc ccg gtt tct tat caa act ttc ccg gct gag ctg 1603
 Glu Arg Phe Met Arg Pro Val Ser Tyr Gln Thr Phe Pro Ala Glu Leu
 490 495 500

ctt cca gat cca gtt tct gag gcg aat aaa tgg gct gta cct cgg gaa 1651
 Leu Pro Asp Pro Val Ser Glu Ala Asn Lys Trp Ala Val Pro Arg Glu
 505 510 515

ata gac cgt taatagctgg tctttacatt tgc 1683
 Ile Asp Arg
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<210> 588

<211> 520

<212> PRT

<213> Corynebacterium glutamicum

<400> 588

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 20 25 30

Asn Ala Ser Leu Asn Pro Ser Tyr Ser Leu Ala Asn Ser Ala Gln Leu
 35 40 45

Arg Ala Ala Thr Thr Ser Ala Lys Arg Ala Phe Glu Ser Tyr Arg Leu
 50 55 60

Thr Thr Pro Glu Val Arg Ala Asp Phe Leu Asp Ser Ile Ala Asp Asn
 65 70 75 80

Ile Asp Ala Leu Ser Gly Glu Ile Val Gln Arg Ala Ser Leu Glu Thr
 85 90 95

Gly Leu Gly Thr Thr Arg Leu Thr Gly Glu Val Ala Arg Thr Ser Asn
 100 105 110

Gln Leu Arg Leu Phe Ala Glu Thr Val Arg Ser Gly Gln Phe His Arg
 115 120 125

Val Arg Ile Glu Arg Gly Pro Arg Ile Asp Leu Arg Gln Arg Gln Val
 130 135 140

Pro Leu Gly Pro Val Ala Val Phe Gly Ala Ser Asn Phe Pro Val Ala
 145 150 155 160

Phe Ser Thr Ala Gly Gly Asp Thr Ala Ser Ala Leu Ala Ala Gly Cys
 165 170 175
 Pro Val Val Phe Lys Ala His Asn Ala His Pro Gly Thr Ala Glu Leu
 180 185 190
 Val Gly Gln Ala Val Arg Gly Ala Val Glu Lys His Glu Phe Asp Ala
 195 200 205
 Gly Val Phe Asn Leu Val Tyr Gly Arg Gly Val Glu Ile Gly Gln Glu
 210 215 220
 Leu Ala Ala Asp Pro Asn Ile Thr Ala Ile Gly Phe Thr Gly Ser Arg
 225 230 235 240
 Gln Gly Gly Leu Ala Leu Ser Gln Thr Ala Phe Ser Arg Pro Val Pro
 245 250 255
 Val Pro Val Phe Ala Glu Met Ser Ala Thr Asn Pro Val Phe Val Phe
 260 265 270
 Pro Gly Ala Leu Ala Asp Leu Asp Ala Ser Ser Ser Leu Ala Glu Ala
 275 280 285
 Phe Thr Ala Ser Val Thr Gly Ser Ser Gly Gln Leu Cys Thr Lys Pro
 290 295 300
 Gly Leu Val Phe Ile Pro Arg Gly Val Val Gly Asp Ala Phe Val Ala
 305 310 315 320
 Leu Val Ala Ala Lys Phe Lys Glu Thr Thr Gly Gln Thr Met Leu Thr
 325 330 335
 Gln Gly Ile Ala Gln Ala Trp Gln Arg Gly Val Asp Asn Leu Ala Ala
 340 345 350
 Gln Pro Ser Val Lys Ile Leu Ala Gln Gly Thr Pro Gly Asp Gly Glu
 355 360 365
 Asn Ala Pro Gly Pro Val Val Phe Glu Ser Asp Val Gln Ala Leu Leu
 370 375 380
 Asn Asn Val Val Leu Gln Glu Glu Ile Phe Gly Ala Ala Ser Leu Val
 385 390 395 400
 Val Arg Tyr Asp Ser Pro Asp Gln Leu His Gln Val Ala Asn Ser Leu
 405 410 415
 Glu Gly Gln Leu Thr Ala Thr Ile His Ala Ser Gln Asp Asp Phe Gln
 420 425 430
 Glu Val Ser Lys Leu Ile Pro Leu Leu Glu Asp Leu Ala Gly Arg Val
 435 440 445
 Leu Tyr Gly Gly Trp Pro Thr Gly Val Glu Val Gly His Thr Val Ile
 450 455 460
 His Gly Gly Pro Tyr Pro Ala Thr Ser Asn Ala Gln Ser Thr Ser Val
 465 470 475 480

Gly	Thr	Leu	Ala	Ile	Glu	Arg	Phe	Met	Arg	Pro	Val	Ser	Tyr	Gln	Thr
				485					490					495	
Phe	Pro	Ala	Glu	Leu	Leu	Pro	Asp	Pro	Val	Ser	Glu	Ala	Asn	Lys	Trp
			500					505					510		
Ala	Val	Pro	Arg	Glu	Ile	Asp	Arg								
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<211> 1467
<212> DNA
<213> Corynebacterium glutamicum
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<222> (101)..(1444)
<223> RXN02399
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cat	tgc	gaa	tca	gca	ctt	aag	gaa	gtg	act	ttg	atg	tca	aac	gtt	gga	163
His	Cys	Glu	Ser	Ala	Leu	Lys	Glu	Val	Thr	Leu	Met	Ser	Asn	Val	Gly	
				10					15					20		
aag	cca	cgt	acc	gca	cag	gaa	atc	cag	cag	gat	tgg	gac	acc	aac	cct	211
Lys	Pro	Arg	Thr	Ala	Gln	Glu	Ile	Gln	Gln	Asp	Trp	Asp	Thr	Asn	Pro	
			25				30				35					
cgt	tgg	aac	ggc	atc	acc	cgc	gac	tac	acc	gca	gac	cag	gta	gct	gat	259
Arg	Trp	Asn	Gly	Ile	Thr	Arg	Asp	Tyr	Thr	Ala	Asp	Gln	Val	Ala	Asp	
		40					45					50				
ctg	cag	ggc	tcc	gtc	atc	gag	gag	cac	act	ctt	gct	cgc	cgc	ggc	tca	307
Leu	Gln	Gly	Ser	Val	Ile	Glu	Glu	His	Thr	Leu	Ala	Arg	Arg	Gly	Ser	
		55					60					65				
gag	atc	ctc	tgg	gac	gca	gtc	acc	cag	gaa	ggc	gac	gga	tac	atc	aac	355
Glu	Ile	Leu	Trp	Asp	Ala	Val	Thr	Gln	Glu	Gly	Asp	Gly	Tyr	Ile	Asn	
70					75					80					85	
gcg	ctt	ggc	gca	ctc	acc	ggc	aac	cag	gct	gtt	cag	cag	gtt	cgt	gca	403
Ala	Leu	Gly	Ala	Leu	Thr	Gly	Asn	Gln	Ala	Val	Gln	Gln	Val	Arg	Ala	
				90					95					100		
ggc	ctg	aag	gct	gtc	tac	ctg	tcc	ggc	tgg	cag	gtc	gca	ggc	gac	gcc	451
Gly	Leu	Lys	Ala	Val	Tyr	Leu	Ser	Gly	Trp	Gln	Val	Ala	Gly	Asp	Ala	
			105				110							115		
aac	ctc	tcc	ggc	cac	acc	tac	cct	gac	cag	tcc	ctc	tac	cca	gcg	aac	499
Asn	Leu	Ser	Gly	His	Thr	Tyr	Pro	Asp	Gln	Ser	Leu	Tyr	Pro	Ala	Asn	
			120				125							130		
tcc	gtt	cca	agc	gtc	gtt	cgt	cgc	atc	aac	aac	gca	ctg	ctg	cgt	tcc	547
Ser	Val	Pro	Ser	Val	Val	Arg	Arg	Ile	Asn	Asn	Ala	Leu	Leu	Arg	Ser	

135	140	145	
gat gaa atc gca cgc acc gaa ggc gac acc tcc gtt gac aac tgg gtt Asp Glu Ile Ala Arg Thr Glu Gly Asp Thr Ser Val Asp Asn Trp Val 150 155 160 165			595
gtc cca atc gtc gcg gac ggc gaa gct ggc ttc ggt gga gca ctc aac Val Pro Ile Val Ala Asp Gly Glu Ala Gly Phe Gly Gly Ala Leu Asn 170 175 180			643
gtc tac gaa ctc cag aag gca atg atc gca gct ggc gct gca ggc acc Val Tyr Glu Leu Gln Lys Ala Met Ile Ala Ala Gly Ala Ala Gly Thr 185 190 195			691
cac tgg gaa gac cag ctc gct tct gaa aag aag tgt ggc cac ctc ggc His Trp Glu Asp Gln Leu Ala Ser Glu Lys Lys Cys Gly His Leu Gly 200 205 210			739
ggc aag gtt ctg atc cca acc cag cag cac atc cgc acc ctg aac tct Gly Lys Val Leu Ile Pro Thr Gln Gln His Ile Arg Thr Leu Asn Ser 215 220 225			787
gcc cgc ctt gca gca gac gtt gca aac acc cca act gtt gtt atc gca Ala Arg Leu Ala Ala Asp Val Ala Asn Thr Pro Thr Val Val Ile Ala 230 235 240 245			835
cgt acc gac gct gag gca gca acc ctg atc acc tct gac gtt gat gag Arg Thr Asp Ala Glu Ala Ala Thr Leu Ile Thr Ser Asp Val Asp Glu 250 255 260			883
cgc gac caa cca ttc atc acc ggt gag cgc acc gca gaa ggc tac tac Arg Asp Gln Pro Phe Ile Thr Gly Glu Arg Thr Ala Glu Gly Tyr Tyr 265 270 275			931
cac gtc aag aat ggt ctc gag cca tgt atc gca cgt gca aag tcc tac His Val Lys Asn Gly Leu Glu Pro Cys Ile Ala Arg Ala Lys Ser Tyr 280 285 290			979
gca cca tac gca gat atg atc tgg atg gag acc ggc acc cct gac ctg Ala Pro Tyr Ala Asp Met Ile Trp Met Glu Thr Gly Thr Pro Asp Leu 295 300 305			1027
gag ctc gct aag aag ttc gct gaa ggc gtt cgc tct gag ttc cca gac Glu Leu Ala Lys Lys Phe Ala Glu Gly Val Arg Ser Glu Phe Pro Asp 310 315 320 325			1075
cag ctg ctg tcc tac aac tgc tcc cca tcc ttc aac tgg tct gca cac Gln Leu Leu Ser Tyr Asn Cys Ser Pro Ser Phe Asn Trp Ser Ala His 330 335 340			1123
ctc gag gca gat gag atc gct aag ttc cag aag gaa ctc ggc gca atg Leu Glu Ala Asp Glu Ile Ala Lys Phe Gln Lys Glu Leu Gly Ala Met 345 350 355			1171
ggc ttc aag ttc cag ttc atc acc ctc gca ggc ttc cac tcc ctc aac Gly Phe Lys Phe Gln Phe Ile Thr Leu Ala Gly Phe His Ser Leu Asn 360 365 370			1219
tac ggc atg ttc gac ctg gct tac gga tac gct cgc gaa ggc atg acc Tyr Gly Met Phe Asp Leu Ala Tyr Gly Tyr Ala Arg Glu Gly Met Thr 375 380 385			1267

tcc ttc gtt gac ctg cag aac cgt gag ttc aag gca gct gaa gag cgt 1315
 Ser Phe Val Asp Leu Gln Asn Arg Glu Phe Lys Ala Ala Glu Glu Arg
 390 395 400 405

ggc ttc acc gct gtt aag cac cag cgt gag gtt ggc gca ggc tac ttc 1363
 Gly Phe Thr Ala Val Lys His Gln Arg Glu Val Gly Ala Gly Tyr Phe
 410 415 420

gac cag atc gca acc acc gtt gac ccg aac tct tct acc acc gct ttg 1411
 Asp Gln Ile Ala Thr Thr Val Asp Pro Asn Ser Ser Thr Thr Ala Leu
 425 430 435

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aat 1467

<210> 590

<211> 448

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 590

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Trp Asp Thr Asn Pro Arg Trp Asn Gly Ile Thr Arg Asp Tyr Thr Ala
 35 40 45

Asp Gln Val Ala Asp Leu Gln Gly Ser Val Ile Glu Glu His Thr Leu
 50 55 60

Ala Arg Arg Gly Ser Glu Ile Leu Trp Asp Ala Val Thr Gln Glu Gly
 65 70 75 80

Asp Gly Tyr Ile Asn Ala Leu Gly Ala Leu Thr Gly Asn Gln Ala Val
 85 90 95

Gln Gln Val Arg Ala Gly Leu Lys Ala Val Tyr Leu Ser Gly Trp Gln
 100 105 110

Val Ala Gly Asp Ala Asn Leu Ser Gly His Thr Tyr Pro Asp Gln Ser
 115 120 125

Leu Tyr Pro Ala Asn Ser Val Pro Ser Val Val Arg Arg Ile Asn Asn
 130 135 140

Ala Leu Leu Arg Ser Asp Glu Ile Ala Arg Thr Glu Gly Asp Thr Ser
 145 150 155 160

Val Asp Asn Trp Val Val Pro Ile Val Ala Asp Gly Glu Ala Gly Phe
 165 170 175

Gly Gly Ala Leu Asn Val Tyr Glu Leu Gln Lys Ala Met Ile Ala Ala
 180 185 190

Gly Ala Ala Gly Thr His Trp Glu Asp Gln Leu Ala Ser Glu Lys Lys
 195 200 205
 Cys Gly His Leu Gly Gly Lys Val Leu Ile Pro Thr Gln Gln His Ile
 210 215 220
 Arg Thr Leu Asn Ser Ala Arg Leu Ala Ala Asp Val Ala Asn Thr Pro
 225 230 235 240
 Thr Val Val Ile Ala Arg Thr Asp Ala Glu Ala Ala Thr Leu Ile Thr
 245 250 255
 Ser Asp Val Asp Glu Arg Asp Gln Pro Phe Ile Thr Gly Glu Arg Thr
 260 265 270
 Ala Glu Gly Tyr Tyr His Val Lys Asn Gly Leu Glu Pro Cys Ile Ala
 275 280 285
 Arg Ala Lys Ser Tyr Ala Pro Tyr Ala Asp Met Ile Trp Met Glu Thr
 290 295 300
 Gly Thr Pro Asp Leu Glu Leu Ala Lys Lys Phe Ala Glu Gly Val Arg
 305 310 315 320
 Ser Glu Phe Pro Asp Gln Leu Leu Ser Tyr Asn Cys Ser Pro Ser Phe
 325 330 335
 Asn Trp Ser Ala His Leu Glu Ala Asp Glu Ile Ala Lys Phe Gln Lys
 340 345 350
 Glu Leu Gly Ala Met Gly Phe Lys Phe Gln Phe Ile Thr Leu Ala Gly
 355 360 365
 Phe His Ser Leu Asn Tyr Gly Met Phe Asp Leu Ala Tyr Gly Tyr Ala
 370 375 380
 Arg Glu Gly Met Thr Ser Phe Val Asp Leu Gln Asn Arg Glu Phe Lys
 385 390 395 400
 Ala Ala Glu Glu Arg Gly Phe Thr Ala Val Lys His Gln Arg Glu Val
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 Gly Ala Gly Tyr Phe Asp Gln Ile Ala Thr Thr Val Asp Pro Asn Ser
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 <211> 1419
 <212> DNA
 <213> *Corynebacterium glutamicum*

<220>
 <221> CDS
 <222> (101)..(1396)

<223> FRXA02399

<400> 591

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                                   Met Ser Asn Val Gly
                                   1 5

aag cca cgt acc gca cag gaa atc cag cag gat tgg gac acc aac cct 163
Lys Pro Arg Thr Ala Gln Glu Ile Gln Gln Asp Trp Asp Thr Asn Pro
                                   10 15 20

cgt tgg aac ggc atc acc cgc gac tac acc gca gac cag gta gct gat 211
Arg Trp Asn Gly Ile Thr Arg Asp Tyr Thr Ala Asp Gln Val Ala Asp
                                   25 30 35

ctg cag ggt tcc gtc atc gag gag cac act ctt gct cgc cgc ggc tca 259
Leu Gln Gly Ser Val Ile Glu Glu His Thr Leu Ala Arg Arg Gly Ser
                                   40 45 50

gag atc ctc tgg gac gca gtc acc cag gaa ggt gac gga tac atc aac 307
Glu Ile Leu Trp Asp Ala Val Thr Gln Glu Gly Asp Gly Tyr Ile Asn
                                   55 60 65

gcg ctt ggc gca ctc acc ggt aac cag gct gtt cag cag gtt cgt gca 355
Ala Leu Gly Ala Leu Thr Gly Asn Gln Ala Val Gln Gln Val Arg Ala
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ggc ctg aag gct gtc tac ctg tcc ggt tgg cag gtc gca ggt gac gcc 403
Gly Leu Lys Ala Val Tyr Leu Ser Gly Trp Gln Val Ala Gly Asp Ala
                                   90 95 100

aac ctc tcc ggc cac acc tac cct gac cag tcc ctc tac cca gcg aac 451
Asn Leu Ser Gly His Thr Tyr Pro Asp Gln Ser Leu Tyr Pro Ala Asn
                                   105 110 115

tcc gtt cca agc gtc gtt cgt cgc atc aac aac gca ctg ctg cgt tcc 499
Ser Val Pro Ser Val Val Arg Arg Ile Asn Asn Ala Leu Leu Arg Ser
                                   120 125 130

gat gaa atc gca cgc acc gaa ggc gac acc tcc gtt gac aac tgg gtt 547
Asp Glu Ile Ala Arg Thr Glu Gly Asp Thr Ser Val Asp Asn Trp Val
                                   135 140 145

gtc cca atc gtc gcg gac ggc gaa gct ggc ttc ggt gga gca ctc aac 595
Val Pro Ile Val Ala Asp Gly Glu Ala Gly Phe Gly Gly Ala Leu Asn
                                   150 155 160 165

gtc tac gaa ctc cag aag gca atg atc gca gct ggc gct gca ggc acc 643
Val Tyr Glu Leu Gln Lys Ala Met Ile Ala Ala Gly Ala Ala Gly Thr
                                   170 175 180

cac tgg gaa gac cag ctc gct tct gaa aag aag tgt ggc cac ctc ggc 691
His Trp Glu Asp Gln Leu Ala Ser Glu Lys Lys Cys Gly His Leu Gly
                                   185 190 195

ggc aag gtt ctg atc cca acc cag cag cac atc cgc acc ctg aac tct 739
Gly Lys Val Leu Ile Pro Thr Gln Gln His Ile Arg Thr Leu Asn Ser
                                   200 205 210

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gcc cgc ctt gca gca gac gtt gca aac acc cca act gtt gtt atc gca 787
Ala Arg Leu Ala Ala Asp Val Ala Asn Thr Pro Thr Val Val Ile Ala
215 220 225

cgt acc gac gct gag gca gca acc ctg atc acc tct gac gtt gat gag 835
Arg Thr Asp Ala Glu Ala Ala Thr Leu Ile Thr Ser Asp Val Asp Glu
230 235 240 245

cgc gac caa cca ttc atc acc ggt gag cgc acc gca gaa ggc tac tac 883
Arg Asp Gln Pro Phe Ile Thr Gly Glu Arg Thr Ala Glu Gly Tyr Tyr
250 255 260

cac gtc aag aat ggt ctc gag cca tgt atc gca cgt gca aag tcc tac 931
His Val Lys Asn Gly Leu Glu Pro Cys Ile Ala Arg Ala Lys Ser Tyr
265 270 275

gca cca tac gca gat atg atc tgg atg gag acc ggc acc cct gac ctg 979
Ala Pro Tyr Ala Asp Met Ile Trp Met Glu Thr Gly Thr Pro Asp Leu
280 285 290

gag ctc gct aag aag ttc gct gaa ggc gtt cgc tct gag ttc cca gac 1027
Glu Leu Ala Lys Lys Phe Ala Glu Gly Val Arg Ser Glu Phe Pro Asp
295 300 305

cag ctg ctg tcc tac aac tgc tcc cca tcc ttc aac tgg tct gca cac 1075
Gln Leu Leu Ser Tyr Asn Cys Ser Pro Ser Phe Asn Trp Ser Ala His
310 315 320 325

ctc gag gca gat gag atc gct aag ttc cag aag gaa ctc ggc gca atg 1123
Leu Glu Ala Asp Glu Ile Ala Lys Phe Gln Lys Glu Leu Gly Ala Met
330 335 340

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Gly Phe Lys Phe Gln Phe Ile Thr Leu Ala Gly Phe His Ser Leu Asn
345 350 355

tac ggc atg ttc gac ctg gct tac gga tac gct cgc gaa ggc atg acc 1219
Tyr Gly Met Phe Asp Leu Ala Tyr Gly Tyr Ala Arg Glu Gly Met Thr
360 365 370

tcc ttc gtt gac ctg cag aac cgt gag ttc aag gca gct gaa gag cgt 1267
Ser Phe Val Asp Leu Gln Asn Arg Glu Phe Lys Ala Ala Glu Glu Arg
375 380 385

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Gly Phe Thr Ala Val Lys His Gln Arg Glu Val Gly Ala Gly Tyr Phe
390 395 400 405

gac cag atc gca acc acc gtt gac ccg aac tct tct acc acc gct ttg 1363
Asp Gln Ile Ala Thr Thr Val Asp Pro Asn Ser Ser Thr Thr Ala Leu
410 415 420

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<213> *Corynebacterium glutamicum*

<400> 592

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Ala Arg Arg Gly Ser Glu Ile Leu Trp Asp Ala Val Thr Gln Glu Gly
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Asp Gly Tyr Ile Asn Ala Leu Gly Ala Leu Thr Gly Asn Gln Ala Val
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Gln Gln Val Arg Ala Gly Leu Lys Ala Val Tyr Leu Ser Gly Trp Gln
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Val Ala Gly Asp Ala Asn Leu Ser Gly His Thr Tyr Pro Asp Gln Ser
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Leu Tyr Pro Ala Asn Ser Val Pro Ser Val Val Arg Arg Ile Asn Asn
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Ala Leu Leu Arg Ser Asp Glu Ile Ala Arg Thr Glu Gly Asp Thr Ser
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Val Asp Asn Trp Val Val Pro Ile Val Ala Asp Gly Glu Ala Gly Phe
          145          150          155          160

Gly Gly Ala Leu Asn Val Tyr Glu Leu Gln Lys Ala Met Ile Ala Ala
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Gly Ala Ala Gly Thr His Trp Glu Asp Gln Leu Ala Ser Glu Lys Lys
          180          185          190

Cys Gly His Leu Gly Gly Lys Val Leu Ile Pro Thr Gln Gln His Ile
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Arg Thr Leu Asn Ser Ala Arg Leu Ala Ala Asp Val Ala Asn Thr Pro
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Thr Val Val Ile Ala Arg Thr Asp Ala Glu Ala Ala Thr Leu Ile Thr
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Ser Asp Val Asp Glu Arg Asp Gln Pro Phe Ile Thr Gly Glu Arg Thr
          245          250          255

Ala Glu Gly Tyr Tyr His Val Lys Asn Gly Leu Glu Pro Cys Ile Ala
          260          265          270

Arg Ala Lys Ser Tyr Ala Pro Tyr Ala Asp Met Ile Trp Met Glu Thr
          275          280          285

Gly Thr Pro Asp Leu Glu Leu Ala Lys Lys Phe Ala Glu Gly Val Arg
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Ser Glu Phe Pro Asp Gln Leu Leu Ser Tyr Asn Cys Ser Pro Ser Phe
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Asn Trp Ser Ala His Leu Glu Ala Asp Glu Ile Ala Lys Phe Gln Lys
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Glu Leu Gly Ala Met Gly Phe Lys Phe Gln Phe Ile Thr Leu Ala Gly
 340 345 350

Phe His Ser Leu Asn Tyr Gly Met Phe Asp Leu Ala Tyr Gly Tyr Ala
 355 360 365

Arg Glu Gly Met Thr Ser Phe Val Asp Leu Gln Asn Arg Glu Phe Lys
 370 375 380

Ala Ala Glu Glu Arg Gly Phe Thr Ala Val Lys His Gln Arg Glu Val
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 Met Thr Glu Gln Glu
 1 5

ctg ttg tct gct cag act gcc gac aac gct gga act gac agc acc gaa 163
 Leu Leu Ser Ala Gln Thr Ala Asp Asn Ala Gly Thr Asp Ser Thr Glu
 10 15 20

cgc gtt gac gcg ggc gga atg cag gtt gca aaa gtt ctc tac gac ttt 211
 Arg Val Asp Ala Gly Gly Met Gln Val Ala Lys Val Leu Tyr Asp Phe
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gta acc gaa gcg gta ctc cct cgc gtg ggt gtg gat gcg gaa aag ttc 259
 Val Thr Glu Ala Val Leu Pro Arg Val Gly Val Asp Ala Glu Lys Phe
 40 45 50

tgg tcc gga ttc gcc gcc atc gcc cgg gac ctc acc cca cgc aac cgc 307
 Trp Ser Gly Phe Ala Ala Ile Ala Arg Asp Leu Thr Pro Arg Asn Arg
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Glu Leu Leu Ala Arg Arg Asp Glu Leu Gln Met Leu Ile Asp Asp Tyr	
70 75 80 85	
cac cgc aac aac tcc ggc acc atc gac caa gag gcg tac gag gat ttc	403
His Arg Asn Asn Ser Gly Thr Ile Asp Gln Glu Ala Tyr Glu Asp Phe	
90 95 100	
ctc aaa gaa atc gga tac ttg gtt gag gag cca gaa gct gca gaa atc	451
Leu Lys Glu Ile Gly Tyr Leu Val Glu Glu Pro Glu Ala Ala Glu Ile	
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Arg Thr Gln Asn Val Asp Thr Glu Ile Ser Ser Thr Ala Gly Pro Gln	
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ctg gtt gtt cca att ctg aac gca cgc ttc gcg ctg aac gct gcc aat	547
Leu Val Val Pro Ile Leu Asn Ala Arg Phe Ala Leu Asn Ala Ala Asn	
135 140 145	
gct cgc tgg ggt tcc ctc tac gat gcg ttg tac ggc acc aac gcc atc	595
Ala Arg Trp Gly Ser Leu Tyr Asp Ala Leu Tyr Gly Thr Asn Ala Ile	
150 155 160 165	
cca gaa act gat ggc gct gaa aag ggc aag gag tac aac ccg gtc cgc	643
Pro Glu Thr Asp Gly Ala Glu Lys Gly Lys Glu Tyr Asn Pro Val Arg	
170 175 180	
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Gly Gln Lys Val Ile Glu Trp Gly Arg Glu Phe Leu Asp Ser Val Val	
185 190 195	
cca ctg gac ggt gct tcg cat gcc gat gtt gag aag tac aac atc acc	739
Pro Leu Asp Gly Ala Ser His Ala Asp Val Glu Lys Tyr Asn Ile Thr	
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gat gga aag ctt gca gcc cac att gga gat agc gtc tac cga ctg aaa	787
Asp Gly Lys Leu Ala Ala His Ile Gly Asp Ser Val Tyr Arg Leu Lys	
215 220 225	
aac cgt gaa tcc tac cgt ggc ttc acc ggc aac ttc ctt gat cca gaa	835
Asn Arg Glu Ser Tyr Arg Gly Phe Thr Gly Asn Phe Leu Asp Pro Glu	
230 235 240 245	
gca atc ctg ctg gaa acc aac ggc ctg cac atc gag ctg cag atc gat	883
Ala Ile Leu Leu Glu Thr Asn Gly Leu His Ile Glu Leu Gln Ile Asp	
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cct gtc cac cca atc ggc aag gca gac aag act ggt ctc aaa gac atc	931
Pro Val His Pro Ile Gly Lys Ala Asp Lys Thr Gly Leu Lys Asp Ile	
265 270 275	
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Val Leu Glu Ser Ala Ile Thr Thr Ile Met Asp Phe Glu Asp Ser Val	
280 285 290	
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Ala Ala Val Asp Ala Glu Asp Lys Thr Leu Gly Tyr Ser Asn Trp Phe	
295 300 305	
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Gly 310	Leu	Asn	Thr	Gly	Glu 315	Leu	Lys	Glu	Glu	Met 320	Ser	Lys	Asn	Gly	Arg 325	
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Ile	Phe	Thr	Arg	Glu	Leu	Asn	Lys	Asp	Arg	Val	Tyr	Ile	Gly	Arg	Asn	
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ggc	acc	gag	ctg	gtt	ctg	cac	ggc	cgt	tcc	ctg	ctg	ttc	gtc	cgc	aac	1171
Gly	Thr	Glu	Leu	Val	Leu	His	Gly	Arg	Ser	Leu	Leu	Phe	Val	Arg	Asn	
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gtt	ggc	cac	ctc	atg	caa	aac	cca	tcc	atc	ttg	att	gat	ggc	gag	gag	1219
Val	Gly	His	Leu	Met	Gln	Asn	Pro	Ser	Ile	Leu	Ile	Asp	Gly	Glu	Glu	
			360					365						370		
atc	ttc	gaa	ggc	atc	atg	gat	gct	gtc	ttg	acc	act	gtt	tgt	gcc	atc	1267
Ile	Phe	Glu	Gly	Ile	Met	Asp	Ala	Val	Leu	Thr	Thr	Val	Cys	Ala	Ile	
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cca	gga	att	gct	ccg	cag	aac	aag	atg	cgc	aat	tcc	cgc	aag	ggc	tcc	1315
Pro	Gly	Ile	Ala	Pro	Gln	Asn	Lys	Met	Arg	Asn	Ser	Arg	Lys	Gly	Ser	
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atc	tac	atc	gtg	aag	cct	aag	cag	cac	ggc	cct	gaa	gaa	gtc	gcg	ttc	1363
Ile	Tyr	Ile	Val	Lys	Pro	Lys	Gln	His	Gly	Pro	Glu	Glu	Val	Ala	Phe	
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acc	aac	gag	ctc	ttc	ggc	cgc	gtt	gag	gat	ctg	ctt	gat	ctg	cca	cgc	1411
Thr	Asn	Glu	Leu	Phe	Gly	Arg	Val	Glu	Asp	Leu	Leu	Asp	Leu	Pro	Arg	
				425				430						435		
cac	acc	ttg	aag	gtt	ggc	gtt	atg	gat	gag	gag	cgt	cgc	acg	tcc	gtg	1459
His	Thr	Leu	Lys	Val	Gly	Val	Met	Asp	Glu	Glu	Arg	Arg	Thr	Ser	Val	
				440				445						450		
aac	ctg	gat	gcc	agc	atc	atg	gaa	gtt	gct	gac	cgc	ttg	gca	ttc	atc	1507
Asn	Leu	Asp	Ala	Ser	Ile	Met	Glu	Val	Ala	Asp	Arg	Leu	Ala	Phe	Ile	
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aac	act	ggc	ttc	ctg	gac	cgc	acc	ggc	gat	gaa	atc	cac	acc	tcc	atg	1555
Asn	Thr	Gly	Phe	Leu	Asp	Arg	Thr	Gly	Asp	Glu	Ile	His	Thr	Ser	Met	
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gaa	gca	ggc	gcc	atg	gtg	cgc	aag	gct	gat	atg	cag	acc	gca	ccg	tgg	1603
Glu	Ala	Gly	Ala	Met	Val	Arg	Lys	Ala	Asp	Met	Gln	Thr	Ala	Pro	Trp	
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aag	cag	gcc	tac	gag	aac	aac	aac	gtt	gat	gca	ggc	att	cag	cgt	ggc	1651
Lys	Gln	Ala	Tyr	Glu	Asn	Asn	Asn	Val	Asp	Ala	Gly	Ile	Gln	Arg	Gly	
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ctt	cct	ggc	aag	gct	cag	atc	ggc	aag	ggc	atg	tgg	gcg	atg	act	gaa	1699
Leu	Pro	Gly	Lys	Ala	Gln	Ile	Gly	Lys	Gly	Met	Trp	Ala	Met	Thr	Glu	
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ctc	atg	gca	gaa	atg	ctg	gag	aag	aag	atc	ggc	cag	cca	cgc	gaa	ggc	1747
Leu	Met	Ala	Glu	Met	Leu	Glu	Lys	Lys	Ile	Gly	Gln	Pro	Arg	Glu	Gly	
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gcc	aac	act	gca	tgg	gtt	cct	tca	cca	act	ggc	gcg	acg	ctg	cac	gca	1795
Ala	Asn	Thr	Ala	Trp	Val	Pro	Ser	Pro	Thr	Gly	Ala	Thr	Leu	His	Ala	

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Thr His Tyr His Leu Val Asp Val Phe Lys Val Gln Asp Glu Leu Arg	570	575	580	
gct gcc ggc cgc cgc gac agc ctg cgc aac att ctc acc att tca acc				1891
Ala Ala Gly Arg Arg Asp Ser Leu Arg Asn Ile Leu Thr Ile Ser Thr	585	590	595	
gca cca aac acc aat tgg tct gag gaa gag aag aag gaa gag atg gac				1939
Ala Pro Asn Thr Asn Trp Ser Glu Glu Glu Lys Lys Glu Glu Met Asp	600	605	610	
aac aac tgc cag tcc atc ctc gga tac gtt gtg cgc tgg gtt gag cac				1987
Asn Asn Cys Gln Ser Ile Leu Gly Tyr Val Val Arg Trp Val Glu His	615	620	625	
ggt gtt ggt tgc tcc aag gtt cca gac atc cat gac atc gac ctc atg				2035
Gly Val Gly Cys Ser Lys Val Pro Asp Ile His Asp Ile Asp Leu Met	630	635	640	645
gaa gac cgc gca acg ctg cgt att tcc tcg cag atg ctg gcc aac tgg				2083
Glu Asp Arg Ala Thr Leu Arg Ile Ser Ser Gln Met Leu Ala Asn Trp	650	655	660	
atc cgc cat gat gtt gtc tcg aag gag cag gtc ttg gag tca ctg gaa				2131
Ile Arg His Asp Val Val Ser Lys Glu Gln Val Leu Glu Ser Leu Glu	665	670	675	
cga atg gca gtg gtc gtc gac aag caa aat gcg ggc gac gag gcc tac				2179
Arg Met Ala Val Val Val Asp Lys Gln Asn Ala Gly Asp Glu Ala Tyr	680	685	690	
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Arg Asp Met Ala Pro Lys Tyr Asp Ala Ser Leu Ala Phe Gln Ala Ala	695	700	705	
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Lys Asp Leu Ile Phe Glu Gly Thr Lys Ser Pro Ser Gly Tyr Thr Glu	710	715	720	725
ccc atc ttg cac gca cgc cgc cgc gag ttc aaa gca aaa aac				2317
Pro Ile Leu His Ala Arg Arg Arg Glu Phe Lys Ala Lys Asn	730	735		
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<211> 739

<212> PRT

<213> Corynebacterium glutamicum

<400> 594

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30

Val Leu Tyr Asp Phe Val Thr Glu Ala Val Leu Pro Arg Val Gly Val
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 Thr Pro Arg Asn Arg Glu Leu Leu Ala Arg Arg Asp Glu Leu Gln Met
 65 70 75 80
 Leu Ile Asp Asp Tyr His Arg Asn Asn Ser Gly Thr Ile Asp Gln Glu
 85 90 95
 Ala Tyr Glu Asp Phe Leu Lys Glu Ile Gly Tyr Leu Val Glu Glu Pro
 100 105 110
 Glu Ala Ala Glu Ile Arg Thr Gln Asn Val Asp Thr Glu Ile Ser Ser
 115 120 125
 Thr Ala Gly Pro Gln Leu Val Val Pro Ile Leu Asn Ala Arg Phe Ala
 130 135 140
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 145 150 155 160
 Gly Thr Asn Ala Ile Pro Glu Thr Asp Gly Ala Glu Lys Gly Lys Glu
 165 170 175
 Tyr Asn Pro Val Arg Gly Gln Lys Val Ile Glu Trp Gly Arg Glu Phe
 180 185 190
 Leu Asp Ser Val Val Pro Leu Asp Gly Ala Ser His Ala Asp Val Glu
 195 200 205
 Lys Tyr Asn Ile Thr Asp Gly Lys Leu Ala Ala His Ile Gly Asp Ser
 210 215 220
 Val Tyr Arg Leu Lys Asn Arg Glu Ser Tyr Arg Gly Phe Thr Gly Asn
 225 230 235 240
 Phe Leu Asp Pro Glu Ala Ile Leu Leu Glu Thr Asn Gly Leu His Ile
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 Glu Leu Gln Ile Asp Pro Val His Pro Ile Gly Lys Ala Asp Lys Thr
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 Gly Leu Lys Asp Ile Val Leu Glu Ser Ala Ile Thr Thr Ile Met Asp
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 Phe Glu Asp Ser Val Ala Ala Val Asp Ala Glu Asp Lys Thr Leu Gly
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 Tyr Ser Asn Trp Phe Gly Leu Asn Thr Gly Glu Leu Lys Glu Glu Met
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 Ser Lys Asn Gly Arg Ile Phe Thr Arg Glu Leu Asn Lys Asp Arg Val
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 Tyr Ile Gly Arg Asn Gly Thr Glu Leu Val Leu His Gly Arg Ser Leu
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 Leu Phe Val Arg Asn Val Gly His Leu Met Gln Asn Pro Ser Ile Leu

355	360	365
Ile Asp Gly Glu Glu Ile 370	Phe Glu Gly Ile Met 375	Asp Ala Val Leu Thr 380
Thr Val Cys Ala Ile Pro Gly Ile Ala Pro Gln Asn Lys Met Arg Asn 385	390	395 400
Ser Arg Lys Gly Ser Ile Tyr Ile Val Lys Pro Lys Gln His Gly Pro 405	410	415
Glu Glu Val Ala Phe Thr Asn Glu Leu Phe Gly Arg Val Glu Asp Leu 420	425	430
Leu Asp Leu Pro Arg His Thr Leu Lys Val Gly Val Met Asp Glu Glu 435	440	445
Arg Arg Thr Ser Val Asn Leu Asp Ala Ser Ile Met Glu Val Ala Asp 450	455	460
Arg Leu Ala Phe Ile Asn Thr Gly Phe Leu Asp Arg Thr Gly Asp Glu 465	470	475 480
Ile His Thr Ser Met Glu Ala Gly Ala Met Val Arg Lys Ala Asp Met 485	490	495
Gln Thr Ala Pro Trp Lys Gln Ala Tyr Glu Asn Asn Asn Val Asp Ala 500	505	510
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Trp Ala Met Thr Glu Leu Met Ala Glu Met Leu Glu Lys Lys Ile Gly 530	535	540
Gln Pro Arg Glu Gly Ala Asn Thr Ala Trp Val Pro Ser Pro Thr Gly 545	550	555 560
Ala Thr Leu His Ala Thr His Tyr His Leu Val Asp Val Phe Lys Val 565	570	575
Gln Asp Glu Leu Arg Ala Ala Gly Arg Arg Asp Ser Leu Arg Asn Ile 580	585	590
Leu Thr Ile Ser Thr Ala Pro Asn Thr Asn Trp Ser Glu Glu Glu Lys 595	600	605
Lys Glu Glu Met Asp Asn Asn Cys Gln Ser Ile Leu Gly Tyr Val Val 610	615	620
Arg Trp Val Glu His Gly Val Gly Cys Ser Lys Val Pro Asp Ile His 625	630	635 640
Asp Ile Asp Leu Met Glu Asp Arg Ala Thr Leu Arg Ile Ser Ser Gln 645	650	655
Met Leu Ala Asn Trp Ile Arg His Asp Val Val Ser Lys Glu Gln Val 660	665	670
Leu Glu S r Leu Glu Arg Met Ala Val Val Val Asp Lys Gln Asn Ala 675	680	685

Gly Asp Glu Ala Tyr Arg Asp Met Ala Pro Lys Tyr Asp Ala Ser Leu
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Ala Phe Gln Ala Ala Lys Asp Leu Ile Phe Glu Gly Thr Lys Ser Pro
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Ser Gly Tyr Thr Glu Pro Ile Leu His Ala Arg Arg Arg Glu Phe Lys
 725 730 735

Ala Lys Asn

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<211> 2159

<212> DNA

<213> Corynebacterium glutamicum

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<223> FRXA02404

<400> 595

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 Pro Arg Val Gly Val Asp Ala Glu Lys Phe Trp Ser Gly Phe Ala Ala
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 Ile Ala Arg Asp Leu Thr Pro Arg Asn Arg Glu Leu Ala Arg Arg
 35 40 45

gat gaa ctg cag atg ctt atc gac gac tac cac cgc aac aac tcc ggc 192
 Asp Glu Leu Gln Met Leu Ile Asp Asp Tyr His Arg Asn Asn Ser Gly
 50 55 60

acc atc gac caa gag gcg tac gag gat ttc ctc aaa gaa atc gga tac 240
 Thr Ile Asp Gln Glu Ala Tyr Glu Asp Phe Leu Lys Glu Ile Gly Tyr
 65 70 75 80

ttg gtt gag gag cca gaa gct gca gaa atc cgt acc caa aac gtc gat 288
 Leu Val Glu Glu Pro Glu Ala Ala Glu Ile Arg Thr Gln Asn Val Asp
 85 90 95

acg gaa atc tcc agc acc gca gga cct cag ctg gtt gtt cca att ctg 336
 Thr Glu Ile Ser Ser Thr Ala Gly Pro Gln Leu Val Val Pro Ile Leu
 100 105 110

aac gca cgc ttc gcg ctg aac gct gcc aat gct cgc tgg ggt tcc ctc 384
 Asn Ala Arg Phe Ala Leu Asn Ala Ala Asn Ala Arg Trp Gly Ser Leu
 115 120 125

tac gat gcg ttg tac ggc acc aac gcc atc cca gaa act gat ggc gct 432
 Tyr Asp Ala Leu Tyr Gly Thr Asn Ala Ile Pro Glu Thr Asp Gly Ala
 130 135 140

gaa aag ggc aag gag tac aac ccg gtc cgc ggc cag aag gtc atc gag	480
Glu Lys Gly Lys Glu Tyr Asn Pro Val Arg Gly Gln Lys Val Ile Glu	
145 150 155 160	
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Trp Gly Arg Glu Phe Leu Asp Ser Val Val Pro Leu Asp Gly Ala Ser	
165 170 175	
cat gcc gat gtt gag aag tac aac atc acc gat gga aag ctt gca gcc	576
His Ala Asp Val Glu Lys Tyr Asn Ile Thr Asp Gly Lys Leu Ala Ala	
180 185 190	
cac att gga gat agc gtc tac cga ctg aaa aac cgt gaa tcc tac cgt	624
His Ile Gly Asp Ser Val Tyr Arg Leu Lys Asn Arg Glu Ser Tyr Arg	
195 200 205	
ggc ttc acc ggc aac ttc ctt gat cca gaa gca atc ctg ctg gaa acc	672
Gly Phe Thr Gly Asn Phe Leu Asp Pro Glu Ala Ile Leu Leu Glu Thr	
210 215 220	
aac ggc ctg cac atc gag ctg cag atc gat cct gtc cac cca atc ggc	720
Asn Gly Leu His Ile Glu Leu Gln Ile Asp Pro Val His Pro Ile Gly	
225 230 235 240	
aag gca gac aag act ggt ctc aaa gac atc gtt ttg gaa tct gcg atc	768
Lys Ala Asp Lys Thr Gly Leu Lys Asp Ile Val Leu Glu Ser Ala Ile	
245 250 255	
acc acg atc atg gac ttc gaa gac tcc gtt gca gct gtt gat gct gaa	816
Thr Thr Ile Met Asp Phe Glu Asp Ser Val Ala Ala Val Asp Ala Glu	
260 265 270	
gac aag acc tta ggt tac tct aac tgg ttc gga ctc aac acc ggc gaa	864
Asp Lys Thr Leu Gly Tyr Ser Asn Trp Phe Gly Leu Asn Thr Gly Glu	
275 280 285	
ctg aaa gaa gag atg tcc aag aac gga cgc atc ttc acc cgt gag ctc	912
Leu Lys Glu Glu Met Ser Lys Asn Gly Arg Ile Phe Thr Arg Glu Leu	
290 295 300	
aac aag gac cgc gtc tac att ggc cgc aat ggt acc gag ctg gtt ctg	960
Asn Lys Asp Arg Val Tyr Ile Gly Arg Asn Gly Thr Glu Leu Val Leu	
305 310 315 320	
cac ggt cgt tcc ctg ctg ttc gtc cgc aac gtt ggt cac ctc atg caa	1008
His Gly Arg Ser Leu Leu Phe Val Arg Asn Val Gly His Leu Met Gln	
325 330 335	
aac cca tcc atc ttg att gat ggc gag gag atc ttc gaa ggc atc atg	1056
Asn Pro Ser Ile Leu Ile Asp Gly Glu Glu Ile Phe Glu Gly Ile Met	
340 345 350	
gat gct gtc ttg acc act gtt tgt gcc atc cca gga att gct ccg cag	1104
Asp Ala Val Leu Thr Thr Val Cys Ala Ile Pro Gly Ile Ala Pro Gln	
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aac aag atg cgc aat tcc cgc aag ggc tcc atc tac atc gtg aag cct	1152
Asn Lys Met Arg Asn Ser Arg Lys Gly Ser Ile Tyr Ile Val Lys Pro	
370 375 380	
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Lys	Gln	His	Gly	Pro	Glu	Glu	Val	Ala	Phe	Thr	Asn	Glu	Leu	Phe	Gly		
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cgc	gtt	gag	gat	ctg	ctt	gat	ctg	cca	cgc	cac	acc	ttg	aag	gtt	ggg	1248	
Arg	Val	Glu	Asp	Leu	Leu	Asp	Leu	Pro	Arg	His	Thr	Leu	Lys	Val	Gly		
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gtt	atg	gat	gag	gag	cgt	cgc	acg	tcc	gtg	aac	ctg	gat	gcc	agc	atc	1296	
Val	Met	Asp	Glu	Glu	Arg	Arg	Thr	Ser	Val	Asn	Leu	Asp	Ala	Ser	Ile		
			420					425					430				
atg	gaa	gtt	gct	gac	cgc	ttg	gca	ttc	atc	aac	act	ggc	ttc	ctg	gac	1344	
Met	Glu	Val	Ala	Asp	Arg	Leu	Ala	Phe	Ile	Asn	Thr	Gly	Phe	Leu	Asp		
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cgc	acc	ggc	gat	gaa	atc	cac	acc	tcc	atg	gaa	gca	ggc	gcc	atg	gtg	1392	
Arg	Thr	Gly	Asp	Glu	Ile	His	Thr	Ser	Met	Glu	Ala	Gly	Ala	Met	Val		
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cgc	aag	gct	gat	atg	cag	acc	gca	ccg	tgg	aag	cag	gcc	tac	gag	aac	1440	
Arg	Lys	Ala	Asp	Met	Gln	Thr	Ala	Pro	Trp	Lys	Gln	Ala	Tyr	Glu	Asn		
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Asn	Asn	Val	Asp	Ala	Gly	Ile	Gln	Arg	Gly	Leu	Pro	Gly	Lys	Ala	Gln		
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Ile	Gly	Lys	Gly	Met	Trp	Ala	Met	Thr	Glu	Leu	Met	Ala	Glu	Met	Leu		
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Glu	Lys	Lys	Ile	Gly	Gln	Pro	Arg	Glu	Gly	Ala	Asn	Thr	Ala	Trp	Val		
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cct	tca	cca	act	ggg	gcg	acg	ctg	cac	gca	acg	cac	tac	cac	ttg	gtt	1632	
Pro	Ser	Pro	Thr	Gly	Ala	Thr	Leu	His	Ala	Thr	His	Tyr	His	Leu	Val		
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gat	gtg	ttc	aag	gtt	caa	gac	gaa	ctg	cgt	gct	gcc	ggc	cgc	cgc	gac	1680	
Asp	Val	Phe	Lys	Val	Gln	Asp	Glu	Leu	Arg	Ala	Ala	Gly	Arg	Arg	Asp		
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Ser	Leu	Arg	Asn	Ile	Leu	Thr	Ile	Ser	Thr	Ala	Pro	Asn	Thr	Asn	Trp		
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Ser	Glu	Glu	Glu	Lys	Lys	Glu	Glu	Met	Asp	Asn	Asn	Cys	Gln	Ser	Ile		
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Leu	Gly	Tyr	Val	Val	Arg	Trp	Val	Glu	His	Gly	Val	Gly	Cys	Ser	Lys		
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gtt	cca	gac	atc	cat	gac	atc	gac	ctc	atg	gaa	gac	cgc	gca	acg	ctg	1872	
Val	Pro	Asp	Ile	His	Asp	Ile	Asp	Leu	Met	Glu	Asp	Arg	Ala	Thr	Leu		
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cgt	att	tcc	tgc	cag	atg	ctg	gcc	aac	tgg	atc	cgc	cat	gat	gtt	gtc	1920	
Arg	Ile	Ser	Ser	Gln	Met	Leu	Ala	Asn	Trp	Ile	Arg	His	Asp	Val	Val		

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tcg aag gag cag gtc ttg gag tca ctg gaa cga atg gca gtg gtc gtc				1968
Ser Lys Glu Gln Val Leu Glu Ser Leu Glu Arg Met Ala Val Val Val				
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gac aag caa aat gcg ggc gac gag gcc tac cgc gat atg gcg ccg aag				2016
Asp Lys Gln Asn Ala Gly Asp Glu Ala Tyr Arg Asp Met Ala Pro Lys				
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tac gac gcc tcc ctc gcc ttc cag gcg gct aag gac ttg att ttc gaa				2064
Tyr Asp Ala Ser Leu Ala Phe Gln Ala Ala Lys Asp Leu Ile Phe Glu				
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ggc acc aag tcc cca tcg ggc tac acc gag ccc atc ttg cac gca cgc				2112
Gly Thr Lys Ser Pro Ser Gly Tyr Thr Glu Pro Ile Leu His Ala Arg				
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<213> Corynebacterium glutamicum

<400> 596

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Ile Ala Arg Asp Leu Thr Pro Arg Asn Arg Glu Leu Leu Ala Arg Arg				
	35	40	45	
Asp Glu Leu Gln Met Leu Ile Asp Asp Tyr His Arg Asn Asn Ser Gly				
	50	55	60	
Thr Ile Asp Gln Glu Ala Tyr Glu Asp Phe Leu Lys Glu Ile Gly Tyr				
	65	70	75	80
Leu Val Glu Glu Pro Glu Ala Ala Glu Ile Arg Thr Gln Asn Val Asp				
	85	90	95	
Thr Glu Ile Ser Ser Thr Ala Gly Pro Gln Leu Val Val Pro Ile Leu				
	100	105	110	
Asn Ala Arg Phe Ala Leu Asn Ala Ala Asn Ala Arg Trp Gly Ser Leu				
	115	120	125	
Tyr Asp Ala Leu Tyr Gly Thr Asn Ala Ile Pro Glu Thr Asp Gly Ala				
	130	135	140	
Glu Lys Gly Lys Glu Tyr Asn Pro Val Arg Gly Gln Lys Val Ile Glu				
	145	150	155	160
Trp Gly Arg Glu Phe Leu Asp Ser Val Val Pro Leu Asp Gly Ala Ser				
	165	170	175	

His Ala Asp Val Glu Lys Tyr Asn Ile Thr Asp Gly Lys Leu Ala Ala
 180 185 190
 His Ile Gly Asp Ser Val Tyr Arg Leu Lys Asn Arg Glu Ser Tyr Arg
 195 200 205
 Gly Phe Thr Gly Asn Phe Leu Asp Pro Glu Ala Ile Leu Leu Glu Thr
 210 215 220
 Asn Gly Leu His Ile Glu Leu Gln Ile Asp Pro Val His Pro Ile Gly
 225 230 235 240
 Lys Ala Asp Lys Thr Gly Leu Lys Asp Ile Val Leu Glu Ser Ala Ile
 245 250 255
 Thr Thr Ile Met Asp Phe Glu Asp Ser Val Ala Ala Val Asp Ala Glu
 260 265 270
 Asp Lys Thr Leu Gly Tyr Ser Asn Trp Phe Gly Leu Asn Thr Gly Glu
 275 280 285
 Leu Lys Glu Glu Met Ser Lys Asn Gly Arg Ile Phe Thr Arg Glu Leu
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 Asn Lys Asp Arg Val Tyr Ile Gly Arg Asn Gly Thr Glu Leu Val Leu
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 His Gly Arg Ser Leu Leu Phe Val Arg Asn Val Gly His Leu Met Gln
 325 330 335
 Asn Pro Ser Ile Leu Ile Asp Gly Glu Glu Ile Phe Glu Gly Ile Met
 340 345 350
 Asp Ala Val Leu Thr Thr Val Cys Ala Ile Pro Gly Ile Ala Pro Gln
 355 360 365
 Asn Lys Met Arg Asn Ser Arg Lys Gly Ser Ile Tyr Ile Val Lys Pro
 370 375 380
 Lys Gln His Gly Pro Glu Glu Val Ala Phe Thr Asn Glu Leu Phe Gly
 385 390 395 400
 Arg Val Glu Asp Leu Leu Asp Leu Pro Arg His Thr Leu Lys Val Gly
 405 410 415
 Val Met Asp Glu Glu Arg Arg Thr Ser Val Asn Leu Asp Ala Ser Ile
 420 425 430
 Met Glu Val Ala Asp Arg Leu Ala Phe Ile Asn Thr Gly Phe Leu Asp
 435 440 445
 Arg Thr Gly Asp Glu Ile His Thr Ser Met Glu Ala Gly Ala Met Val
 450 455 460
 Arg Lys Ala Asp Met Gln Thr Ala Pro Trp Lys Gln Ala Tyr Glu Asn
 465 470 475 480
 Asn Asn Val Asp Ala Gly Ile Gln Arg Gly Leu Pro Gly Lys Ala Gln
 485 490 495

Ile Gly Lys Gly Met Trp Ala Met Thr Glu Leu Met Ala Glu Met Leu
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 Glu Lys Lys Ile Gly Gln Pro Arg Glu Gly Ala Asn Thr Ala Trp Val
 515 520 525
 Pro Ser Pro Thr Gly Ala Thr Leu His Ala Thr His Tyr His Leu Val
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 Asp Val Phe Lys Val Gln Asp Glu Leu Arg Ala Ala Gly Arg Arg Asp
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 Ser Leu Arg Asn Ile Leu Thr Ile Ser Thr Ala Pro Asn Thr Asn Trp
 565 570 575
 Ser Glu Glu Glu Lys Lys Glu Glu Met Asp Asn Asn Cys Gln Ser Ile
 580 585 590
 Leu Gly Tyr Val Val Arg Trp Val Glu His Gly Val Gly Cys Ser Lys
 595 600 605
 Val Pro Asp Ile His Asp Ile Asp Leu Met Glu Asp Arg Ala Thr Leu
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 Arg Ile Ser Ser Gln Met Leu Ala Asn Trp Ile Arg His Asp Val Val
 625 630 635 640
 Ser Lys Glu Gln Val Leu Glu Ser Leu Glu Arg Met Ala Val Val Val
 645 650 655
 Asp Lys Gln Asn Ala Gly Asp Glu Ala Tyr Arg Asp Met Ala Pro Lys
 660 665 670
 Tyr Asp Ala Ser Leu Ala Phe Gln Ala Ala Lys Asp Leu Ile Phe Glu
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 Leu Ser Arg Phe Ala
 1 5
 gcc aac ctg tca ttg act ttt act gag cta gat ttc ctg gat cgt ttt 163

Ala	Asn	Leu	Ser	Leu	Thr	Phe	Thr	Glu	Leu	Asp	Phe	Leu	Asp	Arg	Phe		
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gat	gcc	gct	tcg	aag	cat	gct	ttc	agt	gcc	gtg	gag	ttt	cag	tac	cct	211	
Asp	Ala	Ala	Ser	Lys	His	Ala	Phe	Ser	Ala	Val	Glu	Phe	Gln	Tyr	Pro		
			25					30					35				
tac	gat	ttc	gat	gtt	caa	gag	att	aaa	cag	cgt	gct	gat	tcc	gca	ggc	259	
Tyr	Asp	Phe	Asp	Val	Gln	Glu	Ile	Lys	Gln	Arg	Ala	Asp	Ser	Ala	Gly		
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ctg	ccc	att	gaa	ctg	ttc	aat	gcc	cca	cct	ggg	gat	act	ttt	ggc	ctt	307	
Leu	Pro	Ile	Glu	Leu	Phe	Asn	Ala	Pro	Pro	Gly	Asp	Thr	Phe	Gly	Leu		
	55					60					65						
gcg	gca	ctg	gct	tcc	cct	gaa	gac	ttt	caa	caa	tcc	atc	gag	cag	gcc	355	
Ala	Ala	Leu	Ala	Ser	Pro	Glu	Asp	Phe	Gln	Gln	Ser	Ile	Glu	Gln	Ala		
	70				75				80						85		
atc	acg	tac	gcc	aca	gtg	ttg	aag	cca	aag	aag	atg	cat	gtc	atg	gct	403	
Ile	Thr	Tyr	Ala	Thr	Val	Leu	Lys	Pro	Lys	Lys	Met	His	Val	Met	Ala		
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ggc	atc	gcg	gac	gta	acc	tca	gaa	acc	acg	gcg	cgc	tat	gtg	gag	aat	451	
Gly	Ile	Ala	Asp	Val	Thr	Ser	Glu	Thr	Thr	Ala	Arg	Tyr	Val	Glu	Asn		
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Ile	Arg	Trp	Ala	Ala	Gln	Gln	Leu	Asp	Lys	Leu	Asp	Val	Val	Val	Val		
		120					125					130					
att	gaa	cca	att	aat	cac	tat	tcg	gtt	ccc	ggc	tat	ttc	ctg	cac	act	547	
Ile	Glu	Pro	Ile	Asn	His	Tyr	Ser	Val	Pro	Gly	Tyr	Phe	Leu	His	Thr		
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tta	gag	cag	gcg	tat	tgg	ctt	atc	gac	agc	att	gcc	cac	ccc	aat	gtg	595	
Leu	Glu	Gln	Ala	Tyr	Trp	Leu	Ile	Asp	Ser	Ile	Ala	His	Pro	Asn	Val		
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Lys	Ile	Leu	Phe	Asp	Thr	Phe	His	Leu	Gln	Gln	Ile	His	Gly	Asn	Leu		
				170					175					180			
acc	cgc	cgc	ctg	cgc	gag	gtt	cat	ggc	gca	ggc	ctt	ttg	gga	cac	gtg	691	
Thr	Arg	Arg	Leu	Arg	Glu	Val	His	Gly	Ala	Gly	Leu	Leu	Gly	His	Val		
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caa	gtg	gcc	tca	gtt	cct	gat	cga	cac	gaa	cct	ggc	act	ggc	gaa	gtc	739	
Gln	Val	Ala	Ser	Val	Pro	Asp	Arg	His	Glu	Pro	Gly	Thr	Gly	Glu	Val		
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aat	gcg	gcg	tat	atc	ttc	caa	ctc	cta	agc	gaa	ctg	gga	tat	gac	ggc	787	
Asn	Ala	Ala	Tyr	Ile	Phe	Gln	Leu	Leu	Ser	Glu	Leu	Gly	Tyr	Asp	Gly		
	215					220					225						
gtc	atc	gct	ggc	gaa	tac	cac	cct	gct	ggc	gaa	act	aca	gcc	ggc	ttg	835	
Val	Ile	Ala	Gly	Glu	Tyr	His	Pro	Ala	Gly	Glu	Thr	Thr	Ala	Gly	Leu		
	230				235				240						245		
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<213> *Corynebacterium glutamicum*

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 35 40 45
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 50 55 60
 Asp Thr Phe Gly Leu Ala Ala Leu Ala Ser Pro Glu Asp Phe Gln Gln
 65 70 75 80
 Ser Ile Glu Gln Ala Ile Thr Tyr Ala Thr Val Leu Lys Pro Lys Lys
 85 90 95
 Met His Val Met Ala Gly Ile Ala Asp Val Thr Ser Glu Thr Thr Ala
 100 105 110
 Arg Tyr Val Glu Asn Ile Arg Trp Ala Ala Gln Gln Leu Asp Lys Leu
 115 120 125
 Asp Val Val Val Val Ile Glu Pro Ile Asn His Tyr Ser Val Pro Gly
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 Tyr Phe Leu His Thr Leu Glu Gln Ala Tyr Trp Leu Ile Asp Ser Ile
 145 150 155 160
 Ala His Pro Asn Val Lys Ile Leu Phe Asp Thr Phe His Leu Gln Gln
 165 170 175
 Ile His Gly Asn Leu Thr Arg Arg Leu Arg Glu Val His Gly Ala Gly
 180 185 190
 Leu Leu Gly His Val Gln Val Ala Ser Val Pro Asp Arg His Glu Pro
 195 200 205
 Gly Thr Gly Glu Val Asn Ala Ala Tyr Ile Phe Gln Leu Leu Ser Glu
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<223> RXA01886

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               Met Thr Phe Lys Leu
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Ala Ala Cys Ala Glu Met Ile Tyr Gln Asp Leu Pro Phe Glu Glu Arg
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Val Lys Thr Ile Ser Asp Gln Gly Phe Leu Val Glu Ile Trp Asp Trp
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tcc aca aaa gac atc gat gcg ctc gtg gca aca ggc gcg gaa ttt tcc 259
Ser Thr Lys Asp Ile Asp Ala Leu Val Ala Thr Gly Ala Glu Phe Ser
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tcc atg acg ggc tac ctg cgc ggg gat ctg att act gaa cag ggc cgc 307
Ser Met Thr Gly Tyr Leu Arg Gly Asp Leu Ile Thr Glu Gln Gly Arg
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gcg gag ctc ttg gca acc gct tcg gag tcc ttg gcg gtg gcg gaa aag 355
Ala Glu Leu Leu Ala Thr Ala Ser Glu Ser Leu Ala Val Ala Glu Lys
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ctc aac tgc ccc cgg ctg aat ctg cat gga act ggc ctt gga ccg cag 403
Leu Asn Cys Pro Arg Leu Asn Leu His Gly Thr Gly Leu Gly Pro Gln
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gga cta cct gtt act ccc att gaa gtg gtt acc cca gaa atg tgg ctc 451
Gly Leu Pro Val Thr Pro Ile Glu Val Val Thr Pro Glu Met Trp Leu
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tac gct gct gaa acg ctc cgc cag atc gct gag ctg ggg gag cgc gca 499
Tyr Ala Ala Glu Thr Leu Arg Gln Ile Ala Glu Leu Gly Glu Arg Ala
               120 125 130

ggc aag gtt ttc gtg ctg gaa aac ctc aac ctc gca gtc gat cac ccc 547
Gly Lys Val Phe Val Leu Glu Asn Leu Asn Leu Ala Val Asp His Pro
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Gly Thr Pro Phe Ala Lys Ala Thr Asp Thr Leu Ala Leu Val Lys Ala
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Val Asn His Pro Asn Leu Arg Leu Asn Leu Asp Leu Tyr His Ala Gln
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att ggc gaa gga aac ctc att gag ctg ctc cgt gag gcg cag cca ttc 691
Ile Gly Glu Gly Asn Leu Ile Glu Leu Leu Arg Glu Ala Gln Pro Phe
               185 190 195

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 acc ggc gag atc aac tac cag ggc gtc gcg aaa gct ctc gcc gcg atg 787
 Thr Gly Glu Ile Asn Tyr Gln Gly Val Ala Lys Ala Leu Ala Ala Met
 215 220 225
 ggc tac gac ggc gtc atc ggc atg gag gcg tgg gca tcg ggc gac tcc 835
 Gly Tyr Asp Gly Val Ile Gly Met Glu Ala Trp Ala Ser Gly Asp Ser
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 agc gac gcg ctg cag gcg ttg aag tca gcg ttc acg gtc taaattgctt 884
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 Gly Ala Glu Phe Ser Ser Met Thr Gly Tyr Leu Arg Gly Asp Leu Ile
 50 55 60
 Thr Glu Gln Gly Arg Ala Glu Leu Leu Ala Thr Ala Ser Glu Ser Leu
 65 70 75 80
 Ala Val Ala Glu Lys Leu Asn Cys Pro Arg Leu Asn Leu His Gly Thr
 85 90 95
 Gly Leu Gly Pro Gln Gly Leu Pro Val Thr Pro Ile Glu Val Val Thr
 100 105 110
 Pro Glu Met Trp Leu Tyr Ala Ala Glu Thr Leu Arg Gln Ile Ala Glu
 115 120 125
 Leu Gly Glu Arg Ala Gly Lys Val Phe Val Leu Glu Asn Leu Asn Leu
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 Ala Val Asp His Pro Gly Thr Pro Phe Ala Lys Ala Thr Asp Thr Leu
 145 150 155 160
 Ala Leu Val Lys Ala Val Asn His Pro Asn Leu Arg Leu Asn Leu Asp
 165 170 175
 Leu Tyr His Ala Gln Ile Gly Glu Gly Asn Leu Ile Glu Leu Leu Arg
 180 185 190

Glu Ala Gln Pro Phe Ile Gly Glu Ile Gln Val Ala Asp Val Pro Gly
 195 200 205

Arg Met Glu Pro Gly Thr Gly Glu Ile Asn Tyr Gln Gly Val Ala Lys
 210 215 220

Ala Leu Ala Ala Met Gly Tyr Asp Gly Val Ile Gly Met Glu Ala Trp
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Thr Val

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 <223> RXN03117

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 Val Arg Thr His Arg Ser Ala Glu Glu Phe Pro Tyr Lys Lys His Leu
 10 15 20

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 Ala His Lys Met Ala Arg Val Ala Ala Asp Pro Val Glu Val Ala Ala
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gac act cag gaa atg atc atc acc cgc atc atc gac aat gca tcg gtg 199
 Asp Thr Gln Glu Met Ile Ile Thr Arg Ile Ile Asp Asn Ala Ser Val
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cag gca gct tcc gtg ttg cgt cga cca gtt agc tct gcc cgt gcg atg 247
 Gln Ala Ala Ser Val Leu Arg Arg Pro Val Ser Ser Ala Arg Ala Met
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gca cag gtc agg cca gtt acc gat ggt cgg ggt gca tct gtt ttc ggt 295
 Ala Gln Val Arg Pro Val Thr Asp Gly Arg Gly Ala Ser Val Phe Gly
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ctg cca gga cgt tat gcc gcg gaa tgg gct gcg ctt gct aac ggc act 343
 Leu Pro Gly Arg Tyr Ala Ala Glu Trp Ala Ala Leu Ala Asn Gly Thr
 90 95 100

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 Ala Val Arg Glu Leu Asp Phe His Asp Thr Phe Leu Ala Ala Glu Tyr
 105 110 115

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Ser His Pro Gly Asp Asn Ile Pro Pro Ile Leu Ala Ala Ala Gln Gln	
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gct gga aaa ggt ggc aag gat ctg atc cgt ggc atc gct act ggg tat	487
Ala Gly Lys Gly Gly Lys Asp Leu Ile Arg Gly Ile Ala Thr Gly Tyr	
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gag att cag gtt aac ttg gtg cgt gga atg tgc ctg cat gag cac aag	535
Glu Ile Gln Val Asn Leu Val Arg Gly Met Cys Leu His Glu His Lys	
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Ile Asp His Val Ala His Leu Gly Pro Ser Ala Ala Ala Gly Ile Gly	
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Thr Leu Leu Asp Leu Asp Val Asp Thr Ile Tyr Gln Ala Ile Gly Gln	
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Ala Leu His Thr Thr Thr Ala Thr Arg Gln Ser Arg Lys Gly Ala Ile	
200 205 210	
tct tca tgg aag gca ttt gct cct gcg ttt gcg ggc aag atg tcc atc	727
Ser Ser Trp Lys Ala Phe Ala Pro Ala Phe Ala Gly Lys Met Ser Ile	
215 220 225	
gag gca gta gat cgc gca atg cgt ggc gag ggc gca ccg tca cca atc	775
Glu Ala Val Asp Arg Ala Met Arg Gly Glu Gly Ala Pro Ser Pro Ile	
230 235 240 245	
tgg gaa ggc gaa gac ggc gta atc gcg tgg ctg ctg tcc ggt ctt gat	823
Trp Glu Gly Glu Asp Gly Val Ile Ala Trp Leu Leu Ser Gly Leu Asp	
250 255 260	
cac atc tac acc att cct ttg cct gca gaa ggt gaa gcc aaa cga gca	871
His Ile Tyr Thr Ile Pro Leu Pro Ala Glu Gly Glu Ala Lys Arg Ala	
265 270 275	
atc ttg gat acc tac acc aag gaa cac tcg gcg gaa tac cag tca cag	919
Ile Leu Asp Thr Tyr Thr Lys Glu His Ser Ala Glu Tyr Gln Ser Gln	
280 285 290	
gca ccg atc gac ttg gcg cgc agc atg ggg gag aag ctg gca gca cag	967
Ala Pro Ile Asp Leu Ala Arg Ser Met Gly Glu Lys Leu Ala Ala Gln	
295 300 305	
ggc ttg gac ctg cgt gat gtg gac tcc atc gtt ttg cac acc tcc cac	1015
Gly Leu Asp Leu Arg Asp Val Asp Ser Ile Val Leu His Thr Ser His	
310 315 320 325	
cac act cac tac gtg atc ggc acc gga tct aat gat cca cag aag ttc	1063
His Thr His Tyr Val Ile Gly Thr Gly Ser Asn Asp Pro Gln Lys Phe	
330 335 340	
gat cca gat gca tcg cga gaa acc ctt gat cac tcc atc atg tac att	1111
Asp Pro Asp Ala Ser Arg Glu Thr Leu Asp His Ser Ile Met Tyr Ile	
345 350 355	
ttc gct gtc gcg ctg aag gat cgc gcg tgg cac cac gag cgt tcc tat	1159
Phe Ala Val Ala Leu Lys Asp Arg Ala Trp His His Glu Arg Ser Tyr	

360	365	370	
gct cct gag cga gcc cac cgc cga gag acc atc gag ctg tgg aac aag			1207
Ala Pro Glu Arg Ala His Arg Arg Glu Thr Ile Glu Leu Trp Asn Lys			
375	380	385	
att tcc acg gtg gag gat cct gaa tgg acc agg cgt tac cac tcc gtt			1255
Ile Ser Thr Val Glu Asp Pro Glu Trp Thr Arg Arg Tyr His Ser Val			
390	395	400	405
gat cct gca gaa aag gcc ttc ggc gca cgc gca gtg atc acc ttc aag			1303
Asp Pro Ala Glu Lys Ala Phe Gly Ala Arg Ala Val Ile Thr Phe Lys			
	410	415	420
gat gga acc gtc gtg gaa gat gaa ctg gct gtg gcg aat gcg cat cct			1351
Asp Gly Thr Val Val Glu Asp Glu Leu Ala Val Ala Asn Ala His Pro			
	425	430	435
ctg gga gca cgg cct ttc gct agg gag cag tac att cag aaa ttc cgc			1399
Leu Gly Ala Arg Pro Phe Ala Arg Glu Gln Tyr Ile Gln Lys Phe Arg			
	440	445	450
acc ttg gct gaa ggt gtt gtg tcc gaa aag gaa cag gat cgc ttc ttg			1447
Thr Leu Ala Glu Gly Val Val Ser Glu Lys Glu Gln Asp Arg Phe Leu			
	455	460	465
gat gcg gca cag cgt acg cac gag ctt gag gat ctt tca gaa ctc aac			1495
Asp Ala Ala Gln Arg Thr His Glu Leu Glu Asp Leu Ser Glu Leu Asn			
	470	475	480
att gaa ttg gat gcc gat att ttg gcc aag gct cct gtg att ccg gaa			1543
Ile Glu Leu Asp Ala Asp Ile Leu Ala Lys Ala Pro Val Ile Pro Glu			
	490	495	500
gga ctg ttc tgatggcgagg tttgttttcc tct			1575
Gly Leu Phe			

<210> 602

<211> 504

<212> PRT

<213> Corynebacterium glutamicum

<400> 602

Met	Ile	Thr	His	Glu	Val	Arg	Thr	His	Arg	Ser	Ala	Glu	Glu	Phe	Pro
1				5					10					15	

Tyr	Lys	Lys	His	Leu	Ala	His	Lys	Met	Ala	Arg	Val	Ala	Ala	Asp	Pro
			20					25					30		

Val	Glu	Val	Ala	Ala	Asp	Thr	Gln	Glu	Met	Ile	Ile	Thr	Arg	Ile	Ile
		35					40					45			

Asp	Asn	Ala	Ser	Val	Gln	Ala	Ala	Ser	Val	Leu	Arg	Arg	Pro	Val	Ser
	50					55					60				

Ser	Ala	Arg	Ala	Met	Ala	Gln	Val	Arg	Pro	Val	Thr	Asp	Gly	Arg	Gly
	65				70					75				80	

Ala	Ser	Val	Phe	Gly	Leu	Pro	Gly	Arg	Tyr	Ala	Ala	Glu	Trp	Ala	Ala
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

85								90				95			
Leu	Ala	Asn	Gly	Thr	Ala	Val	Arg	Glu	Leu	Asp	Phe	His	Asp	Thr	Phe
			100					105					110		
Leu	Ala	Ala	Glu	Tyr	Ser	His	Pro	Gly	Asp	Asn	Ile	Pro	Pro	Ile	Leu
		115					120					125			
Ala	Ala	Ala	Gln	Gln	Ala	Gly	Lys	Gly	Gly	Lys	Asp	Leu	Ile	Arg	Gly
		130				135					140				
Ile	Ala	Thr	Gly	Tyr	Glu	Ile	Gln	Val	Asn	Leu	Val	Arg	Gly	Met	Cys
145					150					155					160
Leu	His	Glu	His	Lys	Ile	Asp	His	Val	Ala	His	Leu	Gly	Pro	Ser	Ala
				165					170					175	
Ala	Ala	Gly	Ile	Gly	Thr	Leu	Leu	Asp	Leu	Asp	Val	Asp	Thr	Ile	Tyr
			180						185				190		
Gln	Ala	Ile	Gly	Gln	Ala	Leu	His	Thr	Thr	Thr	Ala	Thr	Arg	Gln	Ser
		195					200					205			
Arg	Lys	Gly	Ala	Ile	Ser	Ser	Trp	Lys	Ala	Phe	Ala	Pro	Ala	Phe	Ala
	210					215					220				
Gly	Lys	Met	Ser	Ile	Glu	Ala	Val	Asp	Arg	Ala	Met	Arg	Gly	Glu	Gly
225					230					235					240
Ala	Pro	Ser	Pro	Ile	Trp	Glu	Gly	Glu	Asp	Gly	Val	Ile	Ala	Trp	Leu
				245					250					255	
Leu	Ser	Gly	Leu	Asp	His	Ile	Tyr	Thr	Ile	Pro	Leu	Pro	Ala	Glu	Gly
			260						265				270		
Glu	Ala	Lys	Arg	Ala	Ile	Leu	Asp	Thr	Tyr	Thr	Lys	Glu	His	Ser	Ala
		275					280					285			
Glu	Tyr	Gln	Ser	Gln	Ala	Pro	Ile	Asp	Leu	Ala	Arg	Ser	Met	Gly	Glu
	290					295					300				
Lys	Leu	Ala	Ala	Gln	Gly	Leu	Asp	Leu	Arg	Asp	Val	Asp	Ser	Ile	Val
305					310					315					320
Leu	His	Thr	Ser	His	His	Thr	His	Tyr	Val	Ile	Gly	Thr	Gly	Ser	Asn
				325					330					335	
Asp	Pro	Gln	Lys	Phe	Asp	Pro	Asp	Ala	Ser	Arg	Glu	Thr	Leu	Asp	His
			340						345				350		
Ser	Ile	Met	Tyr	Ile	Phe	Ala	Val	Ala	Leu	Lys	Asp	Arg	Ala	Trp	His
		355					360					365			
His	Glu	Arg	Ser	Tyr	Ala	Pro	Glu	Arg	Ala	His	Arg	Arg	Glu	Thr	Ile
	370					375					380				
Glu	Leu	Trp	Asn	Lys	Ile	Ser	Thr	Val	Glu	Asp	Pro	Glu	Trp	Thr	Arg
385					390					395					400
Arg	Tyr	His	Ser	Val	Asp	Pro	Ala	Glu	Lys	Ala	Phe	Gly	Ala	Arg	Ala
				405					410					415	

Val Ile Thr Phe Lys Asp Gly Thr Val Val Glu Asp Glu Leu Ala Val
 420 425 430

Ala Asn Ala His Pro Leu Gly Ala Arg Pro Phe Ala Arg Glu Gln Tyr
 435 440 445

Ile Gln Lys Phe Arg Thr Leu Ala Glu Gly Val Val Ser Glu Lys Glu
 450 455 460

Gln Asp Arg Phe Leu Asp Ala Ala Gln Arg Thr His Glu Leu Glu Asp
 465 470 475 480

Leu Ser Glu Leu Asn Ile Glu Leu Asp Ala Asp Ile Leu Ala Lys Ala
 485 490 495

Pro Val Ile Pro Glu Gly Leu Phe
 500

<210> 603
 <211> 975
 <212> DNA
 <213> *Corynebacterium glutamicum*

<220>
 <221> CDS
 <222> (1)..(975)
 <223> FRXA00406

<400> 603

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Asp Pro Val Glu Val Ala Ala Asp Thr Gln Glu Met Ile Ile Thr Arg	
1 5 10 15	
atc atc gac aat gca tcg gtg cag gca gct tcc gtg ttg cgt cga cca	96
Ile Ile Asp Asn Ala Ser Val Gln Ala Ala Ser Val Leu Arg Arg Pro	
20 25 30	
gtt agc tct gcc cgt gcg atg gca cag gtc agg cca gtt acc gat ggt	144
Val Ser Ser Ala Arg Ala Met Ala Gln Val Arg Pro Val Thr Asp Gly	
35 40 45	
cgg ggt gca tct gtt ttc ggt ctg cca gga cgt tat gcc gcg gaa tgg	192
Arg Gly Ala Ser Val Phe Gly Leu Pro Gly Arg Tyr Ala Ala Glu Trp	
50 55 60	
gct gcg ctt gct aac ggc act gcg gtg cgt gag ctt gat ttc cat gac	240
Ala Ala Leu Ala Asn Gly Thr Ala Val Arg Glu Leu Asp Phe His Asp	
65 70 75 80	
acg ttc ctc gct gcg gaa tac tcc cac cca gga gat aac att cct ccg	288
Thr Phe Leu Ala Ala Glu Tyr Ser His Pro Gly Asp Asn Ile Pro Pro	
85 90 95	
att ttg gct gca gca cag cag gct gga aaa ggt ggc aag gat ctg atc	336
Ile Leu Ala Ala Ala Gln Gln Ala Gly Lys Gly Gly Lys Asp Leu Ile	
100 105 110	
cgt ggc atc gct act ggg tat gag att cag gtt aac ttg gtg cgt gga	384
Arg Gly Ile Ala Thr Gly Tyr Glu Ile Gln Val Asn Leu Val Arg Gly	

115	120	125	
atg tgc ctg cat gag cac aag att gat cac gtt gct cat ctt gga cca			432
Met Cys Leu His Glu His Lys Ile Asp His Val Ala His Leu Gly Pro			
130	135	140	
tca gcg gct gct ggt atc gga acc ttg cta gac cta gat gtg gac acc			480
Ser Ala Ala Ala Gly Ile Gly Thr Leu Leu Asp Leu Asp Val Asp Thr			
145	150	155	160
atc tac cag gca att ggt cag gca ttg cac acc acc acg gcg acg agg			528
Ile Tyr Gln Ala Ile Gly Gln Ala Leu His Thr Thr Thr Ala Thr Arg			
	165	170	175
cag tcc cgt aaa ggt gcg att tct tca tgg aag gca ttt gct cct gcg			576
Gln Ser Arg Lys Gly Ala Ile Ser Ser Trp Lys Ala Phe Ala Pro Ala			
	180	185	190
ttt gcg ggc aag atg tcc atc gag gca gta gat cgc gca atg cgt ggc			624
Phe Ala Gly Lys Met Ser Ile Glu Ala Val Asp Arg Ala Met Arg Gly			
	195	200	205
gag ggc gca ccg tca cca atc tgg gaa ggc gaa gac ggc gta atc gcg			672
Glu Gly Ala Pro Ser Pro Ile Trp Glu Gly Glu Asp Gly Val Ile Ala			
	210	215	220
tgg ctg ctg tcc ggt ctt gat cac atc tac acc att cct ttg cct gca			720
Trp Leu Leu Ser Gly Leu Asp His Ile Tyr Thr Ile Pro Leu Pro Ala			
	225	230	235
gaa ggt gaa gcc aaa cga gca atc ttg gat acc tac acc aag gaa cac			768
Glu Gly Glu Ala Lys Arg Ala Ile Leu Asp Thr Tyr Thr Lys Glu His			
	245	250	255
tcg gcg gaa tac cag tca cag gca ccg atc gac ttg gcg cgc agc atg			816
Ser Ala Glu Tyr Gln Ser Gln Ala Pro Ile Asp Leu Ala Arg Ser Met			
	260	265	270
ggg gag aag ctg gca gca cag ggc ttg gac ctg cgt gat gtg gac tcc			864
Gly Glu Lys Leu Ala Ala Gln Gly Leu Asp Leu Arg Asp Val Asp Ser			
	275	280	285
atc gtt ttg cac acc tcc cac cac act cac tac gtg atc ggc acc gga			912
Ile Val Leu His Thr Ser His His Thr His Tyr Val Ile Gly Thr Gly			
	290	295	300
tct aat gat cca cag aag ttc gat cca gat gca tcg cga gaa acc ctt			960
Ser Asn Asp Pro Gln Lys Phe Asp Pro Asp Ala Ser Arg Glu Thr Leu			
	305	310	315
gat cac tcc atc atg			975
Asp His Ser Ile Met			
	325		

<210> 604

<211> 325

<212> PRT

<213> Corynebacterium glutamicum

<400> 604

Asp Pro Val Glu Val Ala Ala Asp Thr Gln Glu Met Ile Ile Thr Arg
 1 5 10 15
 Ile Ile Asp Asn Ala Ser Val Gln Ala Ala Ser Val Leu Arg Arg Pro
 20 25 30
 Val Ser Ser Ala Arg Ala Met Ala Gln Val Arg Pro Val Thr Asp Gly
 35 40 45
 Arg Gly Ala Ser Val Phe Gly Leu Pro Gly Arg Tyr Ala Ala Glu Trp
 50 55 60
 Ala Ala Leu Ala Asn Gly Thr Ala Val Arg Glu Leu Asp Phe His Asp
 65 70 75 80
 Thr Phe Leu Ala Ala Glu Tyr Ser His Pro Gly Asp Asn Ile Pro Pro
 85 90 95
 Ile Leu Ala Ala Ala Gln Gln Ala Gly Lys Gly Gly Lys Asp Leu Ile
 100 105 110
 Arg Gly Ile Ala Thr Gly Tyr Glu Ile Gln Val Asn Leu Val Arg Gly
 115 120 125
 Met Cys Leu His Glu His Lys Ile Asp His Val Ala His Leu Gly Pro
 130 135 140
 Ser Ala Ala Ala Gly Ile Gly Thr Leu Leu Asp Leu Asp Val Asp Thr
 145 150 155 160
 Ile Tyr Gln Ala Ile Gly Gln Ala Leu His Thr Thr Thr Ala Thr Arg
 165 170 175
 Gln Ser Arg Lys Gly Ala Ile Ser Ser Trp Lys Ala Phe Ala Pro Ala
 180 185 190
 Phe Ala Gly Lys Met Ser Ile Glu Ala Val Asp Arg Ala Met Arg Gly
 195 200 205
 Glu Gly Ala Pro Ser Pro Ile Trp Glu Gly Glu Asp Gly Val Ile Ala
 210 215 220
 Trp Leu Leu Ser Gly Leu Asp His Ile Tyr Thr Ile Pro Leu Pro Ala
 225 230 235 240
 Glu Gly Glu Ala Lys Arg Ala Ile Leu Asp Thr Tyr Thr Lys Glu His
 245 250 255
 Ser Ala Glu Tyr Gln Ser Gln Ala Pro Ile Asp Leu Ala Arg Ser Met
 260 265 270
 Gly Glu Lys Leu Ala Ala Gln Gly Leu Asp Leu Arg Asp Val Asp Ser
 275 280 285
 Ile Val Leu His Thr Ser His His Thr His Tyr Val Ile Gly Thr Gly
 290 295 300
 Ser Asn Asp Pro Gln Lys Phe Asp Pro Asp Ala Ser Arg Glu Thr Leu
 305 310 315 320
 Asp His Ser Ile Met

325

<210> 605
 <211> 431
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (1)..(408)
 <223> FRXA00514

<400> 605
 cac gag cgt tcc tat gct cct gag cga gcc ctc cgc cga gag acc atc 48
 His Glu Arg Ser Tyr Ala Pro Glu Arg Ala Leu Arg Arg Glu Thr Ile
 1 5 10 15
 gag ctg tgg aac aag att tcc acg gtg gag gat cct gaa tgg acc agg 96
 Glu Leu Trp Asn Lys Ile Ser Thr Val Glu Asp Pro Glu Trp Thr Arg
 20 25 30
 cgt tac cac tcc gtt gat cct gca gaa aag gcc ttc ggc gca cgc gca 144
 Arg Tyr His Ser Val Asp Pro Ala Glu Lys Ala Phe Gly Ala Arg Ala
 35 40 45
 gtg atc acc ttc aag gat gga acc gtc gtg gaa gat gaa ctg gct gtg 192
 Val Ile Thr Phe Lys Asp Gly Thr Val Val Glu Asp Glu Leu Ala Val
 50 55 60
 gcg aat gcg cat cct ctg gga gca cgg cct ttc gct agg gag cag tac 240
 Ala Asn Ala His Pro Leu Gly Ala Arg Pro Phe Ala Arg Glu Gln Tyr
 65 70 75 80
 att cag aaa ttc cgc acc ttg gct gaa ggt gtt gtg tcc gaa aag gaa 288
 Ile Gln Lys Phe Arg Thr Leu Ala Glu Gly Val Val Ser Glu Lys Glu
 85 90 95
 cag gat cgc ttc ttg gat gcg gca cag cgt acg cac gag ctt gag gat 336
 Gln Asp Arg Phe Leu Asp Ala Ala Gln Arg Thr His Glu Leu Glu Asp
 100 105 110
 ctt tca gaa ctc aac att gaa ttg gat gcc gat att ttg gcc aag gct 384
 Leu Ser Glu Leu Asn Ile Glu Leu Asp Ala Asp Ile Leu Ala Lys Ala
 115 120 125
 cct gtg att ccg gaa gga ctg ttc tgatggcggg tttgttttcc tct. 431
 Pro Val Ile Pro Glu Gly Leu Phe
 130 135

<210> 606
 <211> 136
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 606
 His Glu Arg Ser Tyr Ala Pro Glu Arg Ala Leu Arg Arg Glu Thr Ile
 1 5 10 15
 Glu Leu Trp Asn Lys Ile Ser Thr Val Glu Asp Pro Glu Trp Thr Arg

20 25 30
 Arg Tyr His Ser Val Asp Pro Ala Glu Lys Ala Phe Gly Ala Arg Ala
 35 40 45
 Val Ile Thr Phe Lys Asp Gly Thr Val Val Glu Asp Glu Leu Ala Val
 50 55 60
 Ala Asn Ala His Pro Leu Gly Ala Arg Pro Phe Ala Arg Glu Gln Tyr
 65 70 75 80
 Ile Gln Lys Phe Arg Thr Leu Ala Glu Gly Val Val Ser Glu Lys Glu
 85 90 95
 Gln Asp Arg Phe Leu Asp Ala Ala Gln Arg Thr His Glu Leu Glu Asp
 100 105 110
 Leu Ser Glu Leu Asn Ile Glu Leu Asp Ala Asp Ile Leu Ala Lys Ala
 115 120 125
 Pro Val Ile Pro Glu Gly Leu Phe
 130 135

<210> 607
 <211> 718
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(718)
 <223> RXA00512

<400> 607
 tacaacgagt acaacgcttt cgaccagcaa gtattcacct attccgctga cagctacaag 60
 cccatcttct aaccgccta tatataagga gtgaatcacc atg tcc agc gcc aca 115
 Met Ser Ser Ala Thr
 1 5
 acc act gat gtt cgc aaa ggg ctc tac gga gtc atc gcc gat tac acg 163
 Thr Thr Asp Val Arg Lys Gly Leu Tyr Gly Val Ile Ala Asp Tyr Thr
 10 15 20
 gcc gtt tcc aaa gtc atg cca gag acc aat tca ctg acc tac cgt ggc 211
 Ala Val Ser Lys Val Met Pro Glu Thr Asn Ser Leu Thr Tyr Arg Gly
 25 30 35
 tac gcg gtg gaa gat ttg gtg gaa aac tgc agc ttc gag gag gtg ttt 259
 Tyr Ala Val Glu Asp Leu Val Glu Asn Cys Ser Phe Glu Glu Val Phe
 40 45 50
 tac ctc ctg tgg cac ggc gag ctg ccc act gcg caa caa ctt gcg gag 307
 Tyr Leu Leu Trp His Gly Glu Leu Pro Thr Ala Gln Gln Leu Ala Glu
 55 60 65
 ttc aat gag cgt ggc cgt tcc tac cgc tcc ctg gat gcc ggt ttg atc 355
 Phe Asn Glu Arg Gly Arg Ser Tyr Arg Ser Leu Asp Ala Gly Leu Ile
 70 75 80 85

tcc ctg atc cac tct ttg ccc aaa gaa gcc cac ccg atg gat gtt atg 403
 Ser Leu Ile His Ser Leu Pro Lys Glu Ala His Pro Met Asp Val Met
 90 95 100
 cgc acc gcg gtg tcc tac atg ggc acc aag gat tcc gag tat ttc acc 451
 Arg Thr Ala Val Ser Tyr Met Gly Thr Lys Asp Ser Glu Tyr Phe Thr
 105 110 115
 acc gat tct gag cac atc cgc aaa gtt ggc cac acc ttg ttg gcg cag 499
 Thr Asp Ser Glu His Ile Arg Lys Val Gly His Thr Leu Leu Ala Gln
 120 125 130
 ctt ccg atg gtg cta gcc atg gat att cgt cgc cgc aag ggc ctc gat 547
 Leu Pro Met Val Leu Ala Met Asp Ile Arg Arg Arg Lys Gly Leu Asp
 135 140 145
 atc atc gcc cct gac tcc agc aag tca gtc gcc gaa aac ctg ctg tct 595
 Ile Ile Ala Pro Asp Ser Ser Lys Ser Val Ala Glu Asn Leu Leu Ser
 150 155 160 165
 atg gtg ttt ggt act ggc ccg gaa tca cct gca tcc aac cca gct gac 643
 Met Val Phe Gly Thr Gly Pro Glu Ser Pro Ala Ser Asn Pro Ala Asp
 170 175 180
 gtc cgc gat ttt gag aaa tca ctg atc ctc tac gcc gag cac tcc ttc 691
 Val Arg Asp Phe Glu Lys Ser Leu Ile Leu Tyr Ala Glu His Ser Phe
 185 190 195
 aac gcc tcc acc ttc acc gcc cgc gtg 718
 Asn Ala Ser Thr Phe Thr Ala Arg Val
 200 205

<210> 608
 <211> 206
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 608
 Met Ser Ser Ala Thr Thr Thr Asp Val Arg Lys Gly Leu Tyr Gly Val
 1 5 10 15
 Ile Ala Asp Tyr Thr Ala Val Ser Lys Val Met Pro Glu Thr Asn Ser
 20 25 30
 Leu Thr Tyr Arg Gly Tyr Ala Val Glu Asp Leu Val Glu Asn Cys Ser
 35 40 45
 Phe Glu Glu Val Phe Tyr Leu Leu Trp His Gly Glu Leu Pro Thr Ala
 50 55 60
 Gln Gln Leu Ala Glu Phe Asn Glu Arg Gly Arg Ser Tyr Arg Ser Leu
 65 70 75 80
 Asp Ala Gly Leu Ile Ser Leu Ile His Ser Leu Pro Lys Glu Ala His
 85 90 95
 Pro Met Asp Val Met Arg Thr Ala Val Ser Tyr Met Gly Thr Lys Asp
 100 105 110
 Ser Glu Tyr Phe Thr Thr Asp Ser Glu His Ile Arg Lys Val Gly His

115	120	125
Thr Leu Leu Ala Gln Leu Pro Met Val Leu Ala Met Asp Ile Arg Arg		
130	135	140
Arg Lys Gly Leu Asp Ile Ile Ala Pro Asp Ser Ser Lys Ser Val Ala		
145	150	155
Glu Asn Leu Leu Ser Met Val Phe Gly Thr Gly Pro Glu Ser Pro Ala		
165	170	175
Ser Asn Pro Ala Asp Val Arg Asp Phe Glu Lys Ser Leu Ile Leu Tyr		
180	185	190
Ala Glu His Ser Phe Asn Ala Ser Thr Phe Thr Ala Arg Val		
195	200	205

<210> 609
 <211> 320
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (1)..(297)
 <223> RXA00518

<400> 609	
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Val Leu Pro Val Leu Ala Ala Arg His Asp Gly Glu Lys Trp Val Ala	
1 5 10 15	
atg tat gaa aac atg cgc gac gcc atg gac gcc cgc acc ggc atc aag	96
Met Tyr Glu Asn Met Arg Asp Ala Met Asp Ala Arg Thr Gly Ile Lys	
20 25 30	
ccg aat ctc gat ttc cct gct ggc cct gcc tac cac ctg ctc ggt ttc	144
Pro Asn Leu Asp Phe Pro Ala Gly Pro Ala Tyr His Leu Leu Gly Phe	
35 40 45	
ccg gtc gat ttc ttc acc ccg ctg ttc gtc atc gcc cgc gtc gcc ggc	192
Pro Val Asp Phe Phe Thr Pro Leu Phe Val Ile Ala Arg Val Ala Gly	
50 55 60	
tgg acg gcc cac atc gtg gag cag tac gaa aac aac tcg ctc atc cgc	240
Trp Thr Ala His Ile Val Glu Gln Tyr Glu Asn Asn Ser Leu Ile Arg	
65 70 75 80	
cca ctg tcc gag tac aac ggc gag gag cag cgc gag gtc gcg ccc att	288
Pro Leu Ser Glu Tyr Asn Gly Glu Glu Gln Arg Glu Val Ala Pro Ile	
85 90 95	
gaa aag cgc taaaagattt tcgcttttcg acg	320
Glu Lys Arg	

<210> 610
 <211> 99
 <212> PRT

<213> Corynebacterium glutamicum

<400> 610

Val Leu Pro Val Leu Ala Ala Arg His Asp Gly Glu Lys Trp Val Ala
 1 5 10 15

Met Tyr Glu Asn Met Arg Asp Ala Met Asp Ala Arg Thr Gly Ile Lys
 20 25 30

Pro Asn Leu Asp Phe Pro Ala Gly Pro Ala Tyr His Leu Leu Gly Phe
 35 40 45

Pro Val Asp Phe Phe Thr Pro Leu Phe Val Ile Ala Arg Val Ala Gly
 50 55 60

Trp Thr Ala His Ile Val Glu Gln Tyr Glu Asn Asn Ser Leu Ile Arg
 65 70 75 80

Pro Leu Ser Glu Tyr Asn Gly Glu Glu Gln Arg Glu Val Ala Pro Ile
 85 90 95

Glu Lys Arg

<210> 611

<211> 1494

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1471)

<223> RXA01077

<400> 611

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aatgaaggca agccaaactt aactagtaga taggattgca atg acc gaa tcg caa 115
 Met Thr Glu Ser Gln
 1 5

gat ctc gcc gca ttc gtg gaa gct gcc aaa ctc aat gat gca agc ccc 163
 Asp Leu Ala Ala Phe Val Glu Ala Ala Lys Leu Asn Asp Ala Ser Pro
 10 15 20

gaa gcc gta gag caa ttg aaa atc aga gtg cta gac acc gta ggc gtt 211
 Glu Ala Val Glu Gln Leu Lys Ile Arg Val Leu Asp Thr Val Gly Val
 25 30 35

gcc att ggc gca ctg gat gcc gaa ccg att gtc gcc att cga gga ctc 259
 Ala Ile Gly Ala Leu Asp Ala Glu Pro Ile Val Ala Ile Arg Gly Leu
 40 45 50

ctg gaa gac ctc ggg gga acc gaa cag tca aca ctt att ggt ggt ggc 307
 Leu Glu Asp Leu Gly Gly Thr Glu Gln Ser Thr Leu Ile Gly Gly Gly
 55 60 65

aaa acc agt ccg gaa cgt gca gca ttt ttc aac agc gca tta agc cgc 355
 Lys Thr Ser Pro Glu Arg Ala Ala Phe Phe Asn Ser Ala Leu Ser Arg
 70 75 80 85

tac ctc gac ttc atg gac gcc tac cta gca aag ggc gaa acc aac cac	403
Tyr Leu Asp Phe Met Asp Ala Tyr Leu Ala Lys Gly Glu Thr Asn His	
90 95 100	
ccc tcg gat aac ttc gga gca gtg ctc gct gca gcc gaa agc gtt ggc	451
Pro Ser Asp Asn Phe Gly Ala Val Leu Ala Ala Ala Glu Ser Val Gly	
105 110 115	
gcc tct gga aaa gac ctg ctc acc gca ttc gcc gtg gcc tac cag gta	499
Ala Ser Gly Lys Asp Leu Leu Thr Ala Phe Ala Val Ala Tyr Gln Val	
120 125 130	
cac acc aga ctt tca gat gtc gca cca gtt cgc gcc aaa ggt ttc gat	547
His Thr Arg Leu Ser Asp Val Ala Pro Val Arg Ala Lys Gly Phe Asp	
135 140 145	
cac acc acc caa gga gca ttc gca gcg ggc gca tct gct gcc aag gca	595
His Thr Thr Gln Gly Ala Phe Ala Ala Gly Ala Ser Ala Ala Lys Ala	
150 155 160 165	
ctg ggt ttg cca gct gat caa atc gcc aac gca ctg gcc atc gca gga	643
Leu Gly Leu Pro Ala Asp Gln Ile Ala Asn Ala Leu Ala Ile Ala Gly	
170 175 180	
aca gcc aat gtt gca ctt cgt gtc act cgc act gga aac ttg agc cac	691
Thr Ala Asn Val Ala Leu Arg Val Thr Arg Thr Gly Asn Leu Ser His	
185 190 195	
tgg aaa ggc ctt gcc tac cca cac gtg tcc aaa gaa gga acc tgg gca	739
Trp Lys Gly Leu Ala Tyr Pro His Val Ser Lys Glu Gly Thr Trp Ala	
200 205 210	
gca ctg ctc gca agc cga ggt att acc ggt ccg gaa gaa gtc ttc gaa	787
Ala Leu Leu Ala Ser Arg Gly Ile Thr Gly Pro Glu Glu Val Phe Glu	
215 220 225	
ggc aac aag gga ttc aaa gag tcc gtc tcc gga ccg ttc gag atc gat	835
Gly Asn Lys Gly Phe Lys Glu Ser Val Ser Gly Pro Phe Glu Ile Asp	
230 235 240 245	
tgg tcc aag gaa gac ttg gaa agc gtt aag cgc acc atc atc aag aaa	883
Trp Ser Lys Glu Asp Leu Glu Ser Val Lys Arg Thr Ile Ile Lys Lys	
250 255 260	
cac aac gcg gaa att cac tcg cag tca gcg ctt gat gca gcc caa gaa	931
His Asn Ala Glu Ile His Ser Gln Ser Ala Leu Asp Ala Ala Gln Glu	
265 270 275	
ata cgc gca caa gaa ggc ttc aat gtg gac aac att gaa aag att cac	979
Ile Arg Ala Gln Glu Gly Phe Asn Val Asp Asn Ile Glu Lys Ile His	
280 285 290	
ctg act act ttc gac gtt gcc tac tcc atc att ggc ggc ggc gaa gaa	1027
Leu Thr Thr Phe Asp Val Ala Tyr Ser Ile Ile Gly Gly Gly Glu Glu	
295 300 305	
ggc gac aaa cag ctt att cgc acc aaa gaa gaa gcc gat cac tca ctg	1075
Gly Asp Lys Gln Leu Ile Arg Thr Lys Glu Glu Ala Asp His Ser Leu	
310 315 320 325	

ccg tgg atg ctc gct gta gtt ctg ctg gat ggt cag ctc aat ccc gaa 1123
 Pro Trp Met Leu Ala Val Val Leu Leu Asp Gly Gln Leu Asn Pro Glu
 330 335 340

cag tac gaa cca tca cgc atc gtt gct gat gat gta caa acc ttg atg 1171
 Gln Tyr Glu Pro Ser Arg Ile Val Ala Asp Asp Val Gln Thr Leu Met
 345 350 355

aag aaa atc gaa atc aca ccg tca gat gaa ttc tct gat cgc ttc cct 1219
 Lys Lys Ile Glu Ile Thr Pro Ser Asp Glu Phe Ser Asp Arg Phe Pro
 360 365 370

gac cac atg cca gct gat cta gaa gtc aca cta aac gat ggc tcg gtg 1267
 Asp His Met Pro Ala Asp Leu Glu Val Thr Leu Asn Asp Gly Ser Val
 375 380 385

ttc aaa gct tca caa gat agc tac tta ggc ttc cac gac aat ccc cta 1315
 Phe Lys Ala Ser Gln Asp Ser Tyr Leu Gly Phe His Asp Asn Pro Leu
 390 395 400 405

gat tgg gac aac gcg cgc aag aaa ttc gat gcc ctt gtc aca cca ttc 1363
 Asp Trp Asp Asn Ala Arg Lys Lys Phe Asp Ala Leu Val Thr Pro Phe
 410 415 420

acc ggt gaa gaa cta cgt gaa gaa atc gcc acg atc att cac gag ctc 1411
 Thr Gly Glu Glu Leu Arg Glu Glu Ile Ala Thr Ile Ile His Glu Leu
 425 430 435

gat agc cga cag gtt tct gaa ctc aca gaa gcc ctg gcc aaa gtc tcc 1459
 Asp Ser Arg Gln Val Ser Glu Leu Thr Glu Ala Leu Ala Lys Val Ser
 440 445 450

acc acc cgc agc taaaactttt tgaaaggagc tca 1494
 Thr Thr Arg Ser
 455

<210> 612

<211> 457

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 612

Met Thr Glu Ser Gln Asp Leu Ala Ala Phe Val Glu Ala Ala Lys Leu
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Asn Asp Ala Ser Pro Glu Ala Val Glu Gln Leu Lys Ile Arg Val Leu
 20 25 30

Asp Thr Val Gly Val Ala Ile Gly Ala Leu Asp Ala Glu Pro Ile Val
 35 40 45

Ala Ile Arg Gly Leu Leu Glu Asp Leu Gly Gly Thr Glu Gln Ser Thr
 50 55 60

Leu Ile Gly Gly Gly Lys Thr Ser Pro Glu Arg Ala Ala Phe Phe Asn
 65 70 75 80

Ser Ala Leu Ser Arg Tyr Leu Asp Phe Met Asp Ala Tyr Leu Ala Lys
 85 90 95

Gly Glu Thr Asn His Pro Ser Asp Asn Phe Gly Ala Val Leu Ala Ala
 100 105 110
 Ala Glu Ser Val Gly Ala Ser Gly Lys Asp Leu Leu Thr Ala Phe Ala
 115 120 125
 Val Ala Tyr Gln Val His Thr Arg Leu Ser Asp Val Ala Pro Val Arg
 130 135 140
 Ala Lys Gly Phe Asp His Thr Thr Gln Gly Ala Phe Ala Ala Gly Ala
 145 150 155 160
 Ser Ala Ala Lys Ala Leu Gly Leu Pro Ala Asp Gln Ile Ala Asn Ala
 165 170 175
 Leu Ala Ile Ala Gly Thr Ala Asn Val Ala Leu Arg Val Thr Arg Thr
 180 185 190
 Gly Asn Leu Ser His Trp Lys Gly Leu Ala Tyr Pro His Val Ser Lys
 195 200 205
 Glu Gly Thr Trp Ala Ala Leu Leu Ala Ser Arg Gly Ile Thr Gly Pro
 210 215 220
 Glu Glu Val Phe Glu Gly Asn Lys Gly Phe Lys Glu Ser Val Ser Gly
 225 230 235 240
 Pro Phe Glu Ile Asp Trp Ser Lys Glu Asp Leu Glu Ser Val Lys Arg
 245 250 255
 Thr Ile Ile Lys Lys His Asn Ala Glu Ile His Ser Gln Ser Ala Leu
 260 265 270
 Asp Ala Ala Gln Glu Ile Arg Ala Gln Glu Gly Phe Asn Val Asp Asn
 275 280 285
 Ile Glu Lys Ile His Leu Thr Thr Phe Asp Val Ala Tyr Ser Ile Ile
 290 295 300
 Gly Gly Gly Glu Glu Gly Asp Lys Gln Leu Ile Arg Thr Lys Glu Glu
 305 310 315 320
 Ala Asp His Ser Leu Pro Trp Met Leu Ala Val Val Leu Leu Asp Gly
 325 330 335
 Gln Leu Asn Pro Glu Gln Tyr Glu Pro Ser Arg Ile Val Ala Asp Asp
 340 345 350
 Val Gln Thr Leu Met Lys Lys Ile Glu Ile Thr Pro Ser Asp Glu Phe
 355 360 365
 Ser Asp Arg Phe Pro Asp His Met Pro Ala Asp Leu Glu Val Thr Leu
 370 375 380
 Asn Asp Gly Ser Val Phe Lys Ala Ser Gln Asp Ser Tyr Leu Gly Phe
 385 390 395 400
 His Asp Asn Pro Leu Asp Trp Asp Asn Ala Arg Lys Lys Phe Asp Ala
 405 410 415
 Leu Val Thr Pro Phe Thr Gly Glu Glu Leu Arg Glu Glu Ile Ala Thr

420

425

430

Ile Ile His Glu Leu Asp Ser Arg Gln Val Ser Glu Leu Thr Glu Ala
 435 440 445

Leu Ala Lys Val Ser Thr Thr Arg Ser
 450 455

<210> 613

<211> 923

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(900)

<223> RXN03144

<400> 613

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 Thr Thr Thr Ala Thr Arg Gln Ser Arg Lys Gly Glu Ile Ser Ser Trp
 1 5 10 15

aag gcg ttc gcg cca gcg ttt gcg gga aag atg gcc att gag gcg atg 96
 Lys Ala Phe Ala Pro Ala Phe Ala Gly Lys Met Ala Ile Glu Ala Met
 20 25 30

gat cgt gcg atg cgt ggg gag ggt tcg ccc gca ccg att tgg gag ggc 144
 Asp Arg Ala Met Arg Gly Glu Gly Ser Pro Ala Pro Ile Trp Glu Gly
 35 40 45

gaa gac ggg gtc atc gcg tgg ctg tta tcg ggc aaa gat cat gtt tat 192
 Glu Asp Gly Val Ile Ala Trp Leu Leu Ser Gly Lys Asp His Val Tyr
 50 55 60

cat gtg cca ttg ccg gaa cac ggc gag ccc aag ctg ggg att cta gag 240
 His Val Pro Leu Pro Glu His Gly Glu Pro Lys Leu Gly Ile Leu Glu
 65 70 75 80

act tac aca aag gaa cat tca gcg gaa tat caa tcg cag gca ccg att 288
 Thr Tyr Thr Lys Glu His Ser Ala Glu Tyr Gln Ser Gln Ala Pro Ile
 85 90 95

gat ctg gcg cgc agg atg aag cca ctg gtt gac gcg gct ggc gga acg 336
 Asp Leu Ala Arg Arg Met Lys Pro Leu Val Asp Ala Ala Gly Gly Thr
 100 105 110

gaa cac att gca gag att gtg ctg cgc acc agt cac cac acg cat tat 384
 Glu His Ile Ala Glu Ile Val Leu Arg Thr Ser His His Thr His Tyr
 115 120 125

gtg att ggc act ggg gcg aac gat ccg cag aag atg gat ccg cag gcc 432
 Val Ile Gly Thr Gly Ala Asn Asp Pro Gln Lys Met Asp Pro Gln Ala
 130 135 140

tcg cgt gaa acc ctg gat cat tcc atc atg tac att ttc gcc gtc gcg 480
 Ser Arg Glu Thr Leu Asp His Ser Ile Met Tyr Ile Phe Ala Val Ala
 145 150 155 160

ctt caa gat ggc gtg tgg cac cac gag ttt tcc tac acc cgc aag cgt 528

Leu Gln Asp Gly Val Trp His His Glu Phe Ser Tyr Thr Arg Lys Arg
 165 170 175
 tcc acc cgc ccg gaa act gtg gag ctg tgg cac aag att cgc acc gtg 576
 Ser Thr Arg Pro Glu Thr Val Glu Leu Trp His Lys Ile Arg Thr Val
 180 185 190
 gag gat cct gaa tgg acg cgc cga tac cat tct gat gat cct gca aaa 624
 Glu Asp Pro Glu Trp Thr Arg Arg Tyr His Ser Asp Asp Pro Ala Lys
 195 200 205
 aag gcc ttt ggt gcg aaa gca gtg atc aca atg gct gat ggc acc gtg 672
 Lys Ala Phe Gly Ala Lys Ala Val Ile Thr Met Ala Asp Gly Thr Val
 210 215 220
 att gag gat gaa ttg gct gtc gcg gat gcc cac ccg ctg ggt gct cgg 720
 Ile Glu Asp Glu Leu Ala Val Ala Asp Ala His Pro Leu Gly Ala Arg
 225 230 235 240
 ccg ttt gcg cgg gag aat tac att gaa aaa ttc cgc aca ctc gcg cag 768
 Pro Phe Ala Arg Glu Asn Tyr Ile Glu Lys Phe Arg Thr Leu Ala Gln
 245 250 255
 ggg att gtc att gat tca gaa cag gaa cgc ttc ttg cat gcc gtg caa 816
 Gly Ile Val Ile Asp Ser Glu Gln Glu Arg Phe Leu His Ala Val Gln
 260 265 270
 agc ctg cct gac ctg gat gat ctt gat cag ctc aac atc gaa gtc gac 864
 Ser Leu Pro Asp Leu Asp Asp Leu Asp Gln Leu Asn Ile Glu Val Asp
 275 280 285
 ata agc aac cag gcc gcg acg aaa gcg ggg ctg tta tgaatctctt 910
 Ile Ser Asn Gln Ala Ala Thr Lys Ala Gly Leu Leu
 290 295 300
 ttcgaatggt gtt 923

<210> 614
 <211> 300
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 614
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 Lys Ala Phe Ala Pro Ala Phe Ala Gly Lys Met Ala Ile Glu Ala Met
 20 25 30
 Asp Arg Ala Met Arg Gly Glu Gly Ser Pro Ala Pro Ile Trp Glu Gly
 35 40 45
 Glu Asp Gly Val Ile Ala Trp Leu Leu Ser Gly Lys Asp His Val Tyr
 50 55 60
 His Val Pro Leu Pro Glu His Gly Glu Pro Lys Leu Gly Ile Leu Glu
 65 70 75 80
 Thr Tyr Thr Lys Glu His Ser Ala Glu Tyr Gln Ser Gln Ala Pro Ile
 85 90 95

Asp Leu Ala Arg Arg Met Lys Pro Leu Val Asp Ala Ala Gly Gly Thr
 100 105 110
 Glu His Ile Ala Glu Ile Val Leu Arg Thr Ser His His Thr His Tyr
 115 120 125
 Val Ile Gly Thr Gly Ala Asn Asp Pro Gln Lys Met Asp Pro Gln Ala
 130 135 140
 Ser Arg Glu Thr Leu Asp His Ser Ile Met Tyr Ile Phe Ala Val Ala
 145 150 155 160
 Leu Gln Asp Gly Val Trp His His Glu Phe Ser Tyr Thr Arg Lys Arg
 165 170 175
 Ser Thr Arg Pro Glu Thr Val Glu Leu Trp His Lys Ile Arg Thr Val
 180 185 190
 Glu Asp Pro Glu Trp Thr Arg Arg Tyr His Ser Asp Asp Pro Ala Lys
 195 200 205
 Lys Ala Phe Gly Ala Lys Ala Val Ile Thr Met Ala Asp Gly Thr Val
 210 215 220
 Ile Glu Asp Glu Leu Ala Val Ala Asp Ala His Pro Leu Gly Ala Arg
 225 230 235 240
 Pro Phe Ala Arg Glu Asn Tyr Ile Glu Lys Phe Arg Thr Leu Ala Gln
 245 250 255
 Gly Ile Val Ile Asp Ser Glu Gln Glu Arg Phe Leu His Ala Val Gln
 260 265 270
 Ser Leu Pro Asp Leu Asp Asp Leu Asp Gln Leu Asn Ile Glu Val Asp
 275 280 285
 Ile Ser Asn Gln Ala Ala Thr Lys Ala Gly Leu Leu
 290 295 300

<210> 615

<211> 511

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(511)

<223> FRXA02322

<400> 615

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ctttaaggaa acagtgcaca aataaatctc aaggagcccc atg cgc atc cac gat 115
 Met Arg Ile His Asp
 1 5

gtt tat acc cac ctt tcg gcc gat aac ttt ccc aaa gca gag cac ctt 163
 Val Tyr Thr His Leu Ser Ala Asp Asn Phe Pro Lys Ala Glu His Leu
 10 15 20

gcg tgg aaa ttc tcc gag ctt gcc acc gac ccc gtg gag gtg aca ccg 211
 Ala Trp Lys Phe Ser Glu Leu Ala Thr Asp Pro Val Glu Val Thr Pro
 25 30 35

gat gtt tcg gag atg atc atc aac cgg atc atc gac aac gcg gcg gtg 259
 Asp Val Ser Glu Met Ile Ile Asn Arg Ile Ile Asp Asn Ala Ala Val
 40 45 50

tct gcc gcg tcg gtg ttg cgc cgg cct gtg act gtg gcc agg caa caa 307
 Ser Ala Ala Ser Val Leu Arg Arg Pro Val Thr Val Ala Arg Gln Gln
 55 60 65

gcg cag tcc cat ccg cgg gaa aag ggc gga aaa gtt ttt gga att tca 355
 Ala Gln Ser His Pro Arg Glu Lys Gly Gly Lys Val Phe Gly Ile Ser
 70 75 80 85

ggc agc tac tca cca gag tgg gct gcc ttt gct aat ggt gtg gcc gta 403
 Gly Ser Tyr Ser Pro Glu Trp Ala Ala Phe Ala Asn Gly Val Ala Val
 90 95 100

cgt gaa ttg gac ttc cac gat aca ttt tta gca gct gaa tac tcc cat 451
 Arg Glu Leu Asp Phe His Asp Thr Phe Leu Ala Ala Glu Tyr Ser His
 105 110 115

ccc ggc gac aat att cca cca ctt ctt gca gta gcg cag gct cag aga 499
 Pro Gly Asp Asn Ile Pro Pro Leu Leu Ala Val Ala Gln Ala Gln Arg
 120 125 130

agc agc ggc agg 511
 Ser Ser Gly Arg
 135

<210> 616

<211> 137

<212> PRT

<213> Corynebacterium glutamicum

<400> 616

Met Arg Ile His Asp Val Tyr Thr His Leu Ser Ala Asp Asn Phe Pro
 1 5 10 15

Lys Ala Glu His Leu Ala Trp Lys Phe Ser Glu Leu Ala Thr Asp Pro
 20 25 30

Val Glu Val Thr Pro Asp Val Ser Glu Met Ile Ile Asn Arg Ile Ile
 35 40 45

Asp Asn Ala Ala Val Ser Ala Ala Ser Val Leu Arg Arg Pro Val Thr
 50 55 60

Val Ala Arg Gln Gln Ala Gln Ser His Pro Arg Glu Lys Gly Gly Lys
 65 70 75 80

Val Phe Gly Ile Ser Gly Ser Tyr Ser Pro Glu Trp Ala Ala Phe Ala
 85 90 95

Asn Gly Val Ala Val Arg Glu Leu Asp Phe His Asp Thr Phe Leu Ala
 100 105 110

Ala Glu Tyr Ser His Pro Gly Asp Asn Ile Pro Pro Leu Leu Ala Val
 115 120 125

Ala Gln Ala Gln Arg Ser Ser Gly Arg
 130 135

<210> 617

<211> 603

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(603)

<223> RXA02329

<400> 617

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Thr Ala Thr Arg Gln Ser Arg Lys Gly Glu Ile Ser Ser Trp Lys Ala	
1 5 10 15	
ttc gcg cca gcg ttt gcg gga aag atg gcc att gag gcg atg gat cgt	96
Phe Ala Pro Ala Phe Ala Gly Lys Met Ala Ile Glu Ala Met Asp Arg	
20 25 30	
gcg atg cgt ggg gag ggt tcg ccc gca ccg att tgg gag ggc gaa gac	144
Ala Met Arg Gly Glu Gly Ser Pro Ala Pro Ile Trp Glu Gly Glu Asp	
35 40 45	
ggg gtc atc gcg tgg ctg tta tcg ggc aaa gat cat gtt tat cat gtg	192
Gly Val Ile Ala Trp Leu Leu Ser Gly Lys Asp His Val Tyr His Val	
50 55 60	
cca ttg ccg gaa cac ggc gag ccc aag ctg ggg att cta gag act tac	240
Pro Leu Pro Glu His Gly Glu Pro Lys Leu Gly Ile Leu Glu Thr Tyr	
65 70 75 80	
aca aag gaa cat tca gcg gaa tat caa tcg cag gca ccg att gat ctg	288
Thr Lys Glu His Ser Ala Glu Tyr Gln Ser Gln Ala Pro Ile Asp Leu	
85 90 95	
gcg cgc agg atg aag cca ctg gtt gac gcg gct ggc gga acg gaa cac	336
Ala Arg Arg Met Lys Pro Leu Val Asp Ala Ala Gly Gly Thr Glu His	
100 105 110	
att gca gag att gtg ctg cgc acc agt cac cac acg cat tat gtg att	384
Ile Ala Glu Ile Val Leu Arg Thr Ser His His Thr His Tyr Val Ile	
115 120 125	
ggc act ggg gcg aac gat ccg cag aag atg gat ccg cag gcc tcg cgt	432
Gly Thr Gly Ala Asn Asp Pro Gln Lys Met Asp Pro Gln Ala Ser Arg	
130 135 140	
gaa acc ctg gat cat tcc atc atg tac att ttc gcc gtc gcg ctt caa	480
Glu Thr Leu Asp His Ser Ile Met Tyr Ile Phe Ala Val Ala Leu Gln	
145 150 155 160	
gat ggc gtg tgg cac cac gag ttt tcc tac acc cgc aag cgt tcc acc	528
Asp Gly Val Trp His His Glu Phe Ser Tyr Thr Arg Lys Arg Ser Thr	
165 170 175	

cgc ccg gaa act gtg gag ctg tgg cac aag att cgc acc gtg gag gat 576
 Arg Pro Glu Thr Val Glu Leu Trp His Lys Ile Arg Thr Val Glu Asp
 180 185 190

cct gaa tgg acg cgc cga tac cat tct 603
Pro Glu Trp Thr Arg Arg Tyr His Ser
195 200

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<210> 618
<211> 201
<212> PRT
<213> Corynebacterium glutamicum
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<400> 618
 Thr Ala Thr Arg Gln Ser Arg Lys Gly Glu Ile Ser Ser Trp Lys Ala
 1 5 10 15

Phe Ala Pro Ala Phe Ala Gly Lys Met Ala Ile Glu Ala Met Asp Arg
20 25 30

Ala Met Arg Gly Glu Gly Ser Pro Ala Pro Ile Trp Glu Gly Glu Asp
35 40 45

Gly Val Ile Ala Trp Leu Leu Ser Gly Lys Asp His Val Tyr His Val
50 55 60

Pro Leu Pro Glu His Gly Glu Pro Lys Leu Gly Ile Leu Glu Thr Tyr
65 70 75 80

Thr Lys Glu His Ser Ala Glu Tyr Gln Ser Gln Ala Pro Ile Asp Leu
85 90 95

Ala Arg Arg Met Lys Pro Leu Val Asp Ala Ala Gly Gly Thr Glu His
100 105 110

Ile Ala Glu Ile Val Leu Arg Thr Ser His His Thr His Tyr Val Ile
115 120 125

Gly Thr Gly Ala Asn Asp Pro Gln Lys Met Asp Pro Gln Ala Ser Arg
130 135 140

Glu Thr Leu Asp His Ser Ile Met Tyr Ile Phe Ala Val Ala Leu Gln
145 150 155 160

Asp Gly Val Trp His His Glu Phe Ser Tyr Thr Arg Lys Arg Ser Thr
165 170 175

Arg Pro Glu Thr Val Glu Leu Trp His Lys Ile Arg Thr Val Glu Asp
180 185 190

Pro	Glu	Trp	Thr	Arg	Arg	Tyr	His	Ser
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<210> 619
<211> 1266
<212> DNA
<213> Corynebacterium glutamicum
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<220>

<221> CDS

<222> (101)..(1243)

<223> RXA02332

<400> 619

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tttgaccagc acattttcac ctacagaaaa ggagaaaaaca atg agt gac agc caa 115
                                         Met Ser Asp Ser Gln
                                         1 5

gtc cgc aaa gga ctc aac ggc gtc atc tct gac tac aca agc att tcc 163
Val Arg Lys Gly Leu Asn Gly Val Ile Ser Asp Tyr Thr Ser Ile Ser
                        10 15 20

aaa gtg atg cca gag agc aac tcg ctg act tac cgt ggc tac gcc gtg 211
Lys Val Met Pro Glu Ser Asn Ser Leu Thr Tyr Arg Gly Tyr Ala Val
                        25 30 35

gag gat ttg gtg gaa aac tgc agc ttt gaa gaa gtg atc tac ctc ctg 259
Glu Asp Leu Val Glu Asn Cys Ser Phe Glu Glu Val Ile Tyr Leu Leu
                        40 45 50

tgg ttt ggg gag ctg ccc acc act gaa caa ctc cgg acc ttc aac acg 307
Trp Phe Gly Glu Leu Pro Thr Thr Glu Gln Leu Arg Thr Phe Asn Thr
                        55 60 65

aca ggt cga agc tac cgc tca ctc gac gcc gga ctg att tcc ctc atc 355
Thr Gly Arg Ser Tyr Arg Ser Leu Asp Ala Gly Leu Ile Ser Leu Ile
                        70 75 80 85

cac tcc tta ccc aac acc tgc cac ccc atg gac gtg ctg cgc acc gca 403
His Ser Leu Pro Asn Thr Cys His Pro Met Asp Val Leu Arg Thr Ala
                        90 95 100

gtg tcc tac atg ggt acc ttt gat ccc gat ccg ttt acc cgc gat gcc 451
Val Ser Tyr Met Gly Thr Phe Asp Pro Asp Pro Phe Thr Arg Asp Ala
                        105 110 115

gat cat atc cga agc att gga cac aac ctg ctt gcg cag ctt ccc atg 499
Asp His Ile Arg Ser Ile Gly His Asn Leu Leu Ala Gln Leu Pro Met
                        120 125 130

gtg gtt gcc atg gat atc cgc agg cga agt ggg gaa gag atc atc gca 547
Val Val Ala Met Asp Ile Arg Arg Arg Ser Gly Glu Glu Ile Ile Ala
                        135 140 145

cct gac cac aac aaa ggt atc gct tcg aat ttc tta tcc atg gtg ttt 595
Pro Asp His Asn Lys Gly Ile Ala Ser Asn Phe Leu Ser Met Val Phe
                        150 155 160 165

ggc aat gat gat ggt tct gta gcc aac tcc gca gat gac atc cgc gat 643
Gly Asn Asp Asp Gly Ser Val Ala Asn Ser Ala Asp Asp Ile Arg Asp
                        170 175 180

ttt gaa cgc tcc ctc atc ctc tac gcc gag cac tcc ttc aac gcc tcc 691
Phe Glu Arg Ser Leu Ile Leu Tyr Ala Glu His Ser Phe Asn Ala Ser
                        185 190 195

aca ttc tca gcc cgc gtg atc tca tca acg cga tcc gat acg tat tcg 739

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Thr Phe Ser Ala Arg Val Ile Ser Ser Thr Arg Ser Asp Thr Tyr Ser
 200 205 210
 gcg atc aca ggt gcg atc ggt gct ctc aaa ggc cca ctg cac gga ggt 787
 Ala Ile Thr Gly Ala Ile Gly Ala Leu Lys Gly Pro Leu His Gly Gly
 215 220 225
 gcc aat gag ttt gtc atg cac acc atg ctg gat atc gac gat ccc aac 835
 Ala Asn Glu Phe Val Met His Thr Met Leu Asp Ile Asp Asp Pro Asn
 230 235 240 245
 aat gct gcc gac tgg atg ggc aag gcg ttg gat cgt aaa gaa cgc atc 883
 Asn Ala Ala Asp Trp Met Gly Lys Ala Leu Asp Arg Lys Glu Arg Ile
 250 255 260
 atg gga ttc ggg cac cgc gtg tac aaa aac ggc gac tcc agg gtc ccc 931
 Met Gly Phe Gly His Arg Val Tyr Lys Asn Gly Asp Ser Arg Val Pro
 265 270 275
 tcc atg gag aaa tcc atg cgc tcc ctt gct gct cgt cac cgt ggt caa 979
 Ser Met Glu Lys Ser Met Arg Ser Leu Ala Ala Arg His Arg Gly Gln
 280 285 290
 aaa tgg gtg cac atg tat gag tgc atg caa gaa gtc atg gag gct cgc 1027
 Lys Trp Val His Met Tyr Glu Ser Met Gln Glu Val Met Glu Ala Arg
 295 300 305
 act ggc att aaa ccc aac ctc gac ttc ccg gcc ggc cct gcc tat tac 1075
 Thr Gly Ile Lys Pro Asn Leu Asp Phe Pro Ala Gly Pro Ala Tyr Tyr
 310 315 320 325
 atg ctg gga ttc ccc gtc gac ttc ttc aca cca ctg ttt gtg ctg gcc 1123
 Met Leu Gly Phe Pro Val Asp Phe Phe Thr Pro Leu Phe Val Leu Ala
 330 335 340
 cga gtg tca ggg tgg acg gca cac atc gtg gag caa ttt gaa aac aat 1171
 Arg Val Ser Gly Trp Thr Ala His Ile Val Glu Gln Phe Glu Asn Asn
 345 350 355
 gcg ctg atc cga cca ttg tct gcc tac aac gga gtg gaa gaa agg gag 1219
 Ala Leu Ile Arg Pro Leu Ser Ala Tyr Asn Gly Val Glu Glu Arg Glu
 360 365 370
 gtg gtg ccc att tgc gag aga acc taatcagtgaggctgatttc taa 1266
 Val Val Pro Ile Ser Glu Arg Thr
 375 380

<210> 620

<211> 381

<212> PRT

<213> Corynebacterium glutamicum

<400> 620

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Tyr Thr Ser Ile Ser Lys Val Met Pro Glu Ser Asn Ser Leu Thr Tyr
 20 25 30

Arg Gly Tyr Ala Val Glu Asp Leu Val Glu Asn Cys Ser Phe Glu Glu

35					40					45					
Val	Ile	Tyr	Leu	Leu	Trp	Phe	Gly	Glu	Leu	Pro	Thr	Thr	Glu	Gln	Leu
50						55					60				
Arg	Thr	Phe	Asn	Thr	Thr	Gly	Arg	Ser	Tyr	Arg	Ser	Leu	Asp	Ala	Gly
65					70					75					80
Leu	Ile	Ser	Leu	Ile	His	Ser	Leu	Pro	Asn	Thr	Cys	His	Pro	Met	Asp
				85					90					95	
Val	Leu	Arg	Thr	Ala	Val	Ser	Tyr	Met	Gly	Thr	Phe	Asp	Pro	Asp	Pro
			100					105					110		
Phe	Thr	Arg	Asp	Ala	Asp	His	Ile	Arg	Ser	Ile	Gly	His	Asn	Leu	Leu
		115					120					125			
Ala	Gln	Leu	Pro	Met	Val	Val	Ala	Met	Asp	Ile	Arg	Arg	Arg	Ser	Gly
	130					135					140				
Glu	Glu	Ile	Ile	Ala	Pro	Asp	His	Asn	Lys	Gly	Ile	Ala	Ser	Asn	Phe
145					150					155					160
Leu	Ser	Met	Val	Phe	Gly	Asn	Asp	Asp	Gly	Ser	Val	Ala	Asn	Ser	Ala
				165					170					175	
Asp	Asp	Ile	Arg	Asp	Phe	Glu	Arg	Ser	Leu	Ile	Leu	Tyr	Ala	Glu	His
			180					185					190		
Ser	Phe	Asn	Ala	Ser	Thr	Phe	Ser	Ala	Arg	Val	Ile	Ser	Ser	Thr	Arg
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Ser	Asp	Thr	Tyr	Ser	Ala	Ile	Thr	Gly	Ala	Ile	Gly	Ala	Leu	Lys	Gly
	210					215					220				
Pro	Leu	His	Gly	Gly	Ala	Asn	Glu	Phe	Val	Met	His	Thr	Met	Leu	Asp
225					230					235					240
Ile	Asp	Asp	Pro	Asn	Asn	Ala	Ala	Asp	Trp	Met	Gly	Lys	Ala	Leu	Asp
				245					250					255	
Arg	Lys	Glu	Arg	Ile	Met	Gly	Phe	Gly	His	Arg	Val	Tyr	Lys	Asn	Gly
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Asp	Ser	Arg	Val	Pro	Ser	Met	Glu	Lys	Ser	Met	Arg	Ser	Leu	Ala	Ala
		275					280					285			
Arg	His	Arg	Gly	Gln	Lys	Trp	Val	His	Met	Tyr	Glu	Ser	Met	Gln	Glu
	290					295					300				
Val	Met	Glu	Ala	Arg	Thr	Gly	Ile	Lys	Pro	Asn	Leu	Asp	Phe	Pro	Ala
305					310					315					320
Gly	Pro	Ala	Tyr	Tyr	Met	Leu	Gly	Phe	Pro	Val	Asp	Phe	Phe	Thr	Pro
				325					330					335	
Leu	Phe	Val	Leu	Ala	Arg	Val	Ser	Gly	Trp	Thr	Ala	His	Ile	Val	Glu
			340					345					350		
Gln	Phe	Glu	Asn	Asn	Ala	Leu	Ile	Arg	Pro	Leu	Ser	Ala	Tyr	Asn	Gly
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 <223> RXN02333

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 Met Asn Leu Phe Ser
 1 5
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 Asn Gly Val Asp Val Gly Arg Arg Arg Gln Ala Phe Lys Ala Ala Leu
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 Ala Ala Pro His Ile Ala Arg Leu Pro Gly Ala Phe Ser Pro Leu Ile
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 Ala Arg Ser Ile Glu Glu Ala Gly Phe Glu Gly Val Tyr Val Ser Gly
 40 45 50
 gcc gtc ata gct gct gac ctg gca cta ccc gat atc ggc ttg acg acg 307
 Ala Val Ile Ala Ala Asp Leu Ala Leu Pro Asp Ile Gly Leu Thr Thr
 55 60 65
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 Leu Thr Glu Val Ala His Arg Ala Arg Gln Ile Ala Arg Val Thr Asp
 70 75 80 85
 cta gga gtg ctt gtc gac gcc gac acc ggc ttt ggc gaa ccc atg tcg 403
 Leu Gly Val Leu Val Asp Ala Asp Thr Gly Phe Gly Glu Pro Met Ser
 90 95 100
 gcc gca cgc acc gtc gcc gaa ttg gag gac gcc ggt gtg gcc gga tgc 451
 Ala Ala Arg Thr Val Ala Glu Leu Glu Asp Ala Gly Val Ala Gly Cys
 105 110 115
 cac ctt gaa gac caa gtc aac ccc aaa cgt tgc ggc cac ttg gac ggc 499
 His Leu Glu Asp Gln Val Asn Pro Lys Arg Cys Gly His Leu Asp Gly
 120 125 130
 aaa gaa gtc gtg cgc aca gac gtg atg gtt cga cgc atc gca gcc gcc 547
 Lys Glu Val Val Arg Thr Asp Val Met Val Arg Arg Ile Ala Ala Ala
 135 140 145
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 Val Ser Ala Arg Arg Asp Pro Asn Phe Val Ile Cys Ala Arg Thr Asp
 150 155 160 165

gcc gct gga gtg gaa gga atc gac gcc gcc att gag cgc gcg aaa gcc 643
 Ala Ala Gly Val Glu Gly Ile Asp Ala Ala Ile Glu Arg Ala Lys Ala
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 tac tta gat gcg ggc gcc gac atg att ttc acc gaa gcc ctc cac agc 691
 Tyr Leu Asp Ala Gly Ala Asp Met Ile Phe Thr Glu Ala Leu His Ser
 185 190 195
 gaa gcc gac ttc cga tac ttc cgg cac gcc atc cct gat gcc ttg ttg 739
 Glu Ala Asp Phe Arg Tyr Phe Arg His Ala Ile Pro Asp Ala Leu Leu
 200 205 210
 ctg gcg aat atg acc gaa ttt ggc aaa acg acg ctg ctg tca gcc gac 787
 Leu Ala Asn Met Thr Glu Phe Gly Lys Thr Thr Leu Leu Ser Ala Asp
 215 220 225
 gtg ttg gaa gag att ggc tac aac gcc gtg atc tac ccc gtg acc acg 835
 Val Leu Glu Glu Ile Gly Tyr Asn Ala Val Ile Tyr Pro Val Thr Thr
 230 235 240 245
 ctg cgt att gcc atg gga caa gta gaa caa gca cta gcc gaa atc aaa 883
 Leu Arg Ile Ala Met Gly Gln Val Glu Gln Ala Leu Ala Glu Ile Lys
 250 255 260
 gaa cac ggt acc caa gaa gga tgg ctg gac cgc atg caa cac cgc agc 931
 Glu His Gly Thr Gln Glu Gly Trp Leu Asp Arg Met Gln His Arg Ser
 265 270 275
 aga tta tat gag ctc ctg cga tac gaa gac tac aac gtc ttt gac cag 979
 Arg Leu Tyr Glu Leu Leu Arg Tyr Glu Asp Tyr Asn Val Phe Asp Gln
 280 285 290
 cac att ttc acc tac aga aaa gga gaa aac aat gag tgacagccaa 1025
 His Ile Phe Thr Tyr Arg Lys Gly Glu Asn Asn Glu
 295 300 305
 gtccgcaaaag gac 1038

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 35 40 45
 Val Tyr Val Ser Gly Ala Val Ile Ala Ala Asp Leu Ala Leu Pro Asp
 50 55 60
 Ile Gly Leu Thr Thr Leu Thr Glu Val Ala His Arg Ala Arg Gln Ile
 65 70 75 80

Ala Arg Val Thr Asp Leu Gly Val Leu Val Asp Ala Asp Thr Gly Phe
85 90 95

Gly Glu Pro Met Ser Ala Ala Arg Thr Val Ala Glu Leu Glu Asp Ala
100 105 110

Gly Val Ala Gly Cys His Leu Glu Asp Gln Val Asn Pro Lys Arg Cys
115 120 125

Gly His Leu Asp Gly Lys Glu Val Val Arg Thr Asp Val Met Val Arg
130 135 140

Arg Ile Ala Ala Ala Val Ser Ala Arg Arg Asp Pro Asn Phe Val Ile
145 150 155 160

Cys Ala Arg Thr Asp Ala Ala Gly Val Glu Gly Ile Asp Ala Ala Ile
165 170 175

Glu Arg Ala Lys Ala Tyr Leu Asp Ala Gly Ala Asp Met Ile Phe Thr
180 185 190

Glu Ala Leu His Ser Glu Ala Asp Phe Arg Tyr Phe Arg His Ala Ile
195 200 205

Pro Asp Ala Leu Leu Leu Ala Asn Met Thr Glu Phe Gly Lys Thr Thr
210 215 220

Leu Leu Ser Ala Asp Val Leu Glu Glu Ile Gly Tyr Asn Ala Val Ile
225 230 235 240

Tyr Pro Val Thr Thr Leu Arg Ile Ala Met Gly Gln Val Glu Gln Ala
245 250 255

Leu Ala Glu Ile Lys Glu His Gly Thr Gln Glu Gly Trp Leu Asp Arg
260 265 270

Met Gln His Arg Ser Arg Leu Tyr Glu Leu Leu Arg Tyr Glu Asp Tyr
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Glu
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 Thr Lys Leu Gly Phe Glu Leu Lys His Asp Val Thr Ala Gly Asp Tyr
 25 30 35
 cgc tgg ttg act gtt gtt gat cca gaa aac cca gat ggt gtg cag ctt 259
 Arg Trp Leu Thr Val Val Asp Pro Glu Asn Pro Asp Gly Val Gln Leu
 40 45 50
 ttg ttg gaa cca aac cag cac cca gat gca gcg act tac caa gct gga 307
 Leu Leu Glu Pro Asn Gln His Pro Asp Ala Ala Thr Tyr Gln Ala Gly
 55 60 65
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 Ile Lys Arg Asp Gly Ile Pro Ala Thr Gln Phe Tyr Val Asp Asp Val
 70 75 80 85
 cag gaa gaa tat gac agc ctc aag gat aaa ggc gtg gat ttc atc atg 403
 Gln Glu Glu Tyr Asp Ser Leu Lys Asp Lys Gly Val Asp Phe Ile Met
 90 95 100
 gaa cca acc gat gtg ggc cct tca gtg att gcc att ctc gat gac acc 451
 Glu Pro Thr Asp Val Gly Pro Ser Val Ile Ala Ile Leu Asp Asp Thr
 105 110 115
 gta gga aac cta att cag att gtt caa ttg aag cag aac taacccccgtg 500
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<210> 626

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<212> PRT

<213> Corynebacterium glutamicum

<400> 626

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 35 40 45
 Asp Gly Val Gln Leu Leu Leu Glu Pro Asn Gln His Pro Asp Ala Ala
 50 55 60
 Thr Tyr Gln Ala Gly Ile Lys Arg Asp Gly Ile Pro Ala Thr Gln Phe
 65 70 75 80
 Tyr Val Asp Asp Val Gln Glu Glu Tyr Asp Ser Leu Lys Asp Lys Gly
 85 90 95
 Val Asp Phe Ile Met Glu Pro Thr Asp Val Gly Pro Ser Val Ile Ala
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 115 120 125

Gln Asn
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Met Thr Ser Ile Pro
1 5
aat ttt tca gac atc cca ttg act gct gag aca cgt gca tcg gag tca 163
Asn Phe Ser Asp Ile Pro Leu Thr Ala Glu Thr Arg Ala Ser Glu Ser
10 15 20
cac aac gtt gac gcc ggc aag gtg tgg aac act ccc gaa ggc att gat 211
His Asn Val Asp Ala Gly Lys Val Trp Asn Thr Pro Glu Gly Ile Asp
25 30 35
gtc aag cgc gta ttc acg cag gct gac cgc gac gag gcg caa gcg gcg 259
Val Lys Arg Val Phe Thr Gln Ala Asp Arg Asp Glu Ala Gln Ala Ala
40 45 50
gga cat ccg gtg gat tct ttg cca ggt caa aag cca ttt atg cgc ggg 307
Gly His Pro Val Asp Ser Leu Pro Gly Gln Lys Pro Phe Met Arg Gly
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ccg tac cca act atg tac acc aat cag ccg tgg acg att cgc cag tac 355
Pro Tyr Pro Thr Met Tyr Thr Asn Gln Pro Trp Thr Ile Arg Gln Tyr
70 75 80 85
gca ggc ttt tca acc gcc gcg gaa tcc aat gcg ttt tat cgg agg aac 403
Ala Gly Phe Ser Thr Ala Ala Glu Ser Asn Ala Phe Tyr Arg Arg Asn
90 95 100
ctt gct gcg ggt caa aaa ggt ttg tcg gtt gcg ttc gat cta gcg acc 451
Leu Ala Ala Gly Gln Lys Gly Leu Ser Val Ala Phe Asp Leu Ala Thr
105 110 115
cac cgc ggt tat gac tcg gat aat gag cgc gtg gtc ggc gat gtg ggt 499
His Arg Gly Tyr Asp Ser Asp Asn Glu Arg Val Val Gly Asp Val Gly
120 125 130
atg gcc ggc gtg gcg att gat tcg att ttg gat atg cgt cag ctg ttt 547
Met Ala Gly Val Ala Ile Asp Ser Ile Leu Asp Met Arg Gln Leu Phe
135 140 145
gat ggc att gat ttg tcc agc gtg tcg gtg tcg atg acc atg aat ggc 595
Asp Gly Ile Asp Leu Ser Ser Val Ser Val Ser Met Thr Met Asn Gly
150 155 160 165

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Ala Val Leu Pro Ile Leu Ala Phe Tyr Ile Val Ala Ala Glu Glu Gln	
170 175 180	
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Gly Val Gly Pro Glu Gln Leu Ala Gly Thr Ile Gln Asn Asp Ile Leu	
185 190 195	
aaa gaa ttt atg gtg cgc aac acc tat att tat ccg ccg aag ccg tcg	739
Lys Glu Phe Met Val Arg Asn Thr Tyr Ile Tyr Pro Pro Lys Pro Ser	
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Met Arg Ile Ile Ser Asn Ile Phe Glu Tyr Thr Ser Leu Lys Met Pro	
215 220 225	
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Arg Phe Asn Ser Ile Ser Ile Ser Gly Tyr His Ile Gln Glu Ala Gly	
230 235 240 245	
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Ala Thr Ala Asp Leu Glu Leu Ala Tyr Thr Leu Ala Asp Gly Ile Glu	
250 255 260	
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Tyr Ile Arg Ala Gly Lys Glu Val Gly Leu Asp Val Asp Lys Phe Ala	
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Pro Arg Leu Ser Phe Phe Trp Gly Ile Ser Met Tyr Thr Phe Met Glu	
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Ile Ala Lys Leu Arg Ala Gly Arg Leu Leu Trp Ser Glu Leu Val Ala	
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Lys Phe Asp Pro Lys Asn Ala Lys Ser Gln Ser Leu Arg Thr His Ser	
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Gln Thr Ser Gly Trp Ser Leu Thr Ala Gln Asp Val Tyr Asn Asn Val	
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Ala Arg Thr Ala Ile Glu Ala Met Ala Ala Thr Gln Gly His Thr Gln	
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Ser Leu His Thr Asn Ala Leu Asp Glu Ala Leu Ala Leu Pro Thr Asp	
360 365 370	
ttc tct gct cgt atc gcc cga aac acc cag ctg ttg ctg cag cag gaa	1267
Phe Ser Ala Arg Ile Ala Arg Asn Thr Gln Leu Leu Leu Gln Gln Glu	
375 380 385	
tct ggc acg gtg cgt cca gtt gat cca tgg gcg ggc tcc tat tac gtg	1315
Ser Gly Thr Val Arg Pro Val Asp Pro Trp Ala Gly Ser Tyr Tyr Val	
390 395 400 405	

gag tgg ttg acc aat gag ctg gct aac cgc gcg cgc aag cac atc gat	1363
Glu Trp Leu Thr Asn Glu Leu Ala Asn Arg Ala Arg Lys His Ile Asp	
410 415 420	
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Glu Val Glu Glu Ala Gly Gly Met Ala Gln Ala Thr Ala Gln Gly Ile	
425 430 435	
cct aag ctg cgc att gag gaa tca gcg gca cgc acc cag gct cgc att	1459
Pro Lys Leu Arg Ile Glu Glu Ser Ala Ala Arg Thr Gln Ala Arg Ile	
440 445 450	
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Asp Ser Gly Arg Gln Ala Leu Ile Gly Val Asn Arg Tyr Val Ala Glu	
455 460 465	
gaa gat gag gaa att gaa gtc ctc aag gtt gac aac acc aag gtt cgc	1555
Glu Asp Glu Glu Ile Glu Val Leu Lys Val Asp Asn Thr Lys Val Arg	
470 475 480 485	
gca gaa cag ttg gct aaa ctc gcg caa ctg aaa gca gag cgc aac gat	1603
Ala Glu Gln Leu Ala Lys Leu Ala Gln Leu Lys Ala Glu Arg Asn Asp	
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Ala Glu Val Lys Ala Ala Leu Asp Ala Leu Thr Ala Ala Ala Arg Asn	
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gag cat aaa gag cca ggg gat ttg gat cag aac ctg ctc aaa ctt gcc	1699
Glu His Lys Glu Pro Gly Asp Leu Asp Gln Asn Leu Leu Lys Leu Ala	
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Val Asp Ala Ala Arg Ala Lys Ala Thr Ile Gly Glu Ile Ser Asp Ala	
535 540 545	
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Gly Val Tyr Lys Asp Glu Val Gly Lys Glu Gly Thr Val Ser Asn Val	
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Glu Arg Ala Ile Ala Leu Ala Asp Ala Phe Glu Ala Glu Glu Gly Arg	
585 590 595	
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Arg Pro Arg Ile Phe Ile Ala Lys Met Gly Gln Asp Gly His Asp Arg	
600 605 610	
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Gly Gln Lys Val Val Ala Ser Ala Tyr Ala Asp Leu Gly Met Asp Val	
615 620 625	
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Asp Val Gly Pro Leu Phe Gln Thr Pro Ala Glu Ala Arg Ala Ala	
630 635 640 645	
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Val Asp Ala Asp Val His Val Val Gly Met Ser Ser Leu Ala Ala Gly
650 655 660

cac ctc acc ttg ctg ccc gag ctg aag aaa gaa ctt gca gct ctt ggc 2131
His Leu Thr Leu Leu Pro Glu Leu Lys Lys Glu Leu Ala Ala Leu Gly
665 670 675

cgc gat gac att ctg gtc acc gtg ggc ggc gtc att ccg ccg ggc gat 2179
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680 685 690

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Phe Gln Asp Leu Tyr Asp Met Gly Ala Ala Ala Ile Tyr Pro Ser Gly
695 700 705

acc gtc atc gcg gag tcg gcg atc gat ctg atc acc cga ctc gcc gca 2275
Thr Val Ile Ala Glu Ser Ala Ile Asp Leu Ile Thr Arg Leu Ala Ala
710 715 720 725

cac ctg ggc ttt gac ctg gat gtg gat gtg aat gaa tgatcacggt 2321
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730 735

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Glu Ala Gln Ala Ala Gly His Pro Val Asp Ser Leu Pro Gly Gln Lys
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Pro Phe Met Arg Gly Pro Tyr Pro Thr Met Tyr Thr Asn Gln Pro Trp
65 70 75 80

Thr Ile Arg Gln Tyr Ala Gly Phe Ser Thr Ala Ala Glu Ser Asn Ala
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Phe Tyr Arg Arg Asn Leu Ala Ala Gly Gln Lys Gly Leu Ser Val Ala
100 105 110

Phe Asp Leu Ala Thr His Arg Gly Tyr Asp Ser Asp Asn Glu Arg Val
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Val Gly Asp Val Gly Met Ala Gly Val Ala Ile Asp Ser Ile Leu Asp
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Met Arg Gln Leu Phe Asp Gly Ile Asp Leu Ser Ser Val Ser Val Ser
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Met Thr Met Asn Gly Ala Val Leu Pro Ile Leu Ala Phe Tyr Ile Val
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 225 230 235 240
 Ile Gln Glu Ala Gly Ala Thr Ala Asp Leu Glu Leu Ala Tyr Thr Leu
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 325 330 335
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 465 470 475 480

Asn Thr Lys Val Arg Ala Glu Gln Leu Ala Lys Leu Ala Gln Leu Lys
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 515 520 525
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 Glu Ile Ser Asp Ala Leu Glu Val Val Phe Gly Arg His Glu Ala Glu
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 565 570 575
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 Ala Glu Glu Gly Arg Arg Pro Arg Ile Phe Ile Ala Lys Met Gly Gln
 595 600 605
 Asp Gly His Asp Arg Gly Gln Lys Val Val Ala Ser Ala Tyr Ala Asp
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 Leu Gly Met Asp Val Asp Val Gly Pro Leu Phe Gln Thr Pro Ala Glu
 625 630 635 640
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 645 650 655
 Ser Leu Ala Ala Gly His Leu Thr Leu Leu Pro Glu Leu Lys Lys Glu
 660 665 670
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Val Lys Arg Val Phe Thr Gln Ala Asp Arg Asp Glu Ala Gln Ala Ala
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Gly His Pro Val Asp Ser Leu Pro Gly Gln Lys Pro Phe Met Arg Gly
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ccg tac cca act atg tac acc aat cag ccg tgg acg att cgc cag tac 355
Pro Tyr Pro Thr Met Tyr Thr Asn Gln Pro Trp Thr Ile Arg Gln Tyr
                        70                75                80                85

gca ggc ttt tca acc gcc gcg gaa tcc aat gcg ttt tat cgg agg aac 403
Ala Gly Phe Ser Thr Ala Ala Glu Ser Asn Ala Phe Tyr Arg Arg Asn
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ctt gct gcg ggt caa aaa ggt ttg tcg gtt gcg ttc gat cta gcg acc 451
Leu Ala Ala Gly Gln Lys Gly Leu Ser Val Ala Phe Asp Leu Ala Thr
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cac cgc ggt tat gac tcg gat aat gag cgc gtg gtc ggc gat gtg ggt 499
His Arg Gly Tyr Asp Ser Asp Asn Glu Arg Val Val Gly Asp Val Gly
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atg gcc ggc gtg gcg att gat tcg att ttg gat atg cgt cag ctg ttt 547
Met Ala Gly Val Ala Ile Asp Ser Ile Leu Asp Met Arg Gln Leu Phe
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gat ggc att gat ttg tcc agc gtg tcg gtg tcg atg acc atg aat ggc 595
Asp Gly Ile Asp Leu Ser Ser Val Ser Val Ser Met Thr Met Asn Gly
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gct gtg ctg ccg att ctt gcg ttc tat atc gtg gcg gct gag gaa caa 643
Ala Val Leu Pro Ile Leu Ala Phe Tyr Ile Val Ala Ala Glu Glu Gln
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Gly Val Gly Pro Glu Gln Leu Ala Gly Thr Ile Gln Asn Asp Ile Leu
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aaa gaa ttt atg gtg cgc aac acc tat att tat ccg ccg aag ccg tcg 739
Lys Glu Phe Met Val Arg Asn Thr Tyr Ile Tyr Pro Pro Lys Pro Ser
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atg cgc atc att tcc aac atc ttt gag tac acc tcc ttg aag atg cca 787

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Arg	Phe	Asn	Ser	Ile	Ser	Ile	Ser	Gly	Tyr	His	Ile	Gln	Glu	Ala	Gly	
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gcg	act	gcc	gat	ttg	gag	ctg	gcc	tac	act	ctg	gcg	gat	ggt	att	gaa	883
Ala	Thr	Ala	Asp	Leu	Glu	Leu	Ala	Tyr	Thr	Leu	Ala	Asp	Gly	Ile	Glu	
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tac	atc	cgt	gca	ggt	aaa	gag	gta	ggc	ctt	gac	gtg	gat	aag	ttc	gcg	931
Tyr	Ile	Arg	Ala	Gly	Lys	Glu	Val	Gly	Leu	Asp	Val	Asp	Lys	Phe	Ala	
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cct	cgt	ctg	tcc	ttc	ttc	tgg	ggt	att	tct	atg	tac	acc	ttc	atg	gag	979
Pro	Arg	Leu	Ser	Phe	Phe	Trp	Gly	Ile	Ser	Met	Tyr	Thr	Phe	Met	Glu	
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atc	gca	aag	ctg	cgt	gcg	gga	cga	ctg	ctg	tgg	agc	gag	ttg	gtg	gca	1027
Ile	Ala	Lys	Leu	Arg	Ala	Gly	Arg	Leu	Leu	Trp	Ser	Glu	Leu	Val	Ala	
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Lys	Phe	Asp	Pro	Lys	Asn	Ala	Lys	Ser	Gln	Ser	Leu	Arg	Thr	His	Ser	
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cag	acc	tct	ggt	tgg	tcg	ttg	acc	gcg	cag	gat	gtg	tac	aac	aac	gtc	1123
Gln	Thr	Ser	Gly	Trp	Ser	Leu	Thr	Ala	Gln	Asp	Val	Tyr	Asn	Asn	Val	
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gcc	cgc	acc	gcg	att	gag	gcg	atg	gct	gca	acc	cag	ggc	cac	acc	cag	1171
Ala	Arg	Thr	Ala	Ile	Glu	Ala	Met	Ala	Ala	Thr	Gln	Gly	His	Thr	Gln	
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Ser	Leu	His	Thr	Asn	Ala	Leu	Asp	Glu	Ala	Leu	Ala	Leu	Pro	Thr	Asp	
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Phe	Ser	Ala	Arg	Ile	Ala	Arg	Asn	Thr	Gln	Leu	Leu	Leu	Gln	Gln	Glu	
	375					380					385					
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Ser	Gly	Thr	Val	Arg	Pro	Val	Asp	Pro	Trp	Ala	Gly	Ser	Tyr	Tyr	Val	
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gag	tgg	ttg	acc	aat	gag	ctg	gct	aac	cgc	gcg	cgc	aag	cac	atc	gat	1363
Glu	Trp	Leu	Thr	Asn	Glu	Leu	Ala	Asn	Arg	Ala	Arg	Lys	His	Ile	Asp	
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gag	gtg	gag	gaa	gcc	ggc	gga	atg	gcg	cag	gcc	acc	gcg	cag	gga	att	1411
Glu	Val	Glu	Glu	Ala	Gly	Gly	Met	Ala	Gln	Ala	Thr	Ala	Gln	Gly	Ile	
			425					430					435			
cct	aag	ctg	cgc	att	gag	gaa	tca	gcg	gca	cgc	acc	cag	gct	cgc	att	1459
Pro	Lys	Leu	Arg	Ile	Glu	Glu	Ser	Ala	Ala	Arg	Thr	Gln	Ala	Arg	Ile	
		440					445					450				
gat	tcc	ggc	cgc	cag	gcg	ctg	atc	ggc	gtg	aat	cgc	tac	gtg	gcg	gaa	1507
Asp	Ser	Gly	Arg	Gln	Ala	Leu	Ile	Gly	Val	Asn	Arg	Tyr	Val	Ala	Glu	

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gca gaa cag ttg gct aaa ctc gcg caa ctg aaa gca gag cgc aac gat Ala Glu Gln Leu Ala Lys Leu Ala Gln Leu Lys Ala Glu Arg Asn Asp 490 495 500			1603
gcg gaa gtc aag gct gcg ctg gat gcg ttg aca gct gct gcc cgc aac Ala Glu Val Lys Ala Ala Leu Asp Ala Leu Thr Ala Ala Arg Asn 505 510 515			1651
gag cat aaa gag cca ggg gat ttg gat cag aac ctg ctc aaa ctt gcc Glu His Lys Glu Pro Gly Asp Leu Asp Gln Asn Leu Leu Lys Leu Ala 520 525 530			1699
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gaa cgc gcg atc gcc ctg gct gac gcc ttt gag gct gag gaa ggc cgc Glu Arg Ala Ile Ala Leu Ala Asp Ala Phe Glu Ala Glu Glu Gly Arg 585 590 595			1891
cgc cca cgt atc ttt att gcc aag atg ggc cag gat gga cat gac cgt Arg Pro Arg Ile Phe Ile Ala Lys Met Gly Gln Asp Gly His Asp Arg 600 605 610			1939
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 35 40 45
 Glu Ala Gln Ala Ala Gly His Pro Val Asp Ser Leu Pro Gly Gln Lys
 50 55 60
 Pro Phe Met Arg Gly Pro Tyr Pro Thr Met Tyr Thr Asn Gln Pro Trp
 65 70 75 80
 Thr Ile Arg Gln Tyr Ala Gly Phe Ser Thr Ala Ala Glu Ser Asn Ala
 85 90 95
 Phe Tyr Arg Arg Asn Leu Ala Ala Gly Gln Lys Gly Leu Ser Val Ala
 100 105 110
 Phe Asp Leu Ala Thr His Arg Gly Tyr Asp Ser Asp Asn Glu Arg Val
 115 120 125
 Val Gly Asp Val Gly Met Ala Gly Val Ala Ile Asp Ser Ile Leu Asp
 130 135 140
 Met Arg Gln Leu Phe Asp Gly Ile Asp Leu Ser Ser Val Ser Val Ser
 145 150 155 160
 Met Thr Met Asn Gly Ala Val Leu Pro Ile Leu Ala Phe Tyr Ile Val
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 Ala Ala Glu Glu Gln Gly Val Gly Pro Glu Gln Leu Ala Gly Thr Ile
 180 185 190
 Gln Asn Asp Ile Leu Lys Glu Phe Met Val Arg Asn Thr Tyr Ile Tyr
 195 200 205
 Pro Pro Lys Pro Ser Met Arg Ile Ile Ser Asn Ile Phe Glu Tyr Thr
 210 215 220
 Ser Leu Lys Met Pro Arg Phe Asn Ser Ile Ser Ile Ser Gly Tyr His
 225 230 235 240
 Ile Gln Glu Ala Gly Ala Thr Ala Asp Leu Glu Leu Ala Tyr Thr Leu
 245 250 255
 Ala Asp Gly Ile Glu Tyr Ile Arg Ala Gly Lys Glu Val Gly Leu Asp
 260 265 270
 Val Asp Lys Phe Ala Pro Arg Leu Ser Phe Phe Trp Gly Ile Ser Met
 275 280 285
 Tyr Thr Phe Met Glu Ile Ala Lys Leu Arg Ala Gly Arg Leu Leu Trp
 290 295 300
 Ser Glu Leu Val Ala Lys Phe Asp Pro Lys Asn Ala Lys Ser Gln Ser
 305 310 315 320
 Leu Arg Thr His Ser Gln Thr Ser Gly Trp Ser Leu Thr Ala Gln Asp

325										330										335										
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Gln	Gly	His	Thr	Gln	Ser	Leu	His	Thr	Asn	Ala	Leu	Asp	Glu	Ala	Leu															
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Ala	Leu	Pro	Thr	Asp	Phe	Ser	Ala	Arg	Ile	Ala	Arg	Asn	Thr	Gln	Leu															
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Leu	Leu	Gln	Gln	Glu	Ser	Gly	Thr	Val	Arg	Pro	Val	Asp	Pro	Trp	Ala															
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Gly	Ser	Tyr	Tyr	Val	Glu	Trp	Leu	Thr	Asn	Glu	Leu	Ala	Asn	Arg	Ala															
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Arg	Lys	His	Ile	Asp	Glu	Val	Glu	Glu	Ala	Gly	Gly	Met	Ala	Gln	Ala															
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Thr	Gln	Ala	Arg	Ile	Asp	Ser	Gly	Arg	Gln	Ala	Leu	Ile	Gly	Val	Asn															
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Arg	Tyr	Val	Ala	Glu	Glu	Asp	Glu	Glu	Ile	Glu	Val	Leu	Lys	Val	Asp															
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Asn	Thr	Lys	Val	Arg	Ala	Glu	Gln	Leu	Ala	Lys	Leu	Ala	Gln	Leu	Lys															
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Ala	Glu	Arg	Asn	Asp	Ala	Glu	Val	Lys	Ala	Ala	Leu	Asp	Ala	Leu	Thr															
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Ala	Ala	Ala	Arg	Asn	Glu	His	Lys	Glu	Pro	Gly	Asp	Leu	Asp	Gln	Asn															
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Leu	Leu	Lys	Leu	Ala	Val	Asp	Ala	Ala	Arg	Ala	Lys	Ala	Thr	Ile	Gly															
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Glu	Ile	Ser	Asp	Ala	Leu	Glu	Val	Val	Phe	Gly	Arg	His	Glu	Ala	Glu															
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Ile	Arg	Thr	Leu	Ser	Gly	Val	Tyr	Lys	Asp	Glu	Val	Gly	Lys	Glu	Gly															
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Thr	Val	Ser	Asn	Val	Glu	Arg	Ala	Ile	Ala	Leu	Ala	Asp	Ala	Phe	Glu															
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Ala	Glu	Glu	Gly	Arg	Arg	Pro	Arg	Ile	Phe	Ile	Ala	Lys	Met	Gly	Gln															
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Ala	Ala	Arg	Ala	Ala	Val	Asp	Ala	Asp	Val	His	Val	Val	Gly	Met	Ser															
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 Leu Thr Asp Leu Thr
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 aag act gcg gtg ccc gag gaa ctt tca gag aac ctc gaa act tgg tac 163
 Lys Thr Ala Val Pro Glu Glu Leu Ser Glu Asn Leu Glu Thr Trp Tyr
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 Lys Ala Val Ala Gly Val Phe Ala Arg Thr Gln Lys Lys Asp Ile Gly
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 Asp Ile Ala Val Asp Val Trp Lys Lys Leu Ile Val Thr Thr Pro Asp
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 Gly Val Asp Ile Asn Pro Leu Tyr Thr Arg Ala Asp Glu Ser Gln Arg
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 Lys Phe Thr Glu Val Pro Gly Glu Phe Pro Phe Thr Arg Gly Thr Thr
 70 75 80 85
 gtt gat ggt gaa cgc gtt ggt tgg ggt gtt act gag act ttc gga cat 403
 Val Asp Gly Glu Arg Val Gly Trp Gly Val Thr Glu Thr Phe Gly His
 90 95 100
 gac agc ccg aag aat atc aac gct gcg gtg ctg aat gct ctg aat tct 451
 Asp Ser Pro Lys Asn Ile Asn Ala Ala Val Leu Asn Ala Leu Asn Ser
 105 110 115
 ggc acc acc aca ttg ggt ttt gag ttc tct gag gaa ttc acg gca gct 499
 Gly Thr Thr Thr Leu Gly Phe Glu Phe Ser Glu Glu Phe Thr Ala Ala
 120 125 130
 gat ctt aaa gtt gct ctc gaa ggc gtg tat ctc aac atg gct ccg ttg 547
 Asp Leu Lys Val Ala Leu Glu Gly Val Tyr Leu Asn Met Ala Pro Leu
 135 140 145
 ctg att cat gcg ggt gga tcc acg tca gag gtt gca gcg gcg ttg tat 595
 Leu Ile His Ala Gly Gly Ser Thr Ser Glu Val Ala Ala Ala Leu Tyr
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ctg gga ccg ttg tcc aag cac aat att cgc act ggt ttt act tcc aac 1651
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 505 510 515

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 550 555 560 565

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 Val Glu Lys Leu Arg Glu Ala Gly Val Glu Arg Ile Leu Leu Ala Gly
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 Val Thr Thr Pro Asp Gly Val Asp Ile Asn Pro Leu Tyr Thr Arg Ala
 50 55 60
 Asp Glu Ser Gln Arg Lys Phe Thr Glu Val Pro Gly Glu Phe Pro Phe
 65 70 75 80
 Thr Arg Gly Thr Thr Val Asp Gly Glu Arg Val Gly Trp Gly Val Thr
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 Glu Thr Phe Gly His Asp Ser Pro Lys Asn Ile Asn Ala Ala Val Leu
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 115 120 125
 Glu Phe Thr Ala Ala Asp Leu Lys Val Ala Leu Glu Gly Val Tyr Leu
 130 135 140
 Asn Met Ala Pro Leu Leu Ile His Ala Gly Gly Ser Thr Ser Glu Val
 145 150 155 160
 Ala Ala Ala Leu Tyr Thr Leu Ala Glu Glu Ala Gly Thr Phe Phe Ala
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 Ala Leu Thr Leu Gly Ser Arg Pro Leu Thr Ala Gln Val Asp Gly Ser
 180 185 190
 His Ser Asp Thr Ile Glu Glu Ala Val Gln Leu Ala Val Asn Ala Ser
 195 200 205
 Lys Arg Ala Asn Val Arg Ala Ile Leu Val Asp Gly Ser Ser Phe Ser
 210 215 220
 Asn Gln Gly Ala Ser Asp Ala Gln Glu Ile Gly Leu Ser Ile Ala Ala
 225 230 235 240
 Gly Val Asp Tyr Val Arg Arg Leu Val Asp Ala Gly Leu Ser Thr Glu
 245 250 255
 Ala Ala Leu Lys Gln Val Ala Phe Arg Phe Ala Val Thr Asp Glu Gln
 260 265 270
 Phe Ala Gln Ile Ser Lys Leu Arg Val Ala Arg Arg Leu Trp Ala Arg
 275 280 285
 Val Cys Glu Val Leu Gly Phe Pro Glu Leu Ala Val Ala Pro Gln His
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 Ala Val Thr Ala Arg Ala Met Phe Ser Gln Arg Asp Pro Trp Val Asn
 305 310 315 320

Met Leu Arg Ser Thr Val Ala Ala Phe Ala Ala Gly Val Gly Gly Ala
 325 330 335
 Thr Asp Val Glu Val Arg Thr Phe Asp Asp Ala Ile Pro Asp Gly Val
 340 345 350
 Pro Gly Val Ser Arg Asn Phe Ala His Arg Ile Ala Arg Asn Thr Asn
 355 360 365
 Leu Leu Leu Leu Glu Glu Ser His Leu Gly His Val Val Asp Pro Ala
 370 375 380
 Gly Gly Ser Tyr Phe Val Glu Ser Phe Thr Asp Asp Leu Ala Glu Lys
 385 390 395 400
 Ala Trp Ala Val Phe Ser Gly Ile Glu Ala Glu Gly Gly Tyr Ser Ala
 405 410 415
 Ala Cys Ala Ser Gly Thr Val Thr Ala Met Leu Asp Gln Thr Trp Glu
 420 425 430
 Gln Thr Arg Ala Asp Val Ala Ser Arg Lys Lys Lys Leu Thr Gly Ile
 435 440 445
 Asn Glu Phe Pro Asn Leu Ala Glu Ser Pro Leu Pro Ala Asp Arg Arg
 450 455 460
 Val Glu Pro Ala Gly Val Arg Arg Trp Ala Ala Asp Phe Glu Ala Leu
 465 470 475 480
 Arg Asn Arg Ser Asp Ala Phe Leu Glu Lys Asn Gly Ala Arg Pro Gln
 485 490 495
 Ile Thr Met Ile Pro Leu Gly Pro Leu Ser Lys His Asn Ile Arg Thr
 500 505 510
 Gly Phe Thr Ser Asn Leu Leu Ala Ser Gly Gly Ile Glu Ala Ile Asn
 515 520 525
 Pro Gly Gln Leu Val Pro Gly Thr Asp Ala Phe Ala Glu Ala Ala Gln
 530 535 540
 Ala Ala Gly Ile Val Val Val Cys Gly Thr Asp Gln Glu Tyr Ala Glu
 545 550 555 560
 Thr Gly Glu Gly Ala Val Glu Lys Leu Arg Glu Ala Gly Val Glu Arg
 565 570 575
 Ile Leu Leu Ala Gly Ala Pro Lys Ser Phe Glu Gly Ser Ala His Ala
 580 585 590
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<211> 777

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<223> RXN00317

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                               Val Thr Thr Pro Ser
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aag aaa act ctg ctc ttt gat ctc gac gga acc ctc gtc gat tct ttc 163
Lys Lys Thr Leu Leu Phe Asp Leu Asp Gly Thr Leu Val Asp Ser Phe
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ccc ggt atc cgc act tca ttc ctt cac acc ctg cac gaa aag aac tgg 211
Pro Gly Ile Arg Thr Ser Phe Leu His Thr Leu His Glu Lys Asn Trp
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Glu Trp Thr Phe Gln Asp Leu Gly Met Thr Pro Glu Gln Ala Gln Asp
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Ala Leu Gln Thr Tyr Leu Glu His Tyr Gly Gln Val Gly Trp Asp Leu
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Glu Lys Val Leu Arg Lys Phe Glu Met Phe Asp Leu Phe Glu Phe Met
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Gly Ala Ala Thr Asp Ser Gly Asn Arg Arg Ser Lys Ser Ala Val Ile
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Lys His Val Leu Asp Ser Val Gly Leu Asp Glu Pro Asn Asp Ile Leu
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Met Ile Gly Asp Arg Ser His Asp Ile Glu Gly Ser Ser Glu Phe Gly
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atc gat tgt gtt gcc gta acc tgg ggc tac ggc agc aaa act gaa tgg 691
Ile Asp Cys Val Ala Val Thr Trp Gly Tyr Gly Ser Lys Thr Glu Trp

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185 190 195

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<400> 634

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 35 40 45

Pro Gly Pro Pro Met Glu Trp Thr Phe Gln Asp Leu Gly Met Thr Pro
 50 55 60

Glu Gln Ala Gln Asp Ala Leu Gln Thr Tyr Leu Glu His Tyr Gly Gln
 65 70 75 80

Val Gly Trp Asp Leu Ser Glu Ala Phe Pro Gly Met Arg Asp Leu Leu
 85 90 95

Ile Arg Leu Lys Tyr Glu Gly Phe Arg Leu Cys Thr Ala Thr Ser Lys
 100 105 110

Gly Glu Phe Phe Ala Glu Lys Val Leu Arg Lys Phe Glu Met Phe Asp
 115 120 125

Leu Phe Glu Phe Met Gly Ala Ala Thr Asp Ser Gly Asn Arg Arg Ser
 130 135 140

Lys Ser Ala Val Ile Lys His Val Leu Asp Ser Val Gly Leu Asp Glu
 145 150 155 160

Pro Asn Asp Ile Leu Met Ile Gly Asp Arg Ser His Asp Ile Glu Gly
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Ser Ser Glu Phe Gly Ile Asp Cys Val Ala Val Thr Trp Gly Tyr Gly
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His Glu Lys Asn Trp Glu Ile Pro Ser Glu Glu Arg Ile Ser Gln Val
          35          40          45
Pro Gly Pro Pro Met Glu Trp Thr Phe Gln Asp Leu Gly Met Thr Pro

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Glu Gln Ala Gln Asp Ala Leu Gln Thr Tyr Leu Glu His Tyr Gly Gln
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 Phe Trp Asp Met Asp Gly Thr Met Val Asp Ser Glu Pro Gln Trp Gly
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 Ile Ala Thr Tyr Glu Leu Ser Glu Ala Met Gly Arg Arg Leu Thr Pro
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 Glu Leu Arg Glu Leu Thr Val Gly Ser Ser Leu Pro Arg Thr Met Arg
 40 45 50
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 Leu Cys Ala Glu His Ala Gly Ile Thr Leu Ser Asp Ala Asp Tyr Glu
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 Arg Tyr Arg Ala Gly Met Phe Ala Arg Val His Glu Leu Phe Asp Glu
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 Ser Leu Val Pro Asn Pro Gly Val Thr Glu Leu Leu Thr Glu Leu Lys
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 gcg acc cgt tca gtc gca gcc gtg gga aat gag ttc ttc atc ggt tct 499

Ala Thr Arg Ser Val Ala Ala Val Gly Asn Glu Phe Phe Ile Gly Ser
 120 125 130

atc gct ggt gat gaa gtc cca aca gca aag cca gcc ccc gac atg tac 547
 Ile Ala Gly Asp Glu Val Pro Thr Ala Lys Pro Ala Pro Asp Met Tyr
 135 140 145

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 Leu Glu Ala Ala Arg Arg Val Gly Phe Asp Pro Ser Glu Cys Leu Val
 150 155 160 165

ttc gaa gat tcc tac aac ggc atg ctg ggc gct gtt act gca ggt tgc 643
 Phe Glu Asp Ser Tyr Asn Gly Met Leu Gly Ala Val Thr Ala Gly Cys
 170 175 180

cgc gtc att ggt ctg cac cca gaa gaa gtc caa gcg cca gaa ggt gta 691
 Arg Val Ile Gly Leu His Pro Glu Glu Val Gln Ala Pro Glu Gly Val
 185 190 195

gtg cct ttg cgt tcc ctc cac ggt aaa aac tct ttc gaa ggt gtc acc 739
 Val Pro Leu Arg Ser Leu His Gly Lys Asn Ser Phe Glu Gly Val Thr
 200 205 210

gct gag atg gtc act gcc tgg tac cac cag atc gag ccg gca ggt gtc 787
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 35 40 45

Pro Arg Thr Met Arg Leu Cys Ala Glu His Ala Gly Ile Thr Leu Ser
 50 55 60

Asp Ala Asp Tyr Glu Arg Tyr Arg Ala Gly Met Phe Ala Arg Val His
 65 70 75 80

Glu Leu Phe Asp Glu Ser Leu Val Pro Asn Pro Gly Val Thr Glu Leu
 85 90 95

Leu Thr Glu Leu Lys Ala Leu Glu Ile Pro Met Leu Val Thr Thr Asn
 100 105 110

Thr Glu Arg Asp Leu Ala Thr Arg Ser Val Ala Ala Val Gly Asn Glu
 115 120 125

Phe Phe Ile Gly Ser Ile Ala Gly Asp Glu Val Pro Thr Ala Lys Pro
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 Ala Pro Asp Met Tyr Leu Glu Ala Ala Arg Arg Val Gly Phe Asp Pro
 145 150 155 160
 Ser Glu Cys Leu Val Phe Glu Asp Ser Tyr Asn Gly Met Leu Gly Ala
 165 170 175
 Val Thr Ala Gly Cys Arg Val Ile Gly Leu His Pro Glu Glu Val Gln
 180 185 190
 Ala Pro Glu Gly Val Val Pro Leu Arg Ser Leu His Gly Lys Asn Ser
 195 200 205
 Phe Glu Gly Val Thr Ala Glu Met Val Thr Ala Trp Tyr His Gln Ile
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 Met Arg Gly Leu Ile
 1 5
 gtt gac tac gct gga gta cta gac gga acc gat gag gac cag cgt cgc 163
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 Trp Arg Asn Leu Leu Ala Ala Ala Lys Lys Asn Gly Val Gly Thr Val
 25 30 35
 atc ctc agc aac gat cca ggt ggg ctc ggc gca gcg ccg atc cgg gaa 259
 Ile Leu Ser Asn Asp Pro Gly Gly Leu Gly Ala Ala Pro Ile Arg Glu
 40 45 50
 ctc gaa aca aac ggg gta gtc gat aag gtg ctg ctg tcg gga gaa ctt 307
 Leu Glu Thr Asn Gly Val Val Asp Lys Val Leu Leu Ser Gly Glu Leu
 55 60 65
 ggc gtc gaa aag cca gag gaa gca gct ttc cag gcc gcc gca gac gcc 355
 Gly Val Glu Lys Pro Glu Glu Ala Ala Phe Gln Ala Ala Ala Asp Ala
 70 75 80 85
 atc gac ctg ccc atg cgt gac tgc gtg ctt gtc gac gac tcg atc ctc 403

Ile Asp Leu Pro Met Arg Asp Cys Val Leu Val Asp Asp Ser Ile Leu
 90 95 100

aac gtg cgc ggc gcc gtc gaa gcc gga ctc gta ggc gtc tac tac cag 451
 Asn Val Arg Gly Ala Val Glu Ala Gly Leu Val Gly Val Tyr Tyr Gln
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<210> 640
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 <213> Corynebacterium glutamicum

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 20 25 30

Gly Val Gly Thr Val Ile Leu Ser Asn Asp Pro Gly Gly Leu Gly Ala
 35 40 45

Ala Pro Ile Arg Glu Leu Glu Thr Asn Gly Val Val Asp Lys Val Leu
 50 55 60

Leu Ser Gly Glu Leu Gly Val Glu Lys Pro Glu Glu Ala Ala Phe Gln
 65 70 75 80

Ala Ala Ala Asp Ala Ile Asp Leu Pro Met Arg Asp Cys Val Leu Val
 85 90 95

Asp Asp Ser Ile Leu Asn Val Arg Gly Ala Val Glu Ala Gly Leu Val
 100 105 110

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 <223> RXN01744

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Ile	Ala	Arg	Trp	Gln	Phe	Gly	Ile	Thr	Thr	Val	Tyr	His	Phe	Ile	Phe	
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gtc	cca	ctg	acc	att	ggc	tta	gcg	ccg	ctg	gtc	gca	atc	atg	caa	acg	211
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Phe	Gly	Thr	Val	Leu	Leu	Ile	Asn	Phe	Ala	Val	Gly	Val	Ala	Thr	Gly	
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Ile	Val	Gln	Glu	Phe	Gln	Phe	Gly	Met	Asn	Trp	Ser	Glu	Tyr	Ser	Arg	
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Phe	Val	Gly	Asp	Val	Phe	Gly	Gly	Pro	Leu	Ala	Leu	Glu	Gly	Leu	Ile	
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Ala	Phe	Pro	His	Ala	Val	Ala	Gly	Gly	Phe	Leu	Thr	Ala	Gly	Thr	Phe	
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 Gly Pro Ala Thr Pro Ile Gly Ser Asp Met Pro Met Thr Pro Leu Gln
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<211> 513

<212> PRT

<213> Corynebacterium glutamicum

<400> 642

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 35 40 45

Arg Ala Thr Arg Phe Phe Gly Thr Val Leu Leu Ile Asn Phe Ala Val
 50 55 60

Gly Val Ala Thr Gly Ile Val Gln Glu Phe Gln Phe Gly Met Asn Trp
 65 70 75 80

Ser Glu Tyr Ser Arg Phe Val Gly Asp Val Phe Gly Gly Pro Leu Ala
 85 90 95

Leu Glu Gly Leu Ile Ala Phe Phe Leu Glu Ser Val Phe Leu Gly Leu
 100 105 110

Trp Ile Phe Gly Trp Gly Lys Ile Pro Gly Trp Leu His Thr Ala Ser
 115 120 125

Ile Trp Ile Val Ala Ile Ala Thr Asn Ile Ser Ala Tyr Phe Ile Ile
 130 135 140

Val Ala Asn Ser Phe Met Gln His Pro Val Gly Ala Glu Tyr Asn Pro
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Glu Thr Gly Arg Ala Glu Leu Thr Asp Phe Trp Ala Leu Leu Thr Asn
 165 170 175

Ser Thr Ala Leu Ala Ala Phe Pro His Ala Val Ala Gly Gly Phe Leu
 180 185 190

Thr Ala Gly Thr Phe Val Leu Gly Ile Ser Gly Trp Trp Ile Ile Arg
 195 200 205

Ala His Arg Gln Ala Lys Lys Ala Glu Ser Glu Ile Glu Ser Lys His

210					215					220					
Ser	Met	His	Arg	Pro	Ala	Leu	Trp	Val	Gly	Trp	Trp	Thr	Thr	Val	Val
225					230					235					240
Ser	Ser	Val	Ala	Leu	Phe	Ile	Thr	Gly	Asp	Ile	Gln	Ala	Lys	Leu	Met
				245					250					255	
Phe	Val	Gln	Gln	Pro	Met	Lys	Met	Ala	Ser	Ala	Glu	Ser	Leu	Cys	Glu
			260					265					270		
Thr	Ala	Thr	Asp	Pro	Asn	Phe	Ser	Ile	Leu	Thr	Ile	Gly	Thr	His	Asn
		275					280					285			
Asn	Cys	Asp	Thr	Val	Thr	His	Leu	Ile	Asp	Val	Pro	Phe	Val	Leu	Pro
	290					295					300				
Phe	Leu	Ala	Glu	Gly	Lys	Phe	Thr	Gly	Val	Thr	Leu	Gln	Gly	Val	Asn
305					310					315					320
Gln	Leu	Gln	Ala	Ala	Ala	Glu	Gln	Ala	Tyr	Gly	Pro	Gly	Asn	Tyr	Ser
			325						330					335	
Pro	Asn	Leu	Phe	Val	Thr	Tyr	Trp	Ser	Phe	Arg	Ala	Met	Ile	Gly	Leu
			340					345					350		
Met	Leu	Gly	Ser	Leu	Ala	Ile	Ala	Ala	Ile	Ala	Trp	Leu	Leu	Leu	Arg
		355					360					365			
Lys	Lys	Arg	Thr	Pro	Thr	Gly	Lys	Ile	Ala	Arg	Leu	Phe	Gln	Ile	Gly
	370					375					380				
Ser	Leu	Ile	Ala	Ile	Pro	Phe	Pro	Phe	Leu	Ala	Asn	Ser	Ala	Gly	Trp
385					390					395					400
Ile	Phe	Thr	Glu	Met	Gly	Arg	Gln	Pro	Trp	Val	Val	His	Pro	Asn	Pro
			405						410				415		
Glu	Ser	Ala	Gly	Asp	Ala	Arg	Thr	Glu	Met	Ile	Arg	Met	Thr	Val	Asp
			420					425					430		
Met	Gly	Val	Ser	Asp	His	Ala	Pro	Trp	Gln	Val	Trp	Leu	Thr	Leu	Ile
		435					440					445			
Gly	Phe	Thr	Ile	Leu	Tyr	Leu	Ile	Leu	Phe	Val	Val	Trp	Val	Trp	Leu
	450					455					460				
Ile	Arg	Arg	Ala	Val	Leu	Ile	Gly	Pro	Pro	Glu	Glu	Gly	Ala	Pro	Ser
465					470					475					480
Val	Glu	Ala	Lys	Thr	Gly	Pro	Ala	Thr	Pro	Ile	Gly	Ser	Asp	Met	Pro
			485					490						495	
Met	Thr	Pro	Leu	Gln	Phe	Thr	Ala	Ala	Ala	Pro	Thr	Thr	Gly	Glu	Lys
			500				505						510		

Glu

<210> 643

<211> 238
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(238)
 <223> FRXA00055

<400> 643
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 gttcctgtca acctgcaatg gaagaggaag tgtacctagc gtg gat gtc gtc gac 115
 Val Asp Val Val Asp
 1 5
 atc gca cgg tgg caa ttc gga att acc acc gtc tat cac ttc att ttt 163
 Ile Ala Arg Trp Gln Phe Gly Ile Thr Thr Val Tyr His Phe Ile Phe
 10 15 20
 gtc cca ctg acc att ggc tta gca ccg ctg gtc gcg atc atg caa acg 211
 Val Pro Leu Thr Ile Gly Leu Ala Pro Leu Val Ala Ile Met Gln Thr
 25 30 35
 ttt tgg caa gtt acc ggc aaa gag cac 238
 Phe Trp Gln Val Thr Gly Lys Glu His
 40 45

<210> 644
 <211> 46
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 644
 Val Asp Val Val Asp Ile Ala Arg Trp Gln Phe Gly Ile Thr Thr Val
 1 5 10 15
 Tyr His Phe Ile Phe Val Pro Leu Thr Ile Gly Leu Ala Pro Leu Val
 20 25 30
 Ala Ile Met Gln Thr Phe Trp Gln Val Thr Gly Lys Glu His
 35 40 45

<210> 645
 <211> 1325
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (1)..(1302)
 <223> FRXA01744

<400> 645
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 Trp Ser Glu Tyr Ser Arg Phe Val Gly Asp Val Phe Gly Gly Pro Leu
 1 5 10 15
 gct ttg gag ggt ctt atc gcg ttc ttc ctt gag tct gta ttc ctg gga 96

Ala	Leu	Glu	Gly	Leu	Ile	Ala	Phe	Phe	Leu	Glu	Ser	Val	Phe	Leu	Gly	
			20					25						30		
ctg	tgg	att	ttc	gga	tgg	ggg	aag	att	cct	ggt	tgg	ttg	cac	act	gca	144
Leu	Trp	Ile	Phe	Gly	Trp	Gly	Lys	Ile	Pro	Gly	Trp	Leu	His	Thr	Ala	
			35				40					45				
tcc	att	tgg	atc	gtt	gct	att	gcg	acg	aat	att	tct	gcc	tat	ttc	atc	192
Ser	Ile	Trp	Ile	Val	Ala	Ile	Ala	Thr	Asn	Ile	Ser	Ala	Tyr	Phe	Ile	
			50			55					60					
atc	gtg	gcc	aac	tcg	ttt	atg	cag	cat	ccg	gtg	ggt	gct	gag	tat	aac	240
Ile	Val	Ala	Asn	Ser	Phe	Met	Gln	His	Pro	Val	Gly	Ala	Glu	Tyr	Asn	
			65			70				75					80	
cct	gag	act	ggt	cgt	gcg	gag	ctt	act	gat	ttt	tgg	gct	ctt	ctc	aca	288
Pro	Glu	Thr	Gly	Arg	Ala	Glu	Leu	Thr	Asp	Phe	Trp	Ala	Leu	Leu	Thr	
				85					90					95		
aac	tcc	acc	gcg	ctg	gct	gcg	ttc	ccg	cat	gct	gtt	gcc	ggt	ggt	ttt	336
Asn	Ser	Thr	Ala	Leu	Ala	Ala	Phe	Pro	His	Ala	Val	Ala	Gly	Gly	Phe	
			100					105					110			
tta	aca	gct	gga	act	ttc	gtt	ctc	gga	att	tcg	ggt	tgg	tgg	att	att	384
Leu	Thr	Ala	Gly	Thr	Phe	Val	Leu	Gly	Ile	Ser	Gly	Trp	Trp	Ile	Ile	
			115				120					125				
cgt	gcg	cac	cgt	cag	gcc	aag	aag	gct	gag	tcg	gaa	atc	gag	tcg	aag	432
Arg	Ala	His	Arg	Gln	Ala	Lys	Lys	Ala	Glu	Ser	Glu	Ile	Glu	Ser	Lys	
			130			135					140					
cat	tcg	atg	cac	agg	ccc	gcg	ttg	tgg	gtt	ggt	tgg	tgg	acc	aca	gtt	480
His	Ser	Met	His	Arg	Pro	Ala	Leu	Trp	Val	Gly	Trp	Trp	Thr	Thr	Val	
					150					155					160	
gtc	tct	tcc	gtg	gcg	ctg	ttc	atc	act	ggc	gat	atc	cag	gcg	aag	ctc	528
Val	Ser	Ser	Val	Ala	Leu	Phe	Ile	Thr	Gly	Asp	Ile	Gln	Ala	Lys	Leu	
				165					170					175		
atg	ttc	gtg	caa	cag	cca	atg	aag	atg	gcg	tcg	gcg	gaa	tcc	ttg	tgt	576
Met	Phe	Val	Gln	Gln	Pro	Met	Lys	Met	Ala	Ser	Ala	Glu	Ser	Leu	Cys	
			180				185						190			
gaa	acc	gcc	aca	gat	cca	aac	ttc	tcc	att	ctg	aca	att	ggt	acg	cac	624
Glu	Thr	Ala	Thr	Asp	Pro	Asn	Phe	Ser	Ile	Leu	Thr	Ile	Gly	Thr	His	
			195				200					205				
aac	aac	tgc	gat	acg	gta	acc	cac	ctg	atc	gat	gtt	ccg	ttt	gtg	ctt	672
Asn	Asn	Cys	Asp	Thr	Val	Thr	His	Leu	Ile	Asp	Val	Pro	Phe	Val	Leu	
		210				215					220					
cca	ttc	ttg	gct	gaa	gga	aaa	ttc	acc	ggt	gtg	act	ttg	cag	ggt	gta	720
Pro	Phe	Leu	Ala	Glu	Gly	Lys	Phe	Thr	Gly	Val	Thr	Leu	Gln	Gly	Val	
			225		230					235					240	
aac	cag	ctc	caa	gct	gca	gcg	gag	caa	gca	tac	ggt	cct	ggc	aac	tac	768
Asn	Gln	Leu	Gln	Ala	Ala	Ala	Glu	Gln	Ala	Tyr	Gly	Pro	Gly	Asn	Tyr	
				245					250					255		
tcc	cct	aac	ttg	ttt	gtc	acc	tac	tgg	tca	ttc	cgc	gca	atg	atc	ggc	816
Ser	Pro	Asn	Leu	Phe	Val	Thr	Tyr	Trp	Ser	Phe	Arg	Ala	Met	Ile	Gly	

260										265										270										
ctg atg ctt ggt tct ttg gct atc gct gcg att gcg tgg ctg ttg ctg	864																													
Leu Met Leu Gly Ser Leu Ala Ile Ala Ala Ile Ala Trp Leu Leu Leu																														
275	280	285																												
cgt aag aag cgc aca cca act gga aag att gct cgt ctg ttc cag atc	912																													
Arg Lys Lys Arg Thr Pro Thr Gly Lys Ile Ala Arg Leu Phe Gln Ile																														
290	295	300																												
ggc agc ctc att gct atc ccg ttc cca ttc ttg gcc aac tct gct ggt	960																													
Gly Ser Leu Ile Ala Ile Pro Phe Pro Phe Leu Ala Asn Ser Ala Gly																														
305	310	315	320																											
tgg atc ttc acc gag atg ggc cgc cag cct tgg gtg gtg cac ccg aac	1008																													
Trp Ile Phe Thr Glu Met Gly Arg Gln Pro Trp Val Val His Pro Asn																														
325	330	335																												
cct gaa tct gcc ggc gat gcc cga aca gag atg atc cgg atg act gtt	1056																													
Pro Glu Ser Ala Gly Asp Ala Arg Thr Glu Met Ile Arg Met Thr Val																														
340	345	350																												
gat atg ggt gta tct gat cat gcg cca tgg caa gtc tgg ctg act ctc	1104																													
Asp Met Gly Val Ser Asp His Ala Pro Trp Gln Val Trp Leu Thr Leu																														
355	360	365																												
att ggc ttc acg att ctc tat ctc att ttg ttc gtg gtg tgg gtg tgg	1152																													
Ile Gly Phe Thr Ile Leu Tyr Leu Ile Leu Phe Val Val Trp Val Trp																														
370	375	380																												
ctg att cgc cgc gca gtt ctg atc gga cca cca gag gaa ggc gct cca	1200																													
Leu Ile Arg Arg Ala Val Leu Ile Gly Pro Pro Glu Glu Gly Ala Pro																														
385	390	395	400																											
tcc gtg gag gca aag act gga ccg gca acc ccg att ggt tca gat atg	1248																													
Ser Val Glu Ala Lys Thr Gly Pro Ala Thr Pro Ile Gly Ser Asp Met																														
405	410	415																												
ccc atg aca ccg ctg caa ttt act gcc gct gcc cca acc aca ggt gaa	1296																													
Pro Met Thr Pro Leu Gln Phe Thr Ala Ala Ala Pro Thr Thr Gly Glu																														
420	425	430																												
aag gaa taaccatgga tctcaatacc ttt	1325																													
Lys Glu																														

<210> 646

<211> 434

<212> PRT

<213> Corynebacterium glutamicum

<400> 646

Trp Ser Glu Tyr Ser Arg Phe Val Gly Asp Val Phe Gly Gly Pro Leu
 1 5 10 15

Ala Leu Glu Gly Leu Ile Ala Phe Phe Leu Glu Ser Val Phe Leu Gly
 20 25 30

Leu Trp Ile Phe Gly Trp Gly Lys Ile Pro Gly Trp Leu His Thr Ala
 35 40 45

Ser Ile Trp Ile Val Ala Ile Ala Thr Asn Ile Ser Ala Tyr Phe Ile
 50 55 60
 Ile Val Ala Asn Ser Phe Met Gln His Pro Val Gly Ala Glu Tyr Asn
 65 70 75 80
 Pro Glu Thr Gly Arg Ala Glu Leu Thr Asp Phe Trp Ala Leu Leu Thr
 85 90 95
 Asn Ser Thr Ala Leu Ala Ala Phe Pro His Ala Val Ala Gly Gly Phe
 100 105 110
 Leu Thr Ala Gly Thr Phe Val Leu Gly Ile Ser Gly Trp Trp Ile Ile
 115 120 125
 Arg Ala His Arg Gln Ala Lys Lys Ala Glu Ser Glu Ile Glu Ser Lys
 130 135 140
 His Ser Met His Arg Pro Ala Leu Trp Val Gly Trp Trp Thr Thr Val
 145 150 155 160
 Val Ser Ser Val Ala Leu Phe Ile Thr Gly Asp Ile Gln Ala Lys Leu
 165 170 175
 Met Phe Val Gln Gln Pro Met Lys Met Ala Ser Ala Glu Ser Leu Cys
 180 185 190
 Glu Thr Ala Thr Asp Pro Asn Phe Ser Ile Leu Thr Ile Gly Thr His
 195 200 205
 Asn Asn Cys Asp Thr Val Thr His Leu Ile Asp Val Pro Phe Val Leu
 210 215 220
 Pro Phe Leu Ala Glu Gly Lys Phe Thr Gly Val Thr Leu Gln Gly Val
 225 230 235 240
 Asn Gln Leu Gln Ala Ala Ala Glu Gln Ala Tyr Gly Pro Gly Asn Tyr
 245 250 255
 Ser Pro Asn Leu Phe Val Thr Tyr Trp Ser Phe Arg Ala Met Ile Gly
 260 265 270
 Leu Met Leu Gly Ser Leu Ala Ile Ala Ala Ile Ala Trp Leu Leu Leu
 275 280 285
 Arg Lys Lys Arg Thr Pro Thr Gly Lys Ile Ala Arg Leu Phe Gln Ile
 290 295 300
 Gly Ser Leu Ile Ala Ile Pro Phe Pro Phe Leu Ala Asn Ser Ala Gly
 305 310 315 320
 Trp Ile Phe Thr Glu Met Gly Arg Gln Pro Trp Val Val His Pro Asn
 325 330 335
 Pro Glu Ser Ala Gly Asp Ala Arg Thr Glu Met Ile Arg Met Thr Val
 340 345 350
 Asp Met Gly Val Ser Asp His Ala Pro Trp Gln Val Trp Leu Thr Leu
 355 360 365

Ile Gly Phe Thr Ile Leu Tyr Leu Ile Leu Phe Val Val Trp Val Trp
 370 375 380

Leu Ile Arg Arg Ala Val Leu Ile Gly Pro Pro Glu Glu Gly Ala Pro
 385 390 395 400

Ser Val Glu Ala Lys Thr Gly Pro Ala Thr Pro Ile Gly Ser Asp Met
 405 410 415

Pro Met Thr Pro Leu Gln Phe Thr Ala Ala Ala Pro Thr Thr Gly Glu
 420 425 430

Lys Glu

<210> 647
 <211> 307
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(307)
 <223> RXA00379

<400> 647
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tgtggtggat gttgcggtgc cattggtaga tgaggcctaa atg tct gag att gtg 115
 Met Ser Glu Ile Val
 1 5

gta gcc caa agc atc ggc cag cag ttt gct gac gtc gca gct tcc ggg 163
 Val Ala Gln Ser Ile Gly Gln Gln Phe Ala Asp Val Ala Ala Ser Gly
 10 15 20

cca ctg ttc ctt ggc atc ctt gcc gca gcg ctc gca ggt ctg gtg tct 211
 Pro Leu Phe Leu Gly Ile Leu Ala Ala Leu Ala Gly Leu Val Ser
 25 30 35

ttt gcc agc ccg tgt gtt gtg ccg ttg gtg cca gga tat att tcc tac 259
 Phe Ala Ser Pro Cys Val Val Pro Leu Val Pro Gly Tyr Ile Ser Tyr
 40 45 50

ctc gcc ggc gtg gtc ggt ggg gaa gtg gaa tac agc gct cat gcc acc 307
 Leu Ala Gly Val Val Gly Gly Glu Val Glu Tyr Ser Ala His Ala Thr
 55 60 65

<210> 648
 <211> 69
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 648
 Met Ser Glu Ile Val Val Ala Gln Ser Ile Gly Gln Gln Phe Ala Asp
 1 5 10 15

Val Ala Ala Ser Gly Pro Leu Phe Leu Gly Ile Leu Ala Ala Ala Leu
 20 25 30

Ala Gly Leu Val Ser Phe Ala Ser Pro Cys Val Val Pro Leu Val Pro
 35 40 45

Gly Tyr Ile Ser Tyr Leu Ala Gly Val Val Gly Gly Glu Val Glu Tyr
 50 55 60

Ser Ala His Ala Thr
 65

<210> 649

<211> 362

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (1) .. (339)

<223> RXA00385

<400> 649

ctt ggc gga gtg ttc gct ctc ggt tgg acc cct tgt ttg ggc ccc acc 48
 Leu Gly Gly Val Phe Ala Leu Gly Trp Thr Pro Cys Leu Gly Pro Thr
 1 5 10 15

ctg gct gcg atc atc tcc att tct gca ggt act gaa ggc atg acc gct 96
 Leu Ala Ala Ile Ile Ser Ile Ser Ala Gly Thr Glu Gly Met Thr Ala
 20 25 30

gcg cgt ggc gtg atc tta att gtg ggt tac tgc ctc gga ctg ggg ctg 144
 Ala Arg Gly Val Ile Leu Ile Val Gly Tyr Cys Leu Gly Leu Gly Leu
 35 40 45

cgc ttc ctg ctg atc gcg ttg ggc tcc agc aag gca ctc acc gga gtc 192
 Pro Phe Leu Leu Ile Ala Leu Gly Ser Ser Lys Ala Leu Thr Gly Val
 50 55 60

gag tgg ttg cgc aag cat tcc cgc acc ctg caa att atc ggc ggt gtg 240
 Glu Trp Leu Arg Lys His Ser Arg Thr Leu Gln Ile Ile Gly Gly Val
 65 70 75 80

ttt ttg atc ttg gtc gga gta gcg ttg ctc tct ggc tca tgg gca att 288
 Phe Leu Ile Leu Val Gly Val Ala Leu Leu Ser Gly Ser Trp Ala Ile
 85 90 95

ttt atc aac tgg gtc cgt cag tgg acc gtt gaa tac ggc gca aca ctg 336
 Phe Ile Asn Trp Val Arg Gln Trp Thr Val Glu Tyr Gly Ala Thr Leu
 100 105 110

ctc tagaaaaaga ctttagtag gaa 362
 Leu

<210> 650

<211> 113

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 650

Leu Gly Gly Val Phe Ala Leu Gly Trp Thr Pro Cys Leu Gly Pro Thr
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 Leu Ala Ala Ile Ile Ser Ile Ser Ala Gly Thr Glu Gly Met Thr Ala
 20 25 30
 Ala Arg Gly Val Ile Leu Ile Val Gly Tyr Cys Leu Gly Leu Gly Leu
 35 40 45
 Pro Phe Leu Leu Ile Ala Leu Gly Ser Ser Lys Ala Leu Thr Gly Val
 50 55 60
 Glu Trp Leu Arg Lys His Ser Arg Thr Leu Gln Ile Ile Gly Gly Val
 65 70 75 80
 Phe Leu Ile Leu Val Gly Val Ala Leu Leu Ser Gly Ser Trp Ala Ile
 85 90 95
 Phe Ile Asn Trp Val Arg Gln Trp Thr Val Glu Tyr Gly Ala Thr Leu
 100 105 110
 Leu

<210> 651
 <211> 901
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(901)
 <223> RXA01743

<400> 651
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 ttactgccgc tgccccaacc acagggtgaaa aggaataacc atg gat ctc aat acc 115
 Met Asp Leu Asn Thr
 1 5
 ttt tgg ttt att ctc atc gca ttt ttg ttt gcg gga tac ttt ctc ctc 163
 Phe Trp Phe Ile Leu Ile Ala Phe Leu Phe Ala Gly Tyr Phe Leu Leu
 10 15 20
 gaa gga ttc gac ttc ggc gtc gga att ttg gca ccc atc atc ggt aaa 211
 Glu Gly Phe Asp Phe Gly Val Gly Ile Leu Ala Pro Ile Ile Gly Lys
 25 30 35
 gat tca gcg gct agg aac aca gtg atc cgt acg att ggc cct gtc tgg 259
 Asp Ser Ala Ala Arg Asn Thr Val Ile Arg Thr Ile Gly Pro Val Trp
 40 45 50
 gac gga aat gaa gtg tgg ctg atc gtg gca ggt ggc gct ttg ttt gct 307
 Asp Gly Asn Glu Val Trp Leu Ile Val Ala Gly Gly Ala Leu Phe Ala
 55 60 65
 gcc ttc cct gag tgg tac gca acg atg ttc tcc gga atg tat ctg ccg 355
 Ala Phe Pro Glu Trp Tyr Ala Thr Met Phe Ser Gly Met Tyr Leu Pro
 70 75 80 85

ctg ttc ctc gtg ctt gtg tcg ttg atc atg cgc gtg gtg ggc ctt gaa 403
 Leu Phe Leu Val Leu Val Ser Leu Ile Met Arg Val Val Gly Leu Glu
 90 95 100

tgg cgc aag aaa gtc gat gat cct cgt tgg caa aag tgg tct gac cgg 451
 Trp Arg Lys Lys Val Asp Asp Pro Arg Trp Gln Lys Trp Ser Asp Arg
 105 110 115

gcc atc ttt att ggt tct tgg act cca ccg ctg atg tgg gga ttc atc 499
 Ala Ile Phe Ile Gly Ser Trp Thr Pro Pro Leu Met Trp Gly Phe Ile
 120 125 130

ttc gcc aat att ttg cgt ggc atg ccc ctc aag gcg gat cac acc atc 547
 Phe Ala Asn Ile Leu Arg Gly Met Pro Leu Lys Ala Asp His Thr Ile
 135 140 145

gat gct gcg gca gcc ctt cct ggc atg gtc aac gtc ttc gcc att ctg 595
 Asp Ala Ala Ala Ala Leu Pro Gly Met Val Asn Val Phe Ala Ile Leu
 150 155 160 165

ggt gca ctt gcg ttc acc gca ctg ttc gcc ctt cat ggt ctc gca ttc 643
 Gly Ala Leu Ala Phe Thr Ala Leu Phe Ala Leu His Gly Leu Ala Phe
 170 175 180

atc cgc ctg aaa act gct ggt cgg gtg cgc acc gat gcg gcg aag gca 691
 Ile Arg Leu Lys Thr Ala Gly Arg Val Arg Thr Asp Ala Lys Ala
 185 190 195

gct cca gta gtc gca ctt ctt gct gcg gtg act ggt gga cct ttc gtg 739
 Ala Pro Val Val Ala Leu Leu Ala Ala Val Thr Gly Gly Pro Phe Val
 200 205 210

ttg tgg gct gcc atc gca tac ggc cgt tcc tgg tcc tgg atc ctc gca 787
 Leu Trp Ala Ala Ile Ala Tyr Gly Arg Ser Trp Ser Trp Ile Leu Ala
 215 220 225

gtg ctg atc atc gca gcg gtt ctc ggt gga gct ttc gca ctg atc aaa 835
 Val Leu Ile Ile Ala Ala Val Leu Gly Gly Ala Phe Ala Leu Ile Lys
 230 235 240 245

gac cgc gat gga tta agc ttc ctg tcc act tcc gtc gct gtc atc ggt 883
 Asp Arg Asp Gly Leu Ser Phe Leu Ser Thr Ser Val Ala Val Ile Gly
 250 255 260

gtc gtt gca ctg ctg ttt 901
 Val Val Ala Leu Leu Phe
 265

<210> 652
 <211> 267
 <212> PRT
 <213> *Corynebacterium glutamicum*

<400> 652
 Met Asp Leu Asn Thr Phe Trp Phe Ile Leu Ile Ala Phe Leu Phe Ala
 1 5 10 15
 Gly Tyr Phe Leu Leu Glu Gly Phe Asp Phe Gly Val Gly Ile Leu Ala
 20 25 30

Pro Ile Ile Gly Lys Asp Ser Ala Ala Arg Asn Thr Val Ile Arg Thr
 35 40 45
 Ile Gly Pro Val Trp Asp Gly Asn Glu Val Trp Leu Ile Val Ala Gly
 50 55 60
 Gly Ala Leu Phe Ala Ala Phe Pro Glu Trp Tyr Ala Thr Met Phe Ser
 65 70 75 80
 Gly Met Tyr Leu Pro Leu Phe Leu Val Leu Val Ser Leu Ile Met Arg
 85 90 95
 Val Val Gly Leu Glu Trp Arg Lys Lys Val Asp Asp Pro Arg Trp Gln
 100 105 110
 Lys Trp Ser Asp Arg Ala Ile Phe Ile Gly Ser Trp Thr Pro Pro Leu
 115 120 125
 Met Trp Gly Phe Ile Phe Ala Asn Ile Leu Arg Gly Met Pro Leu Lys
 130 135 140
 Ala Asp His Thr Ile Asp Ala Ala Ala Ala Leu Pro Gly Met Val Asn
 145 150 155 160
 Val Phe Ala Ile Leu Gly Ala Leu Ala Phe Thr Ala Leu Phe Ala Leu
 165 170 175
 His Gly Leu Ala Phe Ile Arg Leu Lys Thr Ala Gly Arg Val Arg Thr
 180 185 190
 Asp Ala Ala Lys Ala Ala Pro Val Val Ala Leu Leu Ala Ala Val Thr
 195 200 205
 Gly Gly Pro Phe Val Leu Trp Ala Ala Ile Ala Tyr Gly Arg Ser Trp
 210 215 220
 Ser Trp Ile Leu Ala Val Leu Ile Ile Ala Ala Val Leu Gly Gly Ala
 225 230 235 240
 Phe Ala Leu Ile Lys Asp Arg Asp Gly Leu Ser Phe Leu Ser Thr Ser
 245 250 255
 Val Ala Val Ile Gly Val Val Ala Leu Leu Phe
 260 265

<210> 653
 <211> 1779
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1756)
 <223> RXN02480

<400> 653
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 gacaggccat gcacgcaagg gcagcaaagc atgggttaatg atg acc acc acc gac 115

930

230	235	240	245	
att gtt tct gag atc att cct gtg ttc tcc cgt aag cca atg ttc ggt				883
Ile Val Ser Glu Ile Ile Pro Val Phe Ser Arg Lys Pro Met Phe Gly	250	255	260	
tac gtc ggc ctg atc ttc gca acc ttg tcc att ggt gca ctg tcc atg				931
Tyr Val Gly Leu Ile Phe Ala Thr Leu Ser Ile Gly Ala Leu Ser Met	265	270	275	
gct gtg tgg gct cac cac atg ttc gtt act ggc gca gtt ttg ctt ccg				979
Ala Val Trp Ala His His Met Phe Val Thr Gly Ala Val Leu Leu Pro	280	285	290	
ttc ttc tcc ttc atg acg ttc ctg att tcg gtt cct acc ggc gtt aag				1027
Phe Phe Ser Phe Met Thr Phe Leu Ile Ser Val Pro Thr Gly Val Lys	295	300	305	
ttc ttc aac tgg gtt gga acc atg tgg aag ggt cac atc act tgg gaa				1075
Phe Phe Asn Trp Val Gly Thr Met Trp Lys Gly His Ile Thr Trp Glu	310	315	320	325
acc cca atg atc tgg tct gtt ggc ttc atg gct acc ttc ctc ttc ggt				1123
Thr Pro Met Ile Trp Ser Val Gly Phe Met Ala Thr Phe Leu Phe Gly	330	335	340	
ggg ctg acc ggc att atg ctg gcg tcc cca cca ctg gac ttc cac ttg				1171
Gly Leu Thr Gly Ile Met Leu Ala Ser Pro Pro Leu Asp Phe His Leu	345	350	355	
gct gac tcc tac ttc ctg atc gcg cac ttc cac tac acc ctc ttc ggt				1219
Ala Asp Ser Tyr Phe Leu Ile Ala His Phe His Tyr Thr Leu Phe Gly	360	365	370	
acc gtg gtg ttc gca tcg tgt gca ggc gtt tac ttc tgg ttc ccg aag				1267
Thr Val Val Phe Ala Ser Cys Ala Gly Val Tyr Phe Trp Phe Pro Lys	375	380	385	
atg act ggc cgc atg atg gac gag cgt ctt ggc aag atc cac ttc tgg				1315
Met Thr Gly Arg Met Met Asp Glu Arg Leu Gly Lys Ile His Phe Trp	390	395	400	405
ttg acc ttc gtc ggt ttc cac gga acc ttc ctc atc cag cac tgg gtg				1363
Leu Thr Phe Val Gly Phe His Gly Thr Phe Leu Ile Gln His Trp Val	410	415	420	
ggc aac atg ggt atg cca cgt cgt tac gct gac tac ctg gat tct gat				1411
Gly Asn Met Gly Met Pro Arg Arg Tyr Ala Asp Tyr Leu Asp Ser Asp	425	430	435	
ggg ttc acc atc tac aac cag atc tcc acc gtg ttc tac ttc ctg ctt				1459
Gly Phe Thr Ile Tyr Asn Gln Ile Ser Thr Val Phe Tyr Phe Leu Leu	440	445	450	
ggc ctg tct gtc att cca ttc atc tgg aac gtc ttc aag tcc tgg cgc				1507
Gly Leu Ser Val Ile Pro Phe Ile Trp Asn Val Phe Lys Ser Trp Arg	455	460	465	
tac ggt gag ctc gtt acc gtt gat gat cct tgg ggt tac ggc aac tcc				1555
Tyr Gly Glu Leu Val Thr Val Asp Asp Pro Trp Gly Tyr Gly Asn Ser	470	475	480	485

ctg gag tgg gca acc tcc tgc cct cct cct cgc cac aac ttc gca tcc 1603
 Leu Glu Trp Ala Thr Ser Cys Pro Pro Pro Arg His Asn Phe Ala Ser
 490 495 500

ttg cct cgt atc cgc tcc gag cgc cct gcg ttc gag ctg cac tac ccg 1651
 Leu Pro Arg Ile Arg Ser Glu Arg Pro Ala Phe Glu Leu His Tyr Pro
 505 510 515

cac atg att gaa cgc atg cgc gca gag gca cac act gga cat cac gat 1699
 His Met Ile Glu Arg Met Arg Ala Glu Ala His Thr Gly His His Asp
 520 525 530

gat att aat gct cca gaa ttg ggt acc gcc cca gcc ctt gca tct gac 1747
 Asp Ile Asn Ala Pro Glu Leu Gly Thr Ala Pro Ala Leu Ala Ser Asp
 535 540 545

tcc agc cgc taaaagcgtc tgatttaagt cgg 1779
 Ser Ser Arg
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<210> 654
 <211> 552
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 654
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Ser Phe Ser Phe Phe Phe Leu Gly Gly Leu Met Ala Leu Leu Ile Arg
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Ala Glu Leu Phe Thr Pro Gly Leu Gln Phe Leu Ser Asn Glu Gln Phe
 35 40 45

Asn Gln Leu Phe Thr Met His Gly Thr Val Met Leu Leu Leu Tyr Gly
 50 55 60

Thr Pro Ile Val Trp Gly Phe Ala Asn Tyr Val Leu Pro Leu Gln Ile
 65 70 75 80

Gly Ala Pro Asp Val Ala Phe Pro Arg Leu Asn Ala Phe Gly Phe Trp
 85 90 95

Ile Thr Thr Val Gly Gly Val Ala Met Leu Thr Gly Phe Leu Thr Pro
 100 105 110

Gly Gly Ala Ala Asp Phe Gly Trp Thr Met Tyr Ser Pro Leu Ser Asp
 115 120 125

Ala Ile His Ser Pro Gly Leu Gly Ser Asp Met Trp Ile Val Gly Val
 130 135 140

Gly Ala Thr Gly Ile Gly Ser Val Ala Ser Ala Ile Asn Met Leu Thr
 145 150 155 160

Thr Ile Leu Cys Leu Arg Ala Pro Gly Met Thr Met Phe Arg Met Pro
 165 170 175

Ile Phe Thr Trp Asn Ile Phe Val Val Ser Val Leu Ala Leu Leu Ile
 180 185 190
 Phe Pro Leu Leu Leu Ala Ala Ala Leu Gly Val Leu Tyr Asp Arg Lys
 195 200 205
 Leu Gly Gly His Leu Tyr Asp Pro Ala Asn Gly Gly Ser Leu Leu Trp
 210 215 220
 Gln His Leu Phe Trp Phe Phe Gly His Pro Glu Val Tyr Val Leu Ala
 225 230 235 240
 Leu Pro Phe Phe Gly Ile Val Ser Glu Ile Ile Pro Val Phe Ser Arg
 245 250 255
 Lys Pro Met Phe Gly Tyr Val Gly Leu Ile Phe Ala Thr Leu Ser Ile
 260 265 270
 Gly Ala Leu Ser Met Ala Val Trp Ala His His Met Phe Val Thr Gly
 275 280 285
 Ala Val Leu Leu Pro Phe Phe Ser Phe Met Thr Phe Leu Ile Ser Val
 290 295 300
 Pro Thr Gly Val Lys Phe Phe Asn Trp Val Gly Thr Met Trp Lys Gly
 305 310 315 320
 His Ile Thr Trp Glu Thr Pro Met Ile Trp Ser Val Gly Phe Met Ala
 325 330 335
 Thr Phe Leu Phe Gly Gly Leu Thr Gly Ile Met Leu Ala Ser Pro Pro
 340 345 350
 Leu Asp Phe His Leu Ala Asp Ser Tyr Phe Leu Ile Ala His Phe His
 355 360 365
 Tyr Thr Leu Phe Gly Thr Val Val Phe Ala Ser Cys Ala Gly Val Tyr
 370 375 380
 Phe Trp Phe Pro Lys Met Thr Gly Arg Met Met Asp Glu Arg Leu Gly
 385 390 395 400
 Lys Ile His Phe Trp Leu Thr Phe Val Gly Phe His Gly Thr Phe Leu
 405 410 415
 Ile Gln His Trp Val Gly Asn Met Gly Met Pro Arg Arg Tyr Ala Asp
 420 425 430
 Tyr Leu Asp Ser Asp Gly Phe Thr Ile Tyr Asn Gln Ile Ser Thr Val
 435 440 445
 Phe Tyr Phe Leu Leu Gly Leu Ser Val Ile Pro Phe Ile Trp Asn Val
 450 455 460
 Phe Lys Ser Trp Arg Tyr Gly Glu Leu Val Thr Val Asp Asp Pro Trp
 465 470 475 480
 Gly Tyr Gly Asn Ser Leu Glu Trp Ala Thr Ser Cys Pro Pro Pro Arg
 485 490 495
 His Asn Phe Ala Ser Leu Pro Arg Ile Arg Ser Glu Arg Pro Ala Phe

500

505

510

Glu Leu His Tyr Pro His Met Ile Glu Arg Met Arg Ala Glu Ala His
 515 520 525

Thr Gly His His Asp Asp Ile Asn Ala Pro Glu Leu Gly Thr Ala Pro
 530 535 540

Ala Leu Ala Ser Asp Ser Ser Arg
 545 550

<210> 655

<211> 385

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(385)

<223> FRXA01919

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gacaggccat gcacgcaagg gcagcaaagc atgggtaatg atg acc acc acc gac 115
 Met Thr Thr Thr Asp
 1 5

cac aag cag ctg ggc att atg tac atc att atg tcc ttc agc ttc ttt 163
 His Lys Gln Leu Gly Ile Met Tyr Ile Ile Met Ser Phe Ser Phe Phe
 10 15 20

ttc ctc ggt ggc ttg atg gcc ctg ctt atc cga gcg gag ctt ttc acc 211
 Phe Leu Gly Gly Leu Met Ala Leu Leu Ile Arg Ala Glu Leu Phe Thr
 25 30 35

cct ggt ctg cag ttc ctg tct aat gag cag ttc aac cag ctg ttc acc 259
 Pro Gly Leu Gln Phe Leu Ser Asn Glu Gln Phe Asn Gln Leu Phe Thr
 40 45 50

atg cac gga act gtc atg ctg ctg ctg tac gga act cca att gtt tgg 307
 Met His Gly Thr Val Met Leu Leu Leu Tyr Gly Thr Pro Ile Val Trp
 55 60 65

ggg ttt gct aac tac gtc ctg cca ctt cca acc acc ang caa gcc ttc 355
 Gly Phe Ala Asn Tyr Val Leu Pro Leu Pro Thr Thr Xaa Gln Ala Phe
 70 75 80 85

tct aaa acc cgg gtg aac tct ccc agg gag 385
 Ser Lys Thr Arg Val Asn Ser Pro Arg Glu
 90 95

<210> 656

<211> 95

<212> PRT

<213> Corynebacterium glutamicum

<400> 656

Met Thr Thr Thr Asp His Lys Gln Leu Gly Ile Met Tyr Ile Ile Met

1	5	10	15
Ser Phe Ser Phe Phe Phe Leu Gly Gly Leu Met Ala Leu Leu Ile Arg	20	25	30
Ala Glu Leu Phe Thr Pro Gly Leu Gln Phe Leu Ser Asn Glu Gln Phe	35	40	45
Asn Gln Leu Phe Thr Met His Gly Thr Val Met Leu Leu Leu Tyr Gly	50	55	60
Thr Pro Ile Val Trp Gly Phe Ala Asn Tyr Val Leu Pro Leu Pro Thr	65	70	75
Thr Xaa Gln Ala Phe Ser Lys Thr Arg Val Asn Ser Pro Arg Glu	85	90	95

<210> 657

<211> 972

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(949)

<223> FRXA02480

<400> 657

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aagccaatgt tcgggttacg tcggcctgat cttcgcaacc ttg tcc att ggt gca 115
                                Leu Ser Ile Gly Ala
                                1 5

ctg tcc atg gct gtg tgg gct cac cac atg ttc gtt act ggc gca gtt 163
Leu Ser Met Ala Val Trp Ala His His Met Phe Val Thr Gly Ala Val
                                10 15 20

ttg ctt ccg ttc ttc tcc ttc atg acg ttc ctg att tcg gtt cct acc 211
Leu Leu Pro Phe Phe Ser Phe Met Thr Phe Leu Ile Ser Val Pro Thr
                                25 30 35

ggc gtt aag ttc ttc aac tgg gtt gga acc atg tgg aag ggt cac atc 259
Gly Val Lys Phe Phe Asn Trp Val Gly Thr Met Trp Lys Gly His Ile
                                40 45 50

act tgg gaa acc cca atg atc tgg tct gtt ggc ttc atg gct acc ttc 307
Thr Trp Glu Thr Pro Met Ile Trp Ser Val Gly Phe Met Ala Thr Phe
                                55 60 65

ctc ttc ggt ggt ctg acc ggc att atg ctg gcg tcc cca cca ctg gac 355
Leu Phe Gly Gly Leu Thr Gly Ile Met Leu Ala Ser Pro Pro Leu Asp
                                70 75 80 85

ttc cac ttg gct gac tcc tac ttc ctg atc gcg cac ttc cac tac acc 403
Phe His Leu Ala Asp Ser Tyr Phe Leu Ile Ala His Phe His Tyr Thr
                                90 95 100

ctc ttc ggt acc gtg gtg ttc gca tcg tgt gca ggc gtt tac ttc tgg 451
Leu Phe Gly Thr Val Val Phe Ala Ser Cys Ala Gly Val Tyr Phe Trp

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105	110	115	
ttc ccg aag atg act ggc cgc atg atg gac gag cgt ctt ggc aag atc			499
Phe Pro Lys Met Thr Gly Arg Met Met Asp Glu Arg Leu Gly Lys Ile			
120	125	130	
cac ttc tgg ttg acc ttc gtc ggt ttc cac gga acc ttc ctc atc cag			547
His Phe Trp Leu Thr Phe Val Gly Phe His Gly Thr Phe Leu Ile Gln			
135	140	145	
cac tgg gtg ggc aac atg ggt atg cca cgt cgt tac gct gac tac ctg			595
His Trp Val Gly Asn Met Gly Met Pro Arg Arg Tyr Ala Asp Tyr Leu			
150	155	160	165
gat tct gat ggt ttc acc atc tac aac cag atc tcc acc gtg ttc tac			643
Asp Ser Asp Gly Phe Thr Ile Tyr Asn Gln Ile Ser Thr Val Phe Tyr			
170	175	180	
ttc ctg ctt ggc ctg tct gtc att cca ttc atc tgg aac gtc ttc aag			691
Phe Leu Leu Gly Leu Ser Val Ile Pro Phe Ile Trp Asn Val Phe Lys			
185	190	195	
tcc tgg cgc tac ggt gag ctc gtt acc gtt gat gat cct tgg ggt tac			739
Ser Trp Arg Tyr Gly Glu Leu Val Thr Val Asp Asp Pro Trp Gly Tyr			
200	205	210	
ggc aac tcc ctg gag tgg gca acc tcc tgc cct cct cct cgc cac aac			787
Gly Asn Ser Leu Glu Trp Ala Thr Ser Cys Pro Pro Pro Arg His Asn			
215	220	225	
ttc gca tcc ttg cct cgt atc cgc tcc gag cgc cct gcg ttc gag ctg			835
Phe Ala Ser Leu Pro Arg Ile Arg Ser Glu Arg Pro Ala Phe Glu Leu			
230	235	240	245
cac tac ccg cac atg att gaa cgc atg cgc gca gag gca cac act gga			883
His Tyr Pro His Met Ile Glu Arg Met Arg Ala Glu Ala His Thr Gly			
250	255	260	
cat cac gat gat att aat gct cca gaa ttg ggt acc gcc cca gcc ctt			931
His His Asp Asp Ile Asn Ala Pro Glu Leu Gly Thr Ala Pro Ala Leu			
265	270	275	
gca tct gac tcc agc cgc taaaagcgtc tgatttaagt cgg			972
Ala Ser Asp Ser Ser Arg			
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<210> 658

<211> 283

<212> PRT

<213> Corynebacterium glutamicum

<400> 658

Leu Ser Ile Gly Ala Leu Ser Met Ala Val Trp Ala His His Met Phe
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Val Thr Gly Ala Val Leu Leu Pro Phe Phe Ser Phe Met Thr Phe Leu
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Ile S r Val Pro Thr Gly Val Lys Phe Phe Asn Trp Val Gly Thr Met
 35 40 45

Trp Lys Gly His Ile Thr Trp Glu Thr Pro Met Ile Trp Ser Val Gly
 50 55 60
 Phe Met Ala Thr Phe Leu Phe Gly Gly Leu Thr Gly Ile Met Leu Ala
 65 70 75 80
 Ser Pro Pro Leu Asp Phe His Leu Ala Asp Ser Tyr Phe Leu Ile Ala
 85 90 95
 His Phe His Tyr Thr Leu Phe Gly Thr Val Val Phe Ala Ser Cys Ala
 100 105 110
 Gly Val Tyr Phe Trp Phe Pro Lys Met Thr Gly Arg Met Met Asp Glu
 115 120 125
 Arg Leu Gly Lys Ile His Phe Trp Leu Thr Phe Val Gly Phe His Gly
 130 135 140
 Thr Phe Leu Ile Gln His Trp Val Gly Asn Met Gly Met Pro Arg Arg
 145 150 155 160
 Tyr Ala Asp Tyr Leu Asp Ser Asp Gly Phe Thr Ile Tyr Asn Gln Ile
 165 170 175
 Ser Thr Val Phe Tyr Phe Leu Leu Gly Leu Ser Val Ile Pro Phe Ile
 180 185 190
 Trp Asn Val Phe Lys Ser Trp Arg Tyr Gly Glu Leu Val Thr Val Asp
 195 200 205
 Asp Pro Trp Gly Tyr Gly Asn Ser Leu Glu Trp Ala Thr Ser Cys Pro
 210 215 220
 Pro Pro Arg His Asn Phe Ala Ser Leu Pro Arg Ile Arg Ser Glu Arg
 225 230 235 240
 Pro Ala Phe Glu Leu His Tyr Pro His Met Ile Glu Arg Met Arg Ala
 245 250 255
 Glu Ala His Thr Gly His His Asp Asp Ile Asn Ala Pro Glu Leu Gly
 260 265 270
 Thr Ala Pro Ala Leu Ala Ser Asp Ser Ser Arg
 275 280

<210> 659
 <211> 735
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(712)
 <223> FRXA02481

<400> 659
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	Met	Leu	Thr	Gly	Phe	
	1				5	
cta acc ccg ggt ggt gct gcc gac ttg ggt gga cca tgt act ccc cac						163
Leu Thr Pro Gly Gly Ala Ala Asp Leu Gly Gly Pro Cys Thr Pro His						
	10			15	20	
tgt ctg acg caa ttc act ccc cag gcc ttg gtt cta aca tgt gga ttg						211
Cys Leu Thr Gln Phe Thr Pro Gln Ala Leu Val Leu Thr Cys Gly Leu						
	25			30	35	
tcg ggt gtc ggt gca act ggt att ggc tcc gtt gct tcc gca att aac						259
Ser Gly Val Gly Ala Thr Gly Ile Gly Ser Val Ala Ser Ala Ile Asn						
	40			45	50	
atg ctc acc acc atc ctc tgc ctc cgc gca cct ggt atg acc atg ttc						307
Met Leu Thr Thr Ile Leu Cys Leu Arg Ala Pro Gly Met Thr Met Phe						
	55			60	65	
cgt atg cct att ttc acc tgg aat atc ttc gtt gtt tcc gtt ctt gct						355
Arg Met Pro Ile Phe Thr Trp Asn Ile Phe Val Val Ser Val Leu Ala						
	70			75	80	85
ctg ctg atc ttc cca ctg ctg ctc gct gct gca ctg ggt gtt ctg tat						403
Leu Leu Ile Phe Pro Leu Leu Leu Ala Ala Ala Leu Gly Val Leu Tyr						
	90			95	100	
gac cgc aag ctt ggt gga cac ctg tac gat cca gct aac ggc ggc tcc						451
Asp Arg Lys Leu Gly Gly His Leu Tyr Asp Pro Ala Asn Gly Gly Ser						
	105			110	115	
ctc ctg tgg cag cac ctg ttc tgg ttc ttc gga cac cct gag gtt tac						499
Leu Leu Trp Gln His Leu Phe Trp Phe Phe Gly His Pro Glu Val Tyr						
	120			125	130	
gtt ctg gcg ctg ccg ttc ttc ggc att gtt tct gag atc att cct gtg						547
Val Leu Ala Leu Pro Phe Phe Gly Ile Val Ser Glu Ile Ile Pro Val						
	135			140	145	
ttc tcc cgt aag cca atg ttc ggg tta cgt cgg cct gat ctt cgc aac						595
Phe Ser Arg Lys Pro Met Phe Gly Leu Arg Arg Pro Asp Leu Arg Asn						
	150			155	160	165
ctt gtc cat tgg tgc act gtc cat ggc tgt gtg ggc tca cca cat gtt						643
Leu Val His Trp Cys Thr Val His Gly Cys Val Gly Ser Pro His Val						
	170			175	180	
cgt tac tgg cgc agt ttt gct tcc gtt ctt ctc ctt cat gac gtt cct						691
Arg Tyr Trp Arg Ser Phe Ala Ser Val Leu Leu Leu His Asp Val Pro						
	185			190	195	
gat ttc ggt tcc tac cgg cgt taagttcttc aactgggttg gaa						735
Asp Phe Gly Ser Tyr Arg Arg						
	200					

<210> 660

<211> 204

<212> PRT

<213> Corynebacterium glutamicum

<400> 660

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 20 25 30

Leu Thr Cys Gly Leu Ser Gly Val Gly Ala Thr Gly Ile Gly Ser Val
 35 40 45

Ala Ser Ala Ile Asn Met Leu Thr Thr Ile Leu Cys Leu Arg Ala Pro
 50 55 60

Gly Met Thr Met Phe Arg Met Pro Ile Phe Thr Trp Asn Ile Phe Val
 65 70 75 80

Val Ser Val Leu Ala Leu Leu Ile Phe Pro Leu Leu Leu Ala Ala Ala
 85 90 95

Leu Gly Val Leu Tyr Asp Arg Lys Leu Gly Gly His Leu Tyr Asp Pro
 100 105 110

Ala Asn Gly Gly Ser Leu Leu Trp Gln His Leu Phe Trp Phe Phe Gly
 115 120 125

His Pro Glu Val Tyr Val Leu Ala Leu Pro Phe Phe Gly Ile Val Ser
 130 135 140

Glu Ile Ile Pro Val Phe Ser Arg Lys Pro Met Phe Gly Leu Arg Arg
 145 150 155 160

Pro Asp Leu Arg Asn Leu Val His Trp Cys Thr Val His Gly Cys Val
 165 170 175

Gly Ser Pro His Val Arg Tyr Trp Arg Ser Phe Ala Ser Val Leu Leu
 180 185 190

Leu His Asp Val Pro Asp Phe Gly Ser Tyr Arg Arg
 195 200

<210> 661

<211> 1200

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1177)

<223> RXA02140

<400> 661

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 Val Glu Gln Gln Asn
 1 5

aag cgt ggt tta aag cgc aag gcc ctg ctt ggc ggt gtc ttg ggc tta 163
 Lys Arg Gly Leu Lys Arg Lys Ala Leu Leu Gly Gly Val Leu Gly Leu
 10 15 20

ggt ggc ctc gcc atg gca ggc tgt gaa gtc gcc cct cct ggc ggt gtg	211
Gly Gly Leu Ala Met Ala Gly Cys Glu Val Ala Pro Pro Gly Gly Val	
25 30 35	
ctt gga gat ttc cta cgt atg ggt tgg cct gat ggc att acc cct gaa	259
Leu Gly Asp Phe Leu Arg Met Gly Trp Pro Asp Gly Ile Thr Pro Glu	
40 45 50	
gca gtg gcc atg ggt aac ttc tgg tca tgg gtc tgg gtt gct gcc tgg	307
Ala Val Ala Met Gly Asn Phe Trp Ser Trp Val Trp Val Ala Ala Trp	
55 60 65	
atc atc ggc atc atc atg tgg ggt cta ttc ctc acc gcc atc ttt gcc	355
Ile Ile Gly Ile Ile Met Trp Gly Leu Phe Leu Thr Ala Ile Phe Ala	
70 75 80 85	
tgg ggc gca aag agg gct gaa aag cgc ggc gag ggt gaa ttc cct aag	403
Trp Gly Ala Lys Arg Ala Glu Lys Arg Gly Glu Gly Glu Phe Pro Lys	
90 95 100	
cag ctc cag tac aac gtt cca ctt gag ctc gtt ctg acg atc gtt ccg	451
Gln Leu Gln Tyr Asn Val Pro Leu Glu Leu Val Leu Thr Ile Val Pro	
105 110 115	
atc atc att gtt atg gtg ctg ttc ttc ttc acc gtt caa act cag gac	499
Ile Ile Ile Val Met Val Leu Phe Phe Phe Thr Val Gln Thr Gln Asp	
120 125 130	
aag gtc acc gct ctg gat aag aac cca gag gtt acc gtg gac gtc acc	547
Lys Val Thr Ala Leu Asp Lys Asn Pro Glu Val Thr Val Asp Val Thr	
135 140 145	
gct tac cag tgg aac tgg aag ttc gga tac tcc gaa att gat ggc tca	595
Ala Tyr Gln Trp Asn Trp Lys Phe Gly Tyr Ser Glu Ile Asp Gly Ser	
150 155 160 165	
ctg gca cct ggt gga cag gat tac caa gga agc gac ccg gag cgt cag	643
Leu Ala Pro Gly Gly Gln Asp Tyr Gln Gly Ser Asp Pro Glu Arg Gln	
170 175 180	
gca gct gcc gag gct tcc aag aag gat cct tct gga gat aac cca att	691
Ala Ala Ala Glu Ala Ser Lys Lys Asp Pro Ser Gly Asp Asn Pro Ile	
185 190 195	
cac ggc aac tca aag tct gac gtt tct tac ctt gag ttc aac cga att	739
His Gly Asn Ser Lys Ser Asp Val Ser Tyr Leu Glu Phe Asn Arg Ile	
200 205 210	
gaa acc ctc gga acc act gat gaa atc cca gtg atg gtt ctt cct gtg	787
Glu Thr Leu Gly Thr Thr Asp Glu Ile Pro Val Met Val Leu Pro Val	
215 220 225	
aac acc cca atc gag ttc aac ctc gca tct gct gac gtt gca cac tcc	835
Asn Thr Pro Ile Glu Phe Asn Leu Ala Ser Ala Asp Val Ala His Ser	
230 235 240 245	
ttc tgg gtt cca gag ttc ctc ttc aag cga gat gct tac gca cac cct	883
Phe Trp Val Pro Glu Phe Leu Phe Lys Arg Asp Ala Tyr Ala His Pro	
250 255 260	

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Pro Pro Gly Gly Val Leu Gly Asp Phe Leu Arg Met Gly Trp Pro Asp
    35            40             45
Gly Ile Thr Pro Glu Ala Val Ala Met Gly Asn Phe Trp Ser Trp Val
   50                55              60
Trp Val Ala Ala Trp Ile Ile Gly Ile Ile Met Trp Gly Leu Phe Leu
  65            70             75              80
Thr Ala Ile Phe Ala Trp Gly Ala Lys Arg Ala Glu Lys Arg Gly Glu
        85                90              95
Gly Glu Phe Pro Lys Gln Leu Gln Tyr Asn Val Pro Leu Glu Leu Val
     100            105           110
Leu Thr Ile Val Pro Ile Ile Ile Val Met Val Leu Phe Phe Phe Thr
    115                120              125
Val Gln Thr Gln Asp Lys Val Thr Ala Leu Asp Lys Asn Pro Glu Val
   130            135           140
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Thr Val Asp Val Thr Ala Tyr Gln Trp Asn Trp Lys Phe Gly Tyr Ser
 145 150 155 160
 Glu Ile Asp Gly Ser Leu Ala Pro Gly Gly Gln Asp Tyr Gln Gly Ser
 165 170 175
 Asp Pro Glu Arg Gln Ala Ala Ala Glu Ala Ser Lys Lys Asp Pro Ser
 180 185 190
 Gly Asp Asn Pro Ile His Gly Asn Ser Lys Ser Asp Val Ser Tyr Leu
 195 200 205
 Glu Phe Asn Arg Ile Glu Thr Leu Gly Thr Thr Asp Glu Ile Pro Val
 210 215 220
 Met Val Leu Pro Val Asn Thr Pro Ile Glu Phe Asn Leu Ala Ser Ala
 225 230 235 240
 Asp Val Ala His Ser Phe Trp Val Pro Glu Phe Leu Phe Lys Arg Asp
 245 250 255
 Ala Tyr Ala His Pro Glu Ala Asn Lys Ser Gln Arg Val Phe Gln Ile
 260 265 270
 Glu Glu Ile Thr Glu Glu Gly Ala Phe Val Gly Arg Cys Ala Glu Met
 275 280 285
 Cys Gly Thr Tyr His Ala Met Met Asn Phe Glu Leu Arg Val Val Asp
 290 295 300
 Arg Asp Ser Phe Ala Glu Tyr Ile Ser Phe Arg Asp Ser Asn Pro Asp
 305 310 315 320
 Ala Thr Asn Ala Gln Ala Leu Glu His Ile Gly Gln Ala Pro Tyr Ala
 325 330 335
 Thr Ser Thr Ser Pro Phe Val Ser Asp Arg Thr Ala Thr Arg Asp Gly
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 Glu Asn Thr Gln Ser Asn Ala
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<210> 663
 <211> 774
 <212> DNA
 <213> *Corynebacterium glutamicum*

<220>
 <221> CDS
 <222> (101)..(751)
 <223> RXA02142

<400> 663
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 aagccgagtt caaactttca attgaaacgg ggggcttgaa gtg act ttg gcc aac 115
 Val Thr Leu Ala Asn
 1 5

caa aca gcc ata cta gat agc gtg acg agc gca gtt gga aat aca ggt 163
 Gln Thr Ala Ile Leu Asp Ser Val Thr Ser Ala Val Gly Asn Thr Gly
 10 15 20

atg gca gca cca caa cgt gtt gcg gca ctg aac cgt ccg aat atg gtc 211
 Met Ala Ala Pro Gln Arg Val Ala Ala Leu Asn Arg Pro Asn Met Val
 25 30 35

agt gtc ggc acc att gtg ttc ctg tct cag gaa tta atg ttc ttc gcc 259
 Ser Val Gly Thr Ile Val Phe Leu Ser Gln Glu Leu Met Phe Phe Ala
 40 45 50

ggg cta ttc gcg atg tac ttc gtg tcc cgt gcg aac gga ctg gca aat 307
 Gly Leu Phe Ala Met Tyr Phe Val Ser Arg Ala Asn Gly Leu Ala Asn
 55 60 65

gga tca tgg gga gag cag aca gat cac ctc aac gtg ccc tac gca ctg 355
 Gly Ser Trp Gly Glu Gln Thr Asp His Leu Asn Val Pro Tyr Ala Leu
 70 75 80 85

ttg att acg gtc att ctg gtg tct tcc tca gtg act tgc cag ttc gga 403
 Leu Ile Thr Val Ile Leu Val Ser Ser Ser Val Thr Cys Gln Phe Gly
 90 95 100

gtt ttt gcg gct gaa agg ggt gac gtt tac ggc ctc cgc aag tgg ttc 451
 Val Phe Ala Ala Glu Arg Gly Asp Val Tyr Gly Leu Arg Lys Trp Phe
 105 110 115

ttg gtc acg att atc ctc gga tca atc ttc gtg atc gga'cag ggc tac 499
 Leu Val Thr Ile Ile Leu Gly Ser Ile Phe Val Ile Gly Gln Gly Tyr
 120 125 130

gag tac atc act ctc gta ggt cac gga ctt aca atc cag agc agt gtc 547
 Glu Tyr Ile Thr Leu Val Gly His Gly Leu Thr Ile Gln Ser Ser Val
 135 140 145

tac gga tcg gca ttc ttt att aca acc ggt ttc cac gca ctg cac gtg 595
 Tyr Gly Ser Ala Phe Phe Ile Thr Thr Gly Phe His Ala Leu His Val
 150 155 160 165

atc gcg ggt gtt atg gcc ttc gtt gtg gtt ctt atg aga atc cat aag 643
 Ile Ala Gly Val Met Ala Phe Val Val Val Leu Met Arg Ile His Lys
 170 175 180

tcg aag ttc act ccg gca cag gca acc gca gca atg gtt gtg tct tat 691
 Ser Lys Phe Thr Pro Ala Gln Ala Thr Ala Ala Met Val Val Ser Tyr
 185 190 195

tac tgg cac ttc gtt gac gtg gtc tgg atc ggc ctc ttc atc act att 739
 Tyr Trp His Phe Val Asp Val Val Trp Ile Gly Leu Phe Ile Thr Ile
 200 205 210

tac ttc att cag taggcagtaa ggaatcctca acg 774
 Tyr Phe Ile Gln
 215

<210> 664

<211> 217

<212> PRT

<213> Corynebacterium glutamicum

<400> 664

Val Thr Leu Ala Asn Gln Thr Ala Ile Leu Asp Ser Val Thr Ser Ala
 1 5 10 15
 Val Gly Asn Thr Gly Met Ala Ala Pro Gln Arg Val Ala Ala Leu Asn
 20 25 30
 Arg Pro Asn Met Val Ser Val Gly Thr Ile Val Phe Leu Ser Gln Glu
 35 40 45
 Leu Met Phe Phe Ala Gly Leu Phe Ala Met Tyr Phe Val Ser Arg Ala
 50 55 60
 Asn Gly Leu Ala Asn Gly Ser Trp Gly Glu Gln Thr Asp His Leu Asn
 65 70 75 80
 Val Pro Tyr Ala Leu Leu Ile Thr Val Ile Leu Val Ser Ser Ser Val
 85 90 95
 Thr Cys Gln Phe Gly Val Phe Ala Ala Glu Arg Gly Asp Val Tyr Gly
 100 105 110
 Leu Arg Lys Trp Phe Leu Val Thr Ile Ile Leu Gly Ser Ile Phe Val
 115 120 125
 Ile Gly Gln Gly Tyr Glu Tyr Ile Thr Leu Val Gly His Gly Leu Thr
 130 135 140
 Ile Gln Ser Ser Val Tyr Gly Ser Ala Phe Phe Ile Thr Thr Gly Phe
 145 150 155 160
 His Ala Leu His Val Ile Ala Gly Val Met Ala Phe Val Val Val Leu
 165 170 175
 Met Arg Ile His Lys Ser Lys Phe Thr Pro Ala Gln Ala Thr Ala Ala
 180 185 190
 Met Val Val Ser Tyr Tyr Trp His Phe Val Asp Val Val Trp Ile Gly
 195 200 205
 Leu Phe Ile Thr Ile Tyr Phe Ile Gln
 210 215

<210> 665

<211> 1347

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(1324)

<223> RXA02144

<400> 665

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 tggtcctcgt ggccgccgct atgtggattg gatcacgttc atg agt aac aac aac 115
 Met Ser Asn Asn Asn
 1 5

gac aaa cag tac aca acc caa gaa ctc aac gcg atg agc aat gag gat	163
Asp Lys Gln Tyr Thr Thr Gln Glu Leu Asn Ala Met Ser Asn Glu Asp	
10 15 20	
ctt gca cga ctt ggt aca gag ctg gac gac gtt acc att gca tac cgc	211
Leu Ala Arg Leu Gly Thr Glu Leu Asp Asp Val Thr Ile Ala Tyr Arg	
25 30 35	
aag gaa cgt ttc cca atc gct aat gac cca gct gag aag cgc gct gca	259
Lys Glu Arg Phe Pro Ile Ala Asn Asp Pro Ala Glu Lys Arg Ala Ala	
40 45 50	
cgt gca gtt act ttc tgg cta gtc ctc ggc atc att ggt gga ctt ggg	307
Arg Ala Val Thr Phe Trp Leu Val Leu Gly Ile Ile Gly Gly Leu Gly	
55 60 65	
ttc ctg gct acc tac att ttc tgg cct tgg gag tac aag gca cac gga	355
Phe Leu Ala Thr Tyr Ile Phe Trp Pro Trp Glu Tyr Lys Ala His Gly	
70 75 80 85	
gat gaa ggt ctc ctg gcg tac acc ttg tac acc cca atg ctg ggt att	403
Asp Glu Gly Leu Leu Ala Tyr Thr Leu Tyr Thr Pro Met Leu Gly Ile	
90 95 100	
act tcc ggt ctt tgc atc ctg tcc ctg gga ttt gca gtt gtc ctt tat	451
Thr Ser Gly Leu Cys Ile Leu Ser Leu Gly Phe Ala Val Val Leu Tyr	
105 110 115	
gtc aag aag ttc att cca gag gaa atc gca gta cag cgt cgc cac gac	499
Val Lys Lys Phe Ile Pro Glu Glu Ile Ala Val Gln Arg Arg His Asp	
120 125 130	
ggt cct tct gaa gaa gtt gac cgc cgc acc atc gtt gca ctt ctc aat	547
Gly Pro Ser Glu Glu Val Asp Arg Arg Thr Ile Val Ala Leu Leu Asn	
135 140 145	
gac tct tgg cag acc tct act ctt ggt cgt cgc aag ctg atc atg gga	595
Asp Ser Trp Gln Thr Ser Thr Leu Gly Arg Arg Lys Leu Ile Met Gly	
150 155 160 165	
ctt gca ggt ggc gga gca gta ctg gcc ggc ctg acc atc atc gct cca	643
Leu Ala Gly Gly Gly Ala Val Leu Ala Gly Leu Thr Ile Ile Ala Pro	
170 175 180	
atg ggc ggt atg atc aag aac cct tgg aat cct aag gaa ggc cca atg	691
Met Gly Gly Met Ile Lys Asn Pro Trp Asn Pro Lys Glu Gly Pro Met	
185 190 195	
gac gtt cag ggt gac ggc acc ctg tgg act tcc ggt tgg act ctc gtt	739
Asp Val Gln Gly Asp Gly Thr Leu Trp Thr Ser Gly Trp Thr Leu Val	
200 205 210	
gag aac gac gtc aag gtt tac ctc ggc cgc gac act gca gca att gcg	787
Glu Asn Asp Val Lys Val Tyr Leu Gly Arg Asp Thr Ala Ala Ile Ala	
215 220 225	
gag tcc cac acc gat gca acc ggt gag cac tgg tca acc act ggt gtt	835
Glu Ser His Thr Asp Ala Thr Gly Glu His Trp Ser Thr Thr Gly Val	
230 235 240 245	

tcc cgc ctg gtt cgt atg cgc cca gaa gat ctg gca gca gca tcc atg 883
 Ser Arg Leu Val Arg Met Arg Pro Glu Asp Leu Ala Ala Ala Ser Met
 250 255 260

gaa act gtc ttc cca ctt cca gct gaa atg gtg aac gac ggt gct gaa 931
 Glu Thr Val Phe Pro Leu Pro Ala Glu Met Val Asn Asp Gly Ala Glu
 265 270 275

tac gat cct gcg aag gac gtc tac gag cac caa atg cac tcg gtg cac 979
 Tyr Asp Pro Ala Lys Asp Val Tyr Glu His Gln Met His Ser Val His
 280 285 290

ggc cca cgc aac gca gtt atg ttg atc cgt ctc cgt acc gct gac gct 1027
 Gly Pro Arg Asn Ala Val Met Leu Ile Arg Leu Arg Thr Ala Asp Ala
 295 300 305

gaa aag gtt atc gaa cgc gaa ggc cag gag tcc ttc cac tac ggt gac 1075
 Glu Lys Val Ile Glu Arg Glu Gly Gln Glu Ser Phe His Tyr Gly Asp
 310 315 320 325

tac tac gct tac tcc aag att tgt aca cac att ggt tgc cca acc tca 1123
 Tyr Tyr Ala Tyr Ser Lys Ile Cys Thr His Ile Gly Cys Pro Thr Ser
 330 335 340

ctg tac gag gct cag acc aat cgt att ctg tgc cca tgt cac cag tcg 1171
 Leu Tyr Glu Ala Gln Thr Asn Arg Ile Leu Cys Pro Cys His Gln Ser
 345 350 355

cag ttt gac gca ttg cac tac gga aag cca gtc ttt gga cct gct gcc 1219
 Gln Phe Asp Ala Leu His Tyr Gly Lys Pro Val Phe Gly Pro Ala Ala
 360 365 370

cgt gca ctg cca cag ctg cca att acc gtt gat gaa gag ggc tac ctc 1267
 Arg Ala Leu Pro Gln Leu Pro Ile Thr Val Asp Glu Glu Gly Tyr Leu
 375 380 385

atc gcc gct ggt aac ttc att gag cca ctc ggc cct gca ttc tgg gag 1315
 Ile Ala Ala Gly Asn Phe Ile Glu Pro Leu Gly Pro Ala Phe Trp Glu
 390 395 400 405

cgt aag tca tgagtctagc taccgtggga aac 1347
 Arg Lys Ser

<210> 666

<211> 408

<212> PRT

<213> Corynebacterium glutamicum

<400> 666

Met Ser Asn Asn Asn Asp Lys Gln Tyr Thr Thr Gln Glu Leu Asn Ala
 1 5 10 15

Met Ser Asn Glu Asp Leu Ala Arg Leu Gly Thr Glu Leu Asp Asp Val
 20 25 30

Thr Ile Ala Tyr Arg Lys Glu Arg Phe Pro Ile Ala Asn Asp Pro Ala
 35 40 45

Glu Lys Arg Ala Ala Arg Ala Val Thr Phe Trp Leu Val Leu Gly Ile

50	55	60
Ile Gly Gly Leu Gly Phe Leu Ala Thr Tyr Ile Phe Trp Pro Trp Glu 65 70 75 80		
Tyr Lys Ala His Gly Asp Glu Gly Leu Leu Ala Tyr Thr Leu Tyr Thr 85 90 95		
Pro Met Leu Gly Ile Thr Ser Gly Leu Cys Ile Leu Ser Leu Gly Phe 100 105 110		
Ala Val Val Leu Tyr Val Lys Lys Phe Ile Pro Glu Glu Ile Ala Val 115 120 125		
Gln Arg Arg His Asp Gly Pro Ser Glu Glu Val Asp Arg Arg Thr Ile 130 135 140		
Val Ala Leu Leu Asn Asp Ser Trp Gln Thr Ser Thr Leu Gly Arg Arg 145 150 155 160		
Lys Leu Ile Met Gly Leu Ala Gly Gly Gly Ala Val Leu Ala Gly Leu 165 170 175		
Thr Ile Ile Ala Pro Met Gly Gly Met Ile Lys Asn Pro Trp Asn Pro 180 185 190		
Lys Glu Gly Pro Met Asp Val Gln Gly Asp Gly Thr Leu Trp Thr Ser 195 200 205		
Gly Trp Thr Leu Val Glu Asn Asp Val Lys Val Tyr Leu Gly Arg Asp 210 215 220		
Thr Ala Ala Ile Ala Glu Ser His Thr Asp Ala Thr Gly Glu His Trp 225 230 235 240		
Ser Thr Thr Gly Val Ser Arg Leu Val Arg Met Arg Pro Glu Asp Leu 245 250 255		
Ala Ala Ala Ser Met Glu Thr Val Phe Pro Leu Pro Ala Glu Met Val 260 265 270		
Asn Asp Gly Ala Glu Tyr Asp Pro Ala Lys Asp Val Tyr Glu His Gln 275 280 285		
Met His Ser Val His Gly Pro Arg Asn Ala Val Met Leu Ile Arg Leu 290 295 300		
Arg Thr Ala Asp Ala Glu Lys Val Ile Glu Arg Glu Gly Gln Glu Ser 305 310 315 320		
Phe His Tyr Gly Asp Tyr Tyr Ala Tyr Ser Lys Ile Cys Thr His Ile 325 330 335		
Gly Cys Pro Thr Ser Leu Tyr Glu Ala Gln Thr Asn Arg Ile Leu Cys 340 345 350		
Pro Cys His Gln Ser Gln Phe Asp Ala Leu His Tyr Gly Lys Pro Val 355 360 365		
Phe Gly Pro Ala Ala Arg Ala Leu Pro Gln Leu Pro Ile Thr Val Asp 370 375 380		

Glu Glu Gly Tyr Leu Ile Ala Ala Gly Asn Phe Ile Glu Pro Leu Gly
 385 390 395 400

Pro Ala Phe Trp Glu Arg Lys Ser
 405

<210> 667
 <211> 1053
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1030)
 <223> RXA02740

<400> 667
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 tatgagtgat ttgaaaatgc aacgttctgg aggagaaccc ttg gac acg atc aag 115
 Leu Asp Thr Ile Lys
 1 5
 gcc tat att gcg cta acg aag ccc agg gtt att gaa ctc ctc ctt gtc 163
 Ala Tyr Ile Ala Leu Thr Lys Pro Arg Val Ile Glu Leu Leu Leu Val
 10 15 20
 gcc aca atc ccc aca atg ctt cag gct gaa cgc ggt gag aac aac att 211
 Ala Thr Ile Pro Thr Met Leu Gln Ala Glu Arg Gly Glu Asn Asn Ile
 25 30 35
 gtg ctc atc ttg ctg act gtg ttc ggt ggc tgg atg ggt gcg gcc gcc 259
 Val Leu Ile Leu Leu Thr Val Phe Gly Gly Trp Met Gly Ala Ala Ala
 40 45 50
 gcc aac acc ttc aac atg gtg gca gac tcc gat att gat cag cgc atg 307
 Ala Asn Thr Phe Asn Met Val Ala Asp Ser Asp Ile Asp Gln Arg Met
 55 60 65
 gga cgc act agg gct cgc cct ttg gtg cgc cac acc gtg agt aat cgc 355
 Gly Arg Thr Arg Ala Arg Pro Leu Val Arg His Thr Val Ser Asn Arg
 70 75 80 85
 gac gcc tcc att ttt gcg tgg gtc ctg aca gtg gcc agc ttc ttg tgg 403
 Asp Ala Ser Ile Phe Ala Trp Val Leu Thr Val Ala Ser Phe Leu Trp
 90 95 100
 ctg tgg ctg ctg tgc gat tcg atg ctc gcc ggc atc ttc gtg ttg atc 451
 Leu Trp Leu Leu Cys Asp Ser Met Leu Ala Gly Ile Phe Val Leu Ile
 105 110 115
 acg att ttc ttc tac att ttt gtc tac acc aag tgg ctg aag cgc cgc 499
 Thr Ile Phe Phe Tyr Ile Phe Val Tyr Thr Lys Trp Leu Lys Arg Arg
 120 125 130
 acg cac atg aat atc gtg tgg ggc gga gcc gca ggt tgt atg cca gtg 547
 Thr His Met Asn Ile Val Trp Gly Gly Ala Ala Gly Cys Met Pro Val
 135 140 145

ctc gtc ggc tgg gca gtg atc gtt gat cag ttt gag cca ggc gtt cca 595
 Leu Val Gly Trp Ala Val Ile Val Asp Gln Phe Glu Pro Gly Val Pro
 150 155 160 165
 cag cag tgg tgg cag gca att gtc ctg ttc atg gtg att ttc ttc tgg 643
 Gln Gln Trp Trp Gln Ala Ile Val Leu Phe Met Val Ile Phe Phe Trp
 170 175 180
 acc cca cct cac acc tgg gct ctg gcc atg aag tac cgc gaa gac tac 691
 Thr Pro Pro His Thr Trp Ala Leu Ala Met Lys Tyr Arg Glu Asp Tyr
 185 190 195
 aag gcg gct ggc gtc cca atg ctt cct gtc gtg cgc acc cca gtc cag 739
 Lys Ala Ala Gly Val Pro Met Leu Pro Val Val Arg Thr Pro Val Gln
 200 205 210
 gtc acc gca caa atc gtg tgg tac tcc gtg gca act gtg ctg acc acc 787
 Val Thr Ala Gln Ile Val Trp Tyr Ser Val Ala Thr Val Leu Thr Thr
 215 220 225
 ttc ttg ctc atc cca gca act ggt tgg atc tac gca gcg atc gcc gtc 835
 Phe Leu Leu Ile Pro Ala Thr Gly Trp Ile Tyr Ala Ala Ile Ala Val
 230 235 240 245
 att tcc ggc gtc acc ttc ttg ttc atg gcc atc aag ctg cac ctc ggc 883
 Ile Ser Gly Val Thr Phe Leu Phe Met Ala Ile Lys Leu His Leu Gly
 250 255 260
 atc aaa aac ggt ggc aag gtc aag cct ctg aag ctg ttt att ttg tcc 931
 Ile Lys Asn Gly Gly Lys Val Lys Pro Leu Lys Leu Phe Ile Leu Ser
 265 270 275
 aac aac tac ttg gca gtc ctc ttc gtg gca ttg tcc gtc gac gcg gtc 979
 Asn Asn Tyr Leu Ala Val Leu Phe Val Ala Leu Ser Val Asp Ala Val
 280 285 290
 ctc ggc ctt gag acc atc ggc gag atg ctc ggc tgg acc acc acc ttc 1027
 Leu Gly Leu Glu Thr Ile Gly Glu Met Leu Gly Trp Thr Thr Thr Phe
 295 300 305
 ttc taaaagcttg cttttcgacg aaa 1053
 Phe
 310

<210> 668
 <211> 310
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 668
 Leu Asp Thr Ile Lys Ala Tyr Ile Ala Leu Thr Lys Pro Arg Val Ile
 1 5 10 15
 Glu Leu Leu Leu Val Ala Thr Ile Pro Thr Met Leu Gln Ala Glu Arg
 20 25 30
 Gly Glu Asn Asn Ile Val Leu Ile Leu Leu Thr Val Phe Gly Gly Trp
 35 40 45
 Met Gly Ala Ala Ala Ala Asn Thr Phe Asn Met Val Ala Asp Ser Asp

50 55 60
 Ile Asp Gln Arg Met Gly Arg Thr Arg Ala Arg Pro Leu Val Arg His
 65 70 75 80
 Thr Val Ser Asn Arg Asp Ala Ser Ile Phe Ala Trp Val Leu Thr Val
 85 90 95
 Ala Ser Phe Leu Trp Leu Trp Leu Leu Cys Asp Ser Met Leu Ala Gly
 100 105 110
 Ile Phe Val Leu Ile Thr Ile Phe Phe Tyr Ile Phe Val Tyr Thr Lys
 115 120 125
 Trp Leu Lys Arg Arg Thr His Met Asn Ile Val Trp Gly Gly Ala Ala
 130 135 140
 Gly Cys Met Pro Val Leu Val Gly Trp Ala Val Ile Val Asp Gln Phe
 145 150 155 160
 Glu Pro Gly Val Pro Gln Gln Trp Trp Gln Ala Ile Val Leu Phe Met
 165 170 175
 Val Ile Phe Phe Trp Thr Pro Pro His Thr Trp Ala Leu Ala Met Lys
 180 185 190
 Tyr Arg Glu Asp Tyr Lys Ala Ala Gly Val Pro Met Leu Pro Val Val
 195 200 205
 Arg Thr Pro Val Gln Val Thr Ala Gln Ile Val Trp Tyr Ser Val Ala
 210 215 220
 Thr Val Leu Thr Thr Phe Leu Leu Ile Pro Ala Thr Gly Trp Ile Tyr
 225 230 235 240
 Ala Ala Ile Ala Val Ile Ser Gly Val Thr Phe Leu Phe Met Ala Ile
 245 250 255
 Lys Leu His Leu Gly Ile Lys Asn Gly Gly Lys Val Lys Pro Leu Lys
 260 265 270
 Leu Phe Ile Leu Ser Asn Asn Tyr Leu Ala Val Leu Phe Val Ala Leu
 275 280 285
 Ser Val Asp Ala Val Leu Gly Leu Glu Thr Ile Gly Glu Met Leu Gly
 290 295 300
 Trp Thr Thr Thr Phe Phe
 305 310

<210> 669

<211> 1161

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1138)

<223> RXA02743

<400> 669

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aattgtataa	aactagccat	gacctgctag	gatcagcgac	gtg tct act tca gat	115	
				Val Ser Thr Ser Asp	5	
				1		
gct ccc tca aat aat cca gtt gag ttg aag ccc att act ttc tgg gca	163					
Ala Pro Ser Asn Asn Pro Val Glu Leu Lys Pro Ile Thr Phe Trp Ala						
	10		15		20	
ccg acc atc aaa gtg cag cgc att ctc gcg ctc cta ctg ttg att ttc	211					
Pro Thr Ile Lys Val Gln Arg Ile Leu Ala Leu Leu Leu Leu Ile Phe						
	25		30		35	
cag gga ggc atc acc gtt acg ggc tct atc gtc cgt gtc aca ggc tcc	259					
Gln Gly Gly Ile Thr Val Thr Gly Ser Ile Val Arg Val Thr Gly Ser						
	40		45		50	
ggc ctc ggt tgt gat acc tgg cca cta tgc cac gaa ggt tca cta gtc	307					
Gly Leu Gly Cys Asp Thr Trp Pro Leu Cys His Glu Gly Ser Leu Val						
	55		60		65	
cca gtc gca ggc gca gca cca tgg atc cac cag gca gtg gaa ttt ggt	355					
Pro Val Ala Gly Ala Ala Pro Trp Ile His Gln Ala Val Glu Phe Gly						
	70		75		80	
					85	
aac cgc atg ctc act ttc gtg ctt gct gcc gca gcg ctt gcg ttg ttc	403					
Asn Arg Met Leu Thr Phe Val Leu Ala Ala Ala Leu Ala Leu Phe						
	90		95		100	
att gca gtt ctt ggc gca aaa cgc cgc cgc gag atc ctg gtc cat tcc	451					
Ile Ala Val Leu Gly Ala Lys Arg Arg Arg Glu Ile Leu Val His Ser						
	105		110		115	
ttc atc cag ggt ttg ggc atc atc ttg cag gct gtc atc ggt ggc atc	499					
Phe Ile Gln Gly Leu Gly Ile Ile Leu Gln Ala Val Ile Gly Gly Ile						
	120		125		130	
acc gtg ctg gtt gat ttg cac tgg tac gcc gtt gct ttg cac ttc ctg	547					
Thr Val Leu Val Asp Leu His Trp Tyr Ala Val Ala Leu His Phe Leu						
	135		140		145	
cca tcc atg atc ctt gtt ttc atg gcc gcg att ttg tac acc cgc atc	595					
Pro Ser Met Ile Leu Val Phe Met Ala Ala Ile Leu Tyr Thr Arg Ile						
	150		155		160	
					165	
ggc gag ccc gat gac ggc gag att acc acc aca ttc ccc acg tgg atc	643					
Gly Glu Pro Asp Asp Gly Glu Ile Thr Thr Thr Phe Pro Thr Trp Ile						
	170		175		180	
cgc aat gta gct gtc att ggt gca gta gcg ctc tcc gta gta ctg atc	691					
Arg Asn Val Ala Val Ile Gly Ala Val Ala Leu Ser Val Val Leu Ile						
	185		190		195	
acc ggc acc atg acc acc ggc gct ggc gtt cac tct ggc gat gca tca	739					
Thr Gly Thr Met Thr Thr Gly Ala Gly Val His Ser Gly Asp Ala Ser						
	200		205		210	
atc acc atggat gat cgc ctc gat gtc agc atc gac ttg atg gcc cac	787					
Ile Thr Met Asp Asp Arg Leu Asp Val Ser Ile Asp Leu Met Ala His						

215	220	225	
atc cac ggc tac agc atg tac atc tac ctc ttc ttc acc ctc atc gtg			835
Ile His Gly Tyr Ser Met Tyr Ile Tyr Leu Phe Phe Thr Leu Ile Val			
230	235	240	245
gtc gcc ggt ctg tac aag gca aaa acc acc aag cac aac aag cag ctt			883
Val Ala Gly Leu Tyr Lys Ala Lys Thr Thr Lys His Asn Lys Gln Leu			
250	255		260
ggc ctc atg ctg att ctg ttc att ctg att cag gca ggt atc ggc atc			931
Gly Leu Met Leu Ile Leu Phe Ile Leu Ile Gln Ala Gly Ile Gly Ile			
265	270		275
ttg cag tac cgc atg ggt gtg cca cgc tgg agc atc cca ttc cac atc			979
Leu Gln Tyr Arg Met Gly Val Pro Arg Trp Ser Ile Pro Phe His Ile			
280	285		290
gca atg tct tct gtc gtt gtt gcc ttc act tcc ctt ctg tgg gcg cag			1027
Ala Met Ser Ser Val Val Val Ala Phe Thr Ser Leu Leu Trp Ala Gln			
295	300		305
ggt cgt ata cgc gtc ggc ggt aaa gcc acc gtt act ggt tct gtt gat			1075
Gly Arg Ile Arg Val Gly Gly Lys Ala Thr Val Thr Gly Ser Val Asp			
310	315	320	325
ggc gat att aag aac gag atc att acg aac ccc ttt gag aag aaa tca			1123
Gly Asp Ile Lys Asn Glu Ile Ile Thr Asn Pro Phe Glu Lys Lys Ser			
330	335		340
aag cag cct gtt aaa taacacgcaa ctgtatcgggt aaa			1161
Lys Gln Pro Val Lys			
345			

<210> 670

<211> 346

<212> PRT

<213> Corynebacterium glutamicum

<400> 670

Val	Ser	Thr	Ser	Asp	Ala	Pro	Ser	Asn	Asn	Pro	Val	Glu	Leu	Lys	Pro
1				5					10					15	

Ile	Thr	Phe	Trp	Ala	Pro	Thr	Ile	Lys	Val	Gln	Arg	Ile	Leu	Ala	Leu
	20						25						30		

Leu	Leu	Leu	Ile	Phe	Gln	Gly	Gly	Ile	Thr	Val	Thr	Gly	Ser	Ile	Val
	35					40						45			

Arg	Val	Thr	Gly	Ser	Gly	Leu	Gly	Cys	Asp	Thr	Trp	Pro	Leu	Cys	His
	50				55					60					

Glu	Gly	Ser	Leu	Val	Pro	Val	Ala	Gly	Ala	Ala	Pro	Trp	Ile	His	Gln
65					70				75						80

Ala	Val	Glu	Phe	Gly	Asn	Arg	Met	Leu	Thr	Phe	Val	Leu	Ala	Ala	Ala
			85						90					95	

Ala	Leu	Ala	Leu	Phe	Ile	Ala	Val	Leu	Gly	Ala	Lys	Arg	Arg	Arg	Glu
		100						105							110

Ile Leu Val His Ser Phe Ile Gln Gly Leu Gly Ile Ile Leu Gln Ala
 115 120 125
 Val Ile Gly Gly Ile Thr Val Leu Val Asp Leu His Trp Tyr Ala Val
 130 135 140
 Ala Leu His Phe Leu Pro Ser Met Ile Leu Val Phe Met Ala Ala Ile
 145 150 155 160
 Leu Tyr Thr Arg Ile Gly Glu Pro Asp Asp Gly Glu Ile Thr Thr Thr
 165 170 175
 Phe Pro Thr Trp Ile Arg Asn Val Ala Val Ile Gly Ala Val Ala Leu
 180 185 190
 Ser Val Val Leu Ile Thr Gly Thr Met Thr Thr Gly Ala Gly Val His
 195 200 205
 Ser Gly Asp Ala Ser Ile Thr Met Asp Asp Arg Leu Asp Val Ser Ile
 210 215 220
 Asp Leu Met Ala His Ile His Gly Tyr Ser Met Tyr Ile Tyr Leu Phe
 225 230 235 240
 Phe Thr Leu Ile Val Val Ala Gly Leu Tyr Lys Ala Lys Thr Thr Lys
 245 250 255
 His Asn Lys Gln Leu Gly Leu Met Leu Ile Leu Phe Ile Leu Ile Gln
 260 265 270
 Ala Gly Ile Gly Ile Leu Gln Tyr Arg Met Gly Val Pro Arg Trp Ser
 275 280 285
 Ile Pro Phe His Ile Ala Met Ser Ser Val Val Val Ala Phe Thr Ser
 290 295 300
 Leu Leu Trp Ala Gln Gly Arg Ile Arg Val Gly Gly Lys Ala Thr Val
 305 310 315 320
 Thr Gly Ser Val Asp Gly Asp Ile Lys Asn Glu Ile Ile Thr Asn Pro
 325 330 335
 Phe Glu Lys Lys Ser Lys Gln Pro Val Lys
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<210> 671

<211> 444

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(421)

<223> RXA01227

<400> 671

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acctattttc caggtcttta tccgtagtat tggagatccg atg acc tac aca atc 115

Met Thr Tyr Thr Ile
1 5

gcc cag ccc tgc gtt gat gtc ctg gat cga gcc tgc gtc gag gaa tgt 163
Ala Gln Pro Cys Val Asp Val Leu Asp Arg Ala Cys Val Glu Glu Cys
10 15 20

ccc gtg gac tgc atc tac gag ggc aaa cgg atg ctc tac atc cac ccc 211
Pro Val Asp Cys Ile Tyr Glu Gly Lys Arg Met Leu Tyr Ile His Pro
25 30 35

gat gag tgc gtc gac tgc ggt gcc tgc gag ccc gtc tgc ccg gtt gaa 259
Asp Glu Cys Val Asp Cys Gly Ala Cys Glu Pro Val Cys Pro Val Glu
40 45 50

gcc atc ttc tac gaa gat gat gtt ccc cac gaa tgg tgg gac tac acc 307
Ala Ile Phe Tyr Glu Asp Asp Val Pro His Glu Trp Trp Asp Tyr Thr
55 60 65

ggc gct aac gcc gcc ttt ttc gac gac ctc ggt tgc cca ggc ggt gcc 355
Gly Ala Asn Ala Ala Phe Phe Asp Asp Leu Gly Ser Pro Gly Gly Ala
70 75 80 85

gcc agc ctg ggt ccg cag gac ttc gac gcc cag ctc gtc gcg gtg ctg 403
Ala Ser Leu Gly Pro Gln Asp Phe Asp Ala Gln Leu Val Ala Val Leu
90 95 100

ccg cca cag aac cag aac taggacctga tatcgccct aaa 444
Pro Pro Gln Asn Gln Asn
105

<210> 672

<211> 107

<212> PRT

<213> Corynebacterium glutamicum

<400> 672

Met Thr Tyr Thr Ile Ala Gln Pro Cys Val Asp Val Leu Asp Arg Ala
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Cys Val Glu Glu Cys Pro Val Asp Cys Ile Tyr Glu Gly Lys Arg Met
20 25 30

Leu Tyr Ile His Pro Asp Glu Cys Val Asp Cys Gly Ala Cys Glu Pro
35 40 45

Val Cys Pro Val Glu Ala Ile Phe Tyr Glu Asp Asp Val Pro His Glu
50 55 60

Trp Trp Asp Tyr Thr Gly Ala Asn Ala Ala Phe Phe Asp Asp Leu Gly
65 70 75 80

Ser Pro Gly Gly Ala Ala Ser Leu Gly Pro Gln Asp Phe Asp Ala Gln
85 90 95

Leu Val Ala Val Leu Pro Pro Gln Asn Gln Asn
100 105

<210> 673

<211> 438
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(415)
 <223> RXA01865

<400> 673

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ttattagcct cttagagttc tcaggagaaa acgaaatccc atg aca tac aca atc 115
                                   Met Thr Tyr Thr Ile
                                   1      5

gca cag ccc tgc gtt gac gtc ttg gat cgt gcc tgc gtt gaa gaa tgc 163
Ala Gln Pro Cys Val Asp Val Leu Asp Arg Ala Cys Val Glu Glu Cys
              10              15              20

cca gta gat tgc atc tac gaa ggt aag cgc atg ctg tac atc cac ccg 211
Pro Val Asp Cys Ile Tyr Glu Gly Lys Arg Met Leu Tyr Ile His Pro
              25              30              35

gat gag tgc gtt gac tgt ggt gca tgt gag cct gct tgc cca gtt gag 259
Asp Glu Cys Val Asp Cys Gly Ala Cys Glu Pro Ala Cys Pro Val Glu
              40              45              50

gca atc ttc tac gag gac gat gtc cca gac gaa tgg ctt gac tac aac 307
Ala Ile Phe Tyr Glu Asp Asp Val Pro Asp Glu Trp Leu Asp Tyr Asn
              55              60              65

gat gcc aac gct gca ttc ttc gat gat ctg ggc tcc cca ggt ggt gcg 355
Asp Ala Asn Ala Ala Phe Phe Asp Asp Leu Gly Ser Pro Gly Gly Ala
              70              75              80              85

gct aag ctt gga cca caa gat ttt gat cac cca atg atc gct gcg ctg 403
Ala Lys Leu Gly Pro Gln Asp Phe Asp His Pro Met Ile Ala Ala Leu
              90              95              100

ccg cct cag gca taatctaacg catgacctct cgc 438
Pro Pro Gln Ala
              105

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<210> 674
 <211> 105
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 674

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Met Thr Tyr Thr Ile Ala Gln Pro Cys Val Asp Val Leu Asp Arg Ala
 1              5              10              15

Cys Val Glu Glu Cys Pro Val Asp Cys Ile Tyr Glu Gly Lys Arg Met
      20              25              30

Leu Tyr Ile His Pro Asp Glu Cys Val Asp Cys Gly Ala Cys Glu Pro
 35              40              45

Ala Cys Pro Val Glu Ala Ile Phe Tyr Glu Asp Asp Val Pro Asp Glu

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50					55					60					
Trp	Leu	Asp	Tyr	Asn	Asp	Ala	Asn	Ala	Ala	Phe	Phe	Asp	Asp	Leu	Gly
65					70					75					80
Ser	Pro	Gly	Gly	Ala	Ala	Lys	Leu	Gly	Pro	Gln	Asp	Phe	Asp	His	Pro
				85					90					95	
Met	Ile	Ala	Ala	Leu	Pro	Pro	Gln	Ala							
			100					105							

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<210> 675
<211> 441
<212> DNA
<213> Corynebacterium glutamicum
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<221> CDS
<222> (101)..(418)
<223> RXA00680
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gacagttcat ctaagtacta aaagtttctaa ggagaagatc										atg	tct	act	att	cat	115		
										Met	Ser	Thr	Ile	His			
										1				5			
ttc	att	gat	cat	gct	ggc	aaa	acc	cgc	acc	atc	gag	gcg	act	gtt	ggt	163	
Phe	Ile	Asp	His	Ala	Gly	Lys	Thr	Arg	Thr	Ile	Glu	Ala	Thr	Val	Gly		
				10					15					20			
gat	tca	gta	atg	gag	acc	gca	gtc	cga	aac	gga	gtg	cct	gga	att	gtt	211	
Asp	Ser	Val	Met	Glu	Thr	Ala	Val	Arg	Asn	Gly	Val	Pro	Gly	Ile	Val		
				25					30					35			
gct	gaa	tgc	ggc	ggg	tcc	tta	tcg	tgt	gca	acc	tgc	cat	gtg	ttt	gtt	259	
Ala	Glu	Cys	Gly	Gly	Ser	Leu	Ser	Cys	Ala	Thr	Cys	His	Val	Phe	Val		
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gac	cct	gca	cag	tat	gat	gcg	ctt	ccc	cca	atg	gag	gag	atg	gaa	gat	307	
Asp	Pro	Ala	Gln	Tyr	Asp	Ala	Leu	Pro	Pro	Met	Glu	Glu	Met	Glu	Asp		
		55					60					65					
gaa	atg	ctg	tgg	ggg	gct	gcc	gtg	gac	cgt	gag	gat	tgc	tcc	cgt	ttg	355	
Glu	Met	Leu	Trp	Gly	Ala	Ala	Val	Asp	Arg	Glu	Asp	Cys	Ser	Arg	Leu		
70					75					80					85		
tct	tgc	caa	atc	aag	gtc	acc	gaa	ggc	atg	gat	ctt	tcg	ttg	acc	acg	403	
Ser	Cys	Gln	Ile	Lys	Val	Thr	Glu	Gly	Met	Asp	Leu	Ser	Leu	Thr	Thr		
				90					95					100			
cca	gaa	acg	caa	gtg	tgaggttgaa	tcatgaatac	ttc									441	
Pro	Glu	Thr	Gln	Val													
105																	

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<210> 676
<211> 106
<212> PRT
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<213> Corynebacterium glutamicum

<400> 676

Met Ser Thr Ile His Phe Ile Asp His Ala Gly Lys Thr Arg Thr Ile
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 Glu Ala Thr Val Gly Asp Ser Val Met Glu Thr Ala Val Arg Asn Gly
 20 25 30
 Val Pro Gly Ile Val Ala Glu Cys Gly Gly Ser Leu Ser Cys Ala Thr
 35 40 45
 Cys His Val Phe Val Asp Pro Ala Gln Tyr Asp Ala Leu Pro Pro Met
 50 55 60
 Glu Glu Met Glu Asp Glu Met Leu Trp Gly Ala Ala Val Asp Arg Glu
 65 70 75 80
 Asp Cys Ser Arg Leu Ser Cys Gln Ile Lys Val Thr Glu Gly Met Asp
 85 90 95
 Leu Ser Leu Thr Thr Pro Glu Thr Gln Val
 100 105

<210> 677

<211> 1389

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1366)

<223> RXA00679

<400> 677

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 Met Asn Thr Ser Ala
 1 5
 gaa act gga atc ttg atc atc ggt gca aac caa tcg ggt gtg cag ctg 163
 Glu Thr Gly Ile Leu Ile Ile Gly Ala Asn Gln Ser Gly Val Gln Leu
 10 15 20
 gcg att tcc ctg cgg gcc acg ggt ttc acc gaa tcg atc acg ctt cta 211
 Ala Ile Ser Leu Arg Ala Thr Gly Phe Thr Glu Ser Ile Thr Leu Leu
 25 30 35
 ggc gag gag gat cac cgc ccc tac cag cgt ccc gcc ttg tcc aag gag 259
 Gly Glu Glu Asp His Arg Pro Tyr Gln Arg Pro Ala Leu Ser Lys Glu
 40 45 50
 ttc ctc cag gac aag atc gac aaa gag cgt ctg att ttc cgt tcc aat 307
 Phe Leu Gln Asp Lys Ile Asp Lys Glu Arg Leu Ile Phe Arg Ser Asn
 55 60 65
 gag tat tgg gaa gaa aat aat att cgc ctg gtc aag ggc gtg cgc atc 355
 Glu Tyr Trp Glu Glu Asn Asn Ile Arg Leu Val Lys Gly Val Arg Ile
 70 75 80 85

gaa cgc att gaa aag aac gac gac gga tca ggg gtc gcc tac ggc gcc	403
Glu Arg Ile Glu Lys Asn Asp Asp Gly Ser Gly Val Ala Tyr Gly Ala	
90 95 100	
gga caa gaa ttc gct ttt cga cgt ctc gct cta gcg gtt ggt gcc cgc	451
Gly Gln Glu Phe Ala Phe Arg Arg Leu Ala Leu Ala Val Gly Ala Arg	
105 110 115	
cct cgc cac ctc gac ctc ccg ggc gcc acc ttg gag ggt gtc acc tac	499
Pro Arg His Leu Asp Leu Pro Gly Ala Thr Leu Glu Gly Val Thr Tyr	
120 125 130	
ctg cgc aac gcg gac gac gcc ttg gcg ctc aaa gcg atg att ggt tct	547
Leu Arg Asn Ala Asp Asp Ala Leu Ala Leu Lys Ala Met Ile Gly Ser	
135 140 145	
gtc acc gat gcc gtt gta gtc ggt ggt ggg ttc atc gga ttg gaa gct	595
Val Thr Asp Ala Val Val Val Gly Gly Gly Phe Ile Gly Leu Glu Ala	
150 155 160 165	
gcg tgt tcg ctt cat gac ctc ggc aaa aat gtc acc gtc ctg gaa tat	643
Ala Cys Ser Leu His Asp Leu Gly Lys Asn Val Thr Val Leu Glu Tyr	
170 175 180	
ggt ccg cgt ctg att ggc cga gcg gtg ggt gaa gaà acc gca gca ttc	691
Gly Pro Arg Leu Ile Gly Arg Ala Val Gly Glu Glu Thr Ala Ala Phe	
185 190 195	
ttc ctc gaa caa cac cgt tcc cgt ggc gta aat atc gtg ctt gat gcc	739
Phe Leu Glu Gln His Arg Ser Arg Gly Val Asn Ile Val Leu Asp Ala	
200 205 210	
cgc atg aaa cag ttt gtg ggc aag gat gga aag ctc agc ggc att gag	787
Arg Met Lys Gln Phe Val Gly Lys Asp Gly Lys Leu Ser Gly Ile Glu	
215 220 225	
cta gaa gat ggc aca gta att cct gcc caa cta gtc att gtg ggc atc	835
Leu Glu Asp Gly Thr Val Ile Pro Ala Gln Leu Val Ile Val Gly Ile	
230 235 240 245	
ggt gtc att ccg aac aca gaa ctt gcc gct gtt ctg ggc tta gac atc	883
Gly Val Ile Pro Asn Thr Glu Leu Ala Ala Val Leu Gly Leu Asp Ile	
250 255 260	
aac aac ggc atc gtg gtg gat aaa cat gcc gtc gcg tca gat ggc acc	931
Asn Asn Gly Ile Val Val Asp Lys His Ala Val Ala Ser Asp Gly Thr	
265 270 275	
acc att gcg att ggc gat gtc gcc aac att ccc aat cca atc cct ggt	979
Thr Ile Ala Ile Gly Asp Val Ala Asn Ile Pro Asn Pro Ile Pro Gly	
280 285 290	
tcc ccc gct gat gaa cgc atc cga cta gaa agc gtc aat aac gcc atc	1027
Ser Pro Ala Asp Glu Arg Ile Arg Leu Glu Ser Val Asn Asn Ala Ile	
295 300 305	
gag cac gca aag atc gct gca tac tca ctc gtc ggc cag ccc gaa gcc	1075
Glu His Ala Lys Ile Ala Ala Tyr Ser Leu Val Gly Gln Pro Glu Ala	
310 315 320 325	

tac gcc gga atc ccc tgg ttc tgg tcc aac caa ggc gat ctc aaa cta 1123
 Tyr Ala Gly Ile Pro Trp Phe Trp Ser Asn Gln Gly Asp Leu Lys Leu
 330 335 340

 caa att gca gga ctt acc ctt ggt tat gac agc aca gta atc cga cag 1171
 Gln Ile Ala Gly Leu Thr Leu Gly Tyr Asp Ser Thr Val Ile Arg Gln
 345 350 355

 gat ccc gag aaa aag aag ttc tct gtc ctt tat tac cgt ggc gac aac 1219
 Asp Pro Glu Lys Lys Lys Phe Ser Val Leu Tyr Tyr Arg Gly Asp Asn
 360 365 370

 atc atc gcc gcc gat tgt gtc aac gct cca ctg gat ttc atg gct gtg 1267
 Ile Ile Ala Ala Asp Cys Val Asn Ala Pro Leu Asp Phe Met Ala Val
 375 380 385

 cgc agt gca ctt tcc agg aac caa aat atc ccc gcc gac ctt gct gca 1315
 Arg Ser Ala Leu Ser Arg Asn Gln Asn Ile Pro Ala Asp Leu Ala Ala
 390 395 400 405

 gat att tcg cag ccg ctg aaa aaa cta gcc gtt gac ctg gag gtt acc 1363
 Asp Ile Ser Gln Pro Leu Lys Lys Leu Ala Val Asp Leu Glu Val Thr
 410 415 420

 cga tgactcgcag taatttaccc gct 1389
 Arg

<210> 678

<211> 422

<212> PRT

<213> Corynebacterium glutamicum

<400> 678

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 20 25 30

 Ser Ile Thr Leu Leu Gly Glu Glu Asp His Arg Pro Tyr Gln Arg Pro
 35 40 45

 Ala Leu Ser Lys Glu Phe Leu Gln Asp Lys Ile Asp Lys Glu Arg Leu
 50 55 60

 Ile Phe Arg Ser Asn Glu Tyr Trp Glu Glu Asn Asn Ile Arg Leu Val
 65 70 75 80

 Lys Gly Val Arg Ile Glu Arg Ile Glu Lys Asn Asp Asp Gly Ser Gly
 85 90 95

 Val Ala Tyr Gly Ala Gly Gln Glu Phe Ala Phe Arg Arg Leu Ala Leu
 100 105 110

 Ala Val Gly Ala Arg Pro Arg His Leu Asp Leu Pro Gly Ala Thr Leu
 115 120 125

 Glu Gly Val Thr Tyr Leu Arg Asn Ala Asp Asp Ala Leu Ala Leu Lys
 130 135 140

Ala Met Ile Gly Ser Val Thr Asp Ala Val Val Val Gly Gly Gly Phe
 145 150 155 160
 Ile Gly Leu Glu Ala Ala Cys Ser Leu His Asp Leu Gly Lys Asn Val
 165 170 175
 Thr Val Leu Glu Tyr Gly Pro Arg Leu Ile Gly Arg Ala Val Gly Glu
 180 185 190
 Glu Thr Ala Ala Phe Phe Leu Glu Gln His Arg Ser Arg Gly Val Asn
 195 200 205
 Ile Val Leu Asp Ala Arg Met Lys Gln Phe Val Gly Lys Asp Gly Lys
 210 215 220
 Leu Ser Gly Ile Glu Leu Glu Asp Gly Thr Val Ile Pro Ala Gln Leu
 225 230 235 240
 Val Ile Val Gly Ile Gly Val Ile Pro Asn Thr Glu Leu Ala Ala Val
 245 250 255
 Leu Gly Leu Asp Ile Asn Asn Gly Ile Val Val Asp Lys His Ala Val
 260 265 270
 Ala Ser Asp Gly Thr Thr Ile Ala Ile Gly Asp Val Ala Asn Ile Pro
 275 280 285
 Asn Pro Ile Pro Gly Ser Pro Ala Asp Glu Arg Ile Arg Leu Glu Ser
 290 295 300
 Val Asn Asn Ala Ile Glu His Ala Lys Ile Ala Ala Tyr Ser Leu Val
 305 310 315 320
 Gly Gln Pro Glu Ala Tyr Ala Gly Ile Pro Trp Phe Trp Ser Asn Gln
 325 330 335
 Gly Asp Leu Lys Leu Gln Ile Ala Gly Leu Thr Leu Gly Tyr Asp Ser
 340 345 350
 Thr Val Ile Arg Gln Asp Pro Glu Lys Lys Lys Phe Ser Val Leu Tyr
 355 360 365
 Tyr Arg Gly Asp Asn Ile Ile Ala Ala Asp Cys Val Asn Ala Pro Leu
 370 375 380
 Asp Phe Met Ala Val Arg Ser Ala Leu Ser Arg Asn Gln Asn Ile Pro
 385 390 395 400
 Ala Asp Leu Ala Ala Asp Ile Ser Gln Pro Leu Lys Lys Leu Ala Val
 405 410 415
 Asp Leu Glu Val Thr Arg
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<210> 679

<211> 1074

<212> DNA

<213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1051)
 <223> RXA00224

<400> 679

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                               Met Ser Ile Ser Tyr
                               1           5

gtg ctg gtt gag cag cta gat ggc cgc cca gaa cca gtt acc ctt gaa 163
Val Leu Val Glu Gln Leu Asp Gly Arg Pro Glu Pro Val Thr Leu Glu
          10                15                20

ttg atc act gct gct cgc gca ctc ggt gac gtc gtt gcc gtt gtc gtt 211
Leu Ile Thr Ala Ala Arg Ala Leu Gly Asp Val Val Ala Val Val Val
          25                30                35

ggc gag cca ggt gcc ggc gta aac ctt gct gct gag ctc ggc aat tgg 259
Gly Glu Pro Gly Ala Gly Val Asn Leu Ala Ala Glu Leu Gly Asn Trp
          40                45                50

ggg gca gca cag gtt gtt tcc gct gaa atc tct ggc gct tcc aac cgt 307
Gly Ala Ala Gln Val Val Ser Ala Glu Ile Ser Gly Ala Ser Asn Arg
          55                60                65

ttg atc ttg cct gct gtt gat gcg ctg cac att ttg gct gcg aac aac 355
Leu Ile Leu Pro Ala Val Asp Ala Leu His Ile Leu Ala Ala Asn Asn
          70                75                80                85

cca ggt cca att gtt atc gct gca act gca agc ggt aat gag atc gct 403
Pro Gly Pro Ile Val Ile Ala Ala Thr Ala Ser Gly Asn Glu Ile Ala
          90                95                100

ggg cgt ttg gct gcc cgt ttg gct tct ggt gtg ctc acc gat gtc gtc 451
Gly Arg Leu Ala Ala Arg Leu Ala Ser Gly Val Leu Thr Asp Val Val
          105                110                115

gga atc aat gcc gac cgc acc gca cag cag tcc att ttc ggc gac acc 499
Gly Ile Asn Ala Asp Arg Thr Ala Gln Gln Ser Ile Phe Gly Asp Thr
          120                125                130

att cag gtg tcc gct gca gtt ggt ggc gct tca ccg ctg tac acc ctg 547
Ile Gln Val Ser Ala Ala Val Gly Gly Ala Ser Pro Leu Tyr Thr Leu
          135                140                145

cgt cca ggt gcc ctt gat ggc gtg gcc gtt cct gca acc ggt gaa ttg 595
Arg Pro Gly Ala Leu Asp Gly Val Ala Val Pro Ala Thr Gly Glu Leu
          150                155                160                165

gca acc att gag atc cca ggc gca acc gcc aag gat gtc acc atc acc 643
Ala Thr Ile Glu Ile Pro Gly Ala Thr Ala Lys Asp Val Thr Ile Thr
          170                175                180

tcc ttc acg cca agc acc cag agc gat cgc cct gag ctg cca cag gca 691
Ser Phe Thr Pro Ser Thr Gln Ser Asp Arg Pro Glu Leu Pro Gln Ala
          185                190                195

aag gtc gtt atc gca ggt gga cgt ggt gtc gga agc gaa gaa aac ttc 739

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Lys Val Val Ile Ala Gly Gly Arg Gly Val Gly Ser Glu Glu Asn Phe
 200 205 210
 cgc agc atc gtt gaa cca ctg gca gat gca ttg ggc ggt gcc gtt ggc 787
 Arg Ser Ile Val Glu Pro Leu Ala Asp Ala Leu Gly Gly Ala Val Gly
 215 220 225
 gca acc cgc gac gcc gtt gat ctg ggc tac tac cca ggc gag tac cag 835
 Ala Thr Arg Asp Ala Val Asp Leu Gly Tyr Tyr Pro Gly Glu Tyr Gln
 230 235 240 245
 gtt ggt cag acc ggt gtc acc gtg tcc cca gac ctc tac atc ggc ctc 883
 Val Gly Gln Thr Gly Val Thr Val Ser Pro Asp Leu Tyr Ile Gly Leu
 250 255 260
 ggc att tcc ggt gca att cag cac act tct ggt atg cag acc gca aag 931
 Gly Ile Ser Gly Ala Ile Gln His Thr Ser Gly Met Gln Thr Ala Lys
 265 270 275
 aag gtt att gtg atc aac aac gat gag gac gcg ccg atc ttc cag att 979
 Lys Val Ile Val Ile Asn Asn Asp Glu Asp Ala Pro Ile Phe Gln Ile
 280 285 290
 gcg gac ctc ggt gtc gtt ggc gac ctc ttt gac atc gcc cct gcg ctc 1027
 Ala Asp Leu Gly Val Val Gly Asp Leu Phe Asp Ile Ala Pro Ala Leu
 295 300 305
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 310 315
 <210> 680
 <211> 317
 <212> PRT
 <213> Corynebacterium glutamicum
 <400> 680
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 20 25 30
 Val Ala Val Val Val Gly Glu Pro Gly Ala Gly Val Asn Leu Ala Ala
 35 40 45
 Glu Leu Gly Asn Trp Gly Ala Ala Gln Val Val Ser Ala Glu Ile Ser
 50 55 60
 Gly Ala Ser Asn Arg Leu Ile Leu Pro Ala Val Asp Ala Leu His Ile
 65 70 75 80
 Leu Ala Ala Asn Asn Pro Gly Pro Ile Val Ile Ala Ala Thr Ala Ser
 85 90 95
 Gly Asn Glu Ile Ala Gly Arg Leu Ala Ala Arg Leu Ala Ser Gly Val
 100 105 110
 Leu Thr Asp Val Val Gly Ile Asn Ala Asp Arg Thr Ala Gln Gln Ser
 115 120 125

Ile Phe Gly Asp Thr Ile Gln Val Ser Ala Ala Val Gly Gly Ala Ser
 130 135 140
 Pro Leu Tyr Thr Leu Arg Pro Gly Ala Leu Asp Gly Val Ala Val Pro
 145 150 155 160
 Ala Thr Gly Glu Leu Ala Thr Ile Glu Ile Pro Gly Ala Thr Ala Lys
 165 170 175
 Asp Val Thr Ile Thr Ser Phe Thr Pro Ser Thr Gln Ser Asp Arg Pro
 180 185 190
 Glu Leu Pro Gln Ala Lys Val Val Ile Ala Gly Gly Arg Gly Val Gly
 195 200 205
 Ser Glu Glu Asn Phe Arg Ser Ile Val Glu Pro Leu Ala Asp Ala Leu
 210 215 220
 Gly Gly Ala Val Gly Ala Thr Arg Asp Ala Val Asp Leu Gly Tyr Tyr
 225 230 235 240
 Pro Gly Glu Tyr Gln Val Gly Gln Thr Gly Val Thr Val Ser Pro Asp
 245 250 255
 Leu Tyr Ile Gly Leu Gly Ile Ser Gly Ala Ile Gln His Thr Ser Gly
 260 265 270
 Met Gln Thr Ala Lys Lys Val Ile Val Ile Asn Asn Asp Glu Asp Ala
 275 280 285
 Pro Ile Phe Gln Ile Ala Asp Leu Gly Val Val Gly Asp Leu Phe Asp
 290 295 300
 Ile Ala Pro Ala Leu Ile Glu Glu Ile Asn Lys Arg Lys
 305 310 315

<210> 681
 <211> 909
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(886)
 <223> RXA00225

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 Met Ser Thr Ile Val
 1 5
 gtt ctg gtt aaa aat gtt cca gac acc tgg tct aag agg act ctg gaa 163
 Val Leu Val Lys Asn Val Pro Asp Thr Trp Ser Lys Arg Thr Leu Glu
 10 15 20
 gct gat ttc acc ctt gac cgt gag ggt gta gat cga gtc ttg gat gag 211
 Ala Asp Phe Thr Leu Asp Arg Glu Gly Val Asp Arg Val Leu Asp Glu

25	30	35	
atc aat gag ttt gct ctg gag cag gca ctg cgc ttg cgg gag tcc aac Ile Asn Glu Phe Ala Leu Glu Gln Ala Leu Arg Leu Arg Glu Ser Asn 40 45 50			259
ccg gat gct ggt tac cgc gtt gtt gcg ctg agc gcc ggc cct gcc ggt Pro Asp Ala Gly Tyr Arg Val Val Ala Leu Ser Ala Gly Pro Ala Gly 55 60 65			307
ggg gaa gag gcg ctg cgt aag gcg ctg tcc atg ggt gct gat gaa gca Gly Glu Glu Ala Leu Arg Lys Ala Leu Ser Met Gly Ala Asp Glu Ala 70 75 80 85			355
atc cag ctc agt gat gat gcc ttg gct ggt tct gat ctt ttg gga acc Ile Gln Leu Ser Asp Asp Ala Leu Ala Gly Ser Asp Leu Leu Gly Thr 90 95 100			403
gct tgg gcg ctg aac aac gct atc aac acc atc gcg ggt gtt gct ctc Ala Trp Ala Leu Asn Asn Ala Ile Asn Thr Ile Ala Gly Val Ala Leu 105 110 115			451
atc gtg acg ggt tgc gct tct tcc gat ggt tcc atg ggt gcg ctt cct Ile Val Thr Gly Ser Ala Ser Ser Asp Gly Ser Met Gly Ala Leu Pro 120 125 130			499
ggc gtg tta gct gag tac cgc cag gtc cca gcg ttg act aac ttg tct Gly Val Leu Ala Glu Tyr Arg Gln Val Pro Ala Leu Thr Asn Leu Ser 135 140 145			547
gcg ctg aag gtc gag ggt gca tct att act gcc act cgc att gat aac Ala Leu Lys Val Glu Gly Ala Ser Ile Thr Ala Thr Arg Ile Asp Asn 150 155 160 165			595
cac ggc acc tat gag ttg cag gct gca ctt cct gcg gtt gtg tgc att His Gly Thr Tyr Glu Leu Gln Ala Ala Leu Pro Ala Val Val Ser Ile 170 175 180			643
tcc gat aag gct gac aag cca cgt ttc cct aac ttc aag ggc atc atg Ser Asp Lys Ala Asp Lys Pro Arg Phe Pro Asn Phe Lys Gly Ile Met 185 190 195			691
gct gct aag aag gct gag atc aag aag ctt tcc ttg gct gaa atc ggc Ala Ala Lys Lys Ala Glu Ile Lys Lys Leu Ser Leu Ala Glu Ile Gly 200 205 210			739
gtg gct cca gag cag gtt ggt ctg tct cac gcg gca act gct gtt act Val Ala Pro Glu Gln Val Gly Leu Ser His Ala Ala Thr Ala Val Thr 215 220 225			787
gct gca gct gat cgt cct gag cgc tcc caa ggt gat gtc att ggt gca Ala Ala Ala Asp Arg Pro Glu Arg Ser Gln Gly Asp Val Ile Gly Ala 230 235 240 245			835
tcg ggt gct gct gaa aag att gct gag tac ctc gct tca gag aac ctc Ser Gly Ala Ala Glu Lys Ile Ala Glu Tyr Leu Ala Ser Glu Asn Leu 250 255 260			883
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<212> PRT

<213> Corynebacterium glutamicum

<400> 682

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 20 25 30

Arg Val Leu Asp Glu Ile Asn Glu Phe Ala Leu Glu Gln Ala Leu Arg
 35 40 45

Leu Arg Glu Ser Asn Pro Asp Ala Gly Tyr Arg Val Val Ala Leu Ser
 50 55 60

Ala Gly Pro Ala Gly Gly Glu Glu Ala Leu Arg Lys Ala Leu Ser Met
 65 70 75 80

Gly Ala Asp Glu Ala Ile Gln Leu Ser Asp Asp Ala Leu Ala Gly Ser
 85 90 95

Asp Leu Leu Gly Thr Ala Trp Ala Leu Asn Asn Ala Ile Asn Thr Ile
 100 105 110

Ala Gly Val Ala Leu Ile Val Thr Gly Ser Ala Ser Ser Asp Gly Ser
 115 120 125

Met Gly Ala Leu Pro Gly Val Leu Ala Glu Tyr Arg Gln Val Pro Ala
 130 135 140

Leu Thr Asn Leu Ser Ala Leu Lys Val Glu Gly Ala Ser Ile Thr Ala
 145 150 155 160

Thr Arg Ile Asp Asn His Gly Thr Tyr Glu Leu Gln Ala Ala Leu Pro
 165 170 175

Ala Val Val Ser Ile Ser Asp Lys Ala Asp Lys Pro Arg Phe Pro Asn
 180 185 190

Phe Lys Gly Ile Met Ala Ala Lys Lys Ala Glu Ile Lys Lys Leu Ser
 195 200 205

Leu Ala Glu Ile Gly Val Ala Pro Glu Gln Val Gly Leu Ser His Ala
 210 215 220

Ala Thr Ala Val Thr Ala Ala Ala Asp Arg Pro Glu Arg Ser Gln Gly
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Asp Val Ile Gly Ala Ser Gly Ala Ala Glu Lys Ile Ala Glu Tyr Leu
 245 250 255

Ala Ser Glu Asn Leu Ile
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 <222> (82)..(2355)
 <223> RXN00606

<400> 683

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tgatttctg cggagaagcc agtg ctc acg ggt gtt att gcg gtg ctg att      111
          Val Leu Thr Gly Val Ile Ala Val Leu Ile
              1              5              10

gca atg tcc gcg ttc act aag tcc gca cag ttc ccg ttc cac ttc tgg      153
Ala Met Ser Ala Phe Thr Lys Ser Ala Gln Phe Pro Phe His Phe Trp
              15              20              25

ctg cct gag gcg atg gct gcg gcc acc cca gtg tcg gcg ttc ctg cac      207
Leu Pro Glu Ala Met Ala Ala Ala Thr Pro Val Ser Ala Phe Leu His
              30              35              40

gct gcg gcc gtg gtc aag gcg ggt att tac ctg ttg ctg cgc ttt agc      255
Ala Ala Ala Val Val Lys Ala Gly Ile Tyr Leu Leu Leu Arg Phe Ser
              45              50              55

att gtg ttc cat gat gtt gcg gtc tgg aat tgg ttg ctg att atc gtc      303
Ile Val Phe His Asp Val Ala Val Trp Asn Trp Leu Leu Ile Ile Val
              60              65              70

ggc atg ggt acg gcc atc atg tcg gcg tat ttc gcg gtg cag aag acc      351
Gly Met Gly Thr Ala Ile Met Ser Ala Tyr Phe Ala Val Gln Lys Thr
              75              80              85              90

gat ctg aag aag ctc acg gca tat tcc acg gtg tcg cat ttg ggt tgg      399
Asp Leu Lys Lys Leu Thr Ala Tyr Ser Thr Val Ser His Leu Gly Trp
              95              100              105

atc gta gcg acc atc ggc gtg ggc act cct ttc gcg ctc ggc gct gcc      447
Ile Val Ala Thr Ile Gly Val Gly Thr Pro Phe Ala Leu Gly Ala Ala
              110              115              120

att gtg cac acg ctc agc cac gcg ctg ttt aag tcc tcg ttg ttc atg      495
Ile Val His Thr Leu Ser His Ala Leu Phe Lys Ser Ser Leu Phe Met
              125              130              135

ctc att ggc gtg att gat cac cag act ggc acg cgc gat att cgt cgc      543
Leu Ile Gly Val Ile Asp His Gln Thr Gly Thr Arg Asp Ile Arg Arg
              140              145              150

ctc ggt ttc ctg gtc aag aag atg ccg ttc acg ttt gtg tct gta tta      591
Leu Gly Phe Leu Val Lys Lys Met Pro Phe Thr Phe Val Ser Val Leu
              155              160              165              170

ata ggt gcg ttg tcg atg gca tcg gtt ccg ccg ttg ctc ggc ttc gtg      639
Ile Gly Ala Leu Ser Met Ala Ser Val Pro Pro Leu Leu Gly Phe Val
              175              180              185

tcc aaa gaa ggc atg atc aca gcg ttc atg gac gcc ccc atc ggc aac      687
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Ser Lys Glu Gly Met Ile Thr Ala Phe Met Asp Ala Pro Ile Gly Asn	
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Ser Tyr Val Val Leu Leu Leu Val Gly Ala Ala Ile Gly Ala Val Leu	
205	210 215
acc ttc aca tac tcc gcg aaa ctc gtg ctc ggc gca ttc gtc gac ggc	783
Thr Phe Thr Tyr Ser Ala Lys Leu Val Leu Gly Ala Phe Val Asp Gly	
220	225 230
cca cgc gac atg tca cac gtc aag gaa gcc ccc gtc tcc ctc tgg ctt	831
Pro Arg Asp Met Ser His Val Lys Glu Ala Pro Val Ser Leu Trp Leu	
235	240 245 250
ccg gcc gcc ctg cct gga ctt atg tct ctg cca cta gtc cta gta ctt	879
Pro Ala Ala Leu Pro Gly Leu Met Ser Leu Pro Leu Val Leu Val Leu	
255	260 265
tcg ctt ttc gac gcc ccc gtc tcc gcc gca gcc acc tcc gcc gcg ggg	927
Ser Leu Phe Asp Ala Pro Val Ser Ala Ala Ala Thr Ser Ala Ala Gly	
270	275 280
gaa gcg gcg cac atg cac ctg gca ttg tgg cac ggc atc aac acc cca	975
Glu Ala Ala His Met His Leu Ala Leu Trp His Gly Ile Asn Thr Pro	
285	290 295
ctg ttg att tcc ttg ggt gtg ctg gtg gcc gga atc ctt ggt gtg ctg	1023
Leu Leu Ile Ser Leu Gly Val Leu Val Ala Gly Ile Leu Gly Val Leu	
300	305 310
ttc cgc aaa gag ctg tgg aaa atc gcc gag acc agc cct ttc ccc atc	1071
Phe Arg Lys Glu Leu Trp Lys Ile Ala Glu Thr Ser Pro Phe Pro Ile	
315	320 325 330
gcc aca ggc aac gac atc cta tcg atg ctg gtt tac cga gcc aac ttg	1119
Ala Thr Gly Asn Asp Ile Leu Ser Met Leu Val Tyr Arg Ala Asn Leu	
335	340 345
ctg ggt aaa ttc ttc ggt cgc atg gct gat tcg atg agc cca cgc agg	1167
Leu Gly Lys Phe Phe Gly Arg Met Ala Asp Ser Met Ser Pro Arg Arg	
350	355 360
cac ttg gtc agc ctc atc gtg ctg ctc tgg gcg ctg gct gct ttt gcc	1215
His Leu Val Ser Leu Ile Val Leu Leu Trp Ala Leu Ala Ala Phe Ala	
365	370 375
acc att cac ccc tcg gtt cag ctt gca cca aag caa ccg gga att gat	1263
Thr Ile His Pro Ser Val Gln Leu Ala Pro Lys Gln Pro Gly Ile Asp	
380	385 390
cgt tgg atc gac ctc att ccg ctt gcc atc atc gcg cta tct gtc ttc	1311
Arg Trp Ile Asp Leu Ile Pro Leu Ala Ile Ile Ala Leu Ser Val Phe	
395	400 405 410
ggc ctg ctc acc acc cga aac cgc ctc agc gca gcc gtg ctt gtg ggt	1359
Gly Leu Leu Thr Thr Arg Asn Arg Leu Ser Ala Ala Val Leu Val Gly	
415	420 425
acc gtt ggt gtg ggt gtt tcc ttc cag atg cta ctt ctg ggc gct ccc	1407
Thr Val Gly Val Gly Val Ser Phe Gln Met Leu Leu Leu Gly Ala Pro	

430	435	440	
gat gtt gca ctt acc cag ttc ctg gta gaa ggc ctc gtc gtg gta atc Asp Val Ala Leu Thr Gln Phe Leu Val Glu Gly Leu Val Val Val Ile 445 450 455			1455
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ccc agc aga agg cgc agc acc gtt ctt gtc gcc gtc ctt gct gcc ttc Pro Ser Arg Arg Arg Ser Thr Val Leu Val Ala Val Leu Ala Ala Phe 475 480 485 490			1551
gcc gca ttc atg gcg gtg tgg gga ttg ctt ggc cgt cac gaa cgt tct Ala Ala Phe Met Ala Val Trp Gly Leu Leu Gly Arg His Glu Arg Ser 495 500 505			1599
gag ctg gcc atg tgg tac ctc aac caa ggt cca gag atc acc tct ggc Glu Leu Ala Met Trp Tyr Leu Asn Gln Gly Pro Glu Ile Thr Ser Gly 510 515 520			1647
gcc aac gtg gtg aac acc atc ctc gtg gaa ttc cgt gca ctg gat acg Ala Asn Val Val Asn Thr Ile Leu Val Glu Phe Arg Ala Leu Asp Thr 525 530 535			1695
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atg gtg gct tcc atg cct cgt cat ccg ttt gcc aag ggc acc cac cct Met Val Ala Ser Met Pro Arg His Pro Phe Ala Lys Gly Thr His Pro 555 560 565 570			1791
cgc ccc ttt ggc caa tca cag ttg aac tcc att ccg ctg cgc atg ctg Arg Pro Phe Gly Gln Ser Gln Leu Asn Ser Ile Pro Leu Arg Met Leu 575 580 585			1839
ctt aag gtg ctg gtt cca gcg cta tgc ttc ttg agc ttc atg gtg ttc Leu Lys Val Leu Val Pro Ala Leu Cys Phe Leu Ser Phe Met Val Phe 590 595 600			1887
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cgc att ttc cgc ccg aat gtt cct ttc att ctc act ggt gcg ggc atc Arg Ile Phe Arg Pro Asn Val Pro Phe Ile Leu Thr Gly Ala Gly Ile 635 640 645 650			2031
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ctg tac gcc atc cac ttc aac ttc gta ggc cag cac tgg acc acc tcg Leu Tyr Ala Ile His Phe Asn Phe Val Gly Gln His Trp Thr Thr Ser 670 675 680			2127

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 Met Ile Phe Asp Leu Gly Val Tyr Leu Ala Val Leu Gly Met Val Ser
 685 690 695

atg gca atc aac ggc ctg ggc gga tac ctg cgc cca ggt acc gac aat 2223
 Met Ala Ile Asn Gly Leu Gly Gly Tyr Leu Arg Pro Gly Thr Asp Asn
 700 705 710

gca gat ctg gac tac gcc cgc cga agt ggc cca ctg cca gca acg cca 2271
 Ala Asp Leu Asp Tyr Ala Arg Arg Ser Gly Pro Leu Pro Ala Thr Pro
 715 720 725 730

acg gtt gaa ccc gaa cca gaa ggc gat gaa gac tgg ccc gaa ccc atc 2319
 Thr Val Glu Pro Glu Pro Glu Gly Asp Glu Asp Trp Pro Glu Pro Ile
 735 740 745

aac ccc gca ggc gat aac aaa gag gag gca aac cga tgattctcgc 2365
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<400> 684

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Ala Ala Thr Pro Val Ser Ala Phe Leu His Ala Ala Ala Val Val Lys
 35 40 45

Ala Gly Ile Tyr Leu Leu Leu Arg Phe Ser Ile Val Phe His Asp Val
 50 55 60

Ala Val Trp Asn Trp Leu Leu Ile Ile Val Gly Met Gly Thr Ala Ile
 65 70 75 80

Met Ser Ala Tyr Phe Ala Val Gln Lys Thr Asp Leu Lys Lys Leu Thr
 85 90 95

Ala Tyr Ser Thr Val Ser His Leu Gly Trp Ile Val Ala Thr Ile Gly
 100 105 110

Val Gly Thr Pro Phe Ala Leu Gly Ala Ala Ile Val His Thr Leu Ser
 115 120 125

His Ala Leu Phe Lys Ser Ser Leu Phe Met Leu Ile Gly Val Ile Asp
 130 135 140

His Gln Thr Gly Thr Arg Asp Ile Arg Arg Leu Gly Phe Leu Val Lys
 145 150 155 160

Lys Met Pro Phe Thr Phe Val Ser Val Leu Ile Gly Ala Leu Ser Met

165										170					175				
Ala	Ser	Val	Pro	Pro	Leu	Leu	Gly	Phe	Val	Val	Ser	Lys	Glu	Gly	Met	Ile			
			180					185						190					
Thr	Ala	Phe	Met	Asp	Ala	Pro	Ile	Gly	Asn	Ser	Tyr	Val	Val	Leu	Leu				
		195					200					205							
Leu	Val	Gly	Ala	Ala	Ile	Gly	Ala	Val	Leu	Thr	Phe	Thr	Tyr	Ser	Ala				
	210					215					220								
Lys	Leu	Val	Leu	Gly	Ala	Phe	Val	Asp	Gly	Pro	Arg	Asp	Met	Ser	His				
225				230						235				240					
Val	Lys	Glu	Ala	Pro	Val	Ser	Leu	Trp	Leu	Pro	Ala	Ala	Leu	Pro	Gly				
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Leu	Met	Ser	Leu	Pro	Leu	Val	Leu	Val	Leu	Ser	Leu	Phe	Asp	Ala	Pro				
		260					265						270						
Val	Ser	Ala	Ala	Ala	Thr	Ser	Ala	Ala	Gly	Glu	Ala	Ala	His	Met	His				
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Leu	Ala	Leu	Trp	His	Gly	Ile	Asn	Thr	Pro	Leu	Leu	Ile	Ser	Leu	Gly				
	290					295					300								
Val	Leu	Val	Ala	Gly	Ile	Leu	Gly	Val	Leu	Phe	Arg	Lys	Glu	Leu	Trp				
305				310						315				320					
Lys	Ile	Ala	Glu	Thr	Ser	Pro	Phe	Pro	Ile	Ala	Thr	Gly	Asn	Asp	Ile				
			325					330					335						
Leu	Ser	Met	Leu	Val	Tyr	Arg	Ala	Asn	Leu	Leu	Gly	Lys	Phe	Phe	Gly				
		340					345						350						
Arg	Met	Ala	Asp	Ser	Met	Ser	Pro	Arg	Arg	His	Leu	Val	Ser	Leu	Ile				
		355					360				365								
Val	Leu	Leu	Trp	Ala	Leu	Ala	Ala	Phe	Ala	Thr	Ile	His	Pro	Ser	Val				
	370					375					380								
Gln	Leu	Ala	Pro	Lys	Gln	Pro	Gly	Ile	Asp	Arg	Trp	Ile	Asp	Leu	Ile				
385				390					395					400					
Pro	Leu	Ala	Ile	Ile	Ala	Leu	Ser	Val	Phe	Gly	Leu	Leu	Thr	Thr	Arg				
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Asn	Arg	Leu	Ser	Ala	Ala	Val	Leu	Val	Gly	Thr	Val	Gly	Val	Gly	Val				
		420					425					430							
Ser	Phe	Gln	Met	Leu	Leu	Leu	Gly	Ala	Pro	Asp	Val	Ala	Leu	Thr	Gln				
	435					440					445								
Phe	Leu	Val	Glu	Gly	Leu	Val	Val	Val	Ile	Ile	Met	Met	Val	Val	Arg				
	450					455					460								
His	Gln	Pro	Ala	Asn	Phe	Lys	Arg	Ile	Lys	Pro	Ser	Arg	Arg	Arg	Ser				
465				470					475					480					
Thr	Val	Leu	Val	Ala	Val	Leu	Ala	Ala	Phe	Ala	Ala	Phe	Met	Ala	Val				
			485				490						495						

Trp Gly Leu Leu Gly Arg His Glu Arg Ser Glu Leu Ala Met Trp Tyr
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 Leu Asn Gln Gly Pro Glu Ile Thr Ser Gly Ala Asn Val Val Asn Thr
 515 520 525
 Ile Leu Val Glu Phe Arg Ala Leu Asp Thr Leu Gly Glu Leu Ser Val
 530 535 540
 Leu Gly Met Ala Ala Val Ile Gly Ala Met Val Ala Ser Met Pro
 545 550 555 560
 Arg His Pro Phe Ala Lys Gly Thr His Pro Arg Pro Phe Gly Gln Ser
 565 570 575
 Gln Leu Asn Ser Ile Pro Leu Arg Met Leu Leu Lys Val Leu Val Pro
 580 585 590
 Ala Leu Cys Phe Leu Ser Phe Met Val Phe Met Arg Gly His Asn Asp
 595 600 605
 Pro Gly Gly Gly Phe Ile Ala Ala Leu Ile Ala Gly Gly Ala Leu Met
 610 615 620
 Leu Leu Tyr Leu Ser Lys Ala Lys Asp Gly Arg Ile Phe Arg Pro Asn
 625 630 635 640
 Val Pro Phe Ile Leu Thr Gly Ala Gly Ile Leu Met Ala Val Phe Ser
 645 650 655
 Gly Val Leu Gly Leu Thr His Gly Ser Phe Leu Tyr Ala Ile His Phe
 660 665 670
 Asn Phe Val Gly Gln His Trp Thr Thr Ser Met Ile Phe Asp Leu Gly
 675 680 685
 Val Tyr Leu Ala Val Leu Gly Met Val Ser Met Ala Ile Asn Gly Leu
 690 695 700
 Gly Gly Tyr Leu Arg Pro Gly Thr Asp Asn Ala Asp Leu Asp Tyr Ala
 705 710 715 720
 Arg Arg Ser Gly Pro Leu Pro Ala Thr Pro Thr Val Glu Pro Glu Pro
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<223> FRXA00606

<400> 685

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                                   Met Ala Ser Val Pro
                                   1 5

ccg ttg ctc ggc ttc gtg tcc aaa gaa ggc atg atc aca gcg ttc atg 163
Pro Leu Leu Gly Phe Val Ser Lys Glu Gly Met Ile Thr Ala Phe Met
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gac gcc ccc atc ggc aac tcc tat gtt gta tta ctg ctg gtc ggc gca 211
Asp Ala Pro Ile Gly Asn Ser Tyr Val Val Leu Leu Leu Val Gly Ala
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gca atc ggc gcg gtc cta acc ttc aca tac tcc gcg aaa ctc gtg ctc 259
Ala Ile Gly Ala Val Leu Thr Phe Thr Tyr Ser Ala Lys Leu Val Leu
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ggc gca ttc gtc gac ggc cca cgc gac atg tca cac gtc aag gaa gcc 307
Gly Ala Phe Val Asp Gly Pro Arg Asp Met Ser His Val Lys Glu Ala
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ccc gtc tcc ctc tgg ctt ccg gcc gcc ctg cct gga ctt atg tct ctg 355
Pro Val Ser Leu Trp Leu Pro Ala Ala Leu Pro Gly Leu Met Ser Leu
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cca cta gtc cta gta ctt tcg ctt ttc gac gcc ccc gtc tcc gcc gca 403
Pro Leu Val Leu Val Leu Ser Leu Phe Asp Ala Pro Val Ser Ala Ala
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gcc acc tcc gcc gcg ggg gaa gcg gcg cac atg cac ctg gca ttg tgg 451
Ala Thr Ser Ala Ala Gly Glu Ala Ala His Met His Leu Ala Leu Trp
                                   105 110 115

cac ggc atc aac acc cca ctg ttg att tcc ttg ggt gtg ctg gtg gcc 499
His Gly Ile Asn Thr Pro Leu Leu Ile Ser Leu Gly Val Leu Val Ala
                                   120 125 130

gga atc ctt ggt gtg ctg ttc cgc aaa gag ctg tgg aaa atc gcc gag 547
Gly Ile Leu Gly Val Leu Phe Arg Lys Glu Leu Trp Lys Ile Ala Glu
                                   135 140 145

acc agc cct ttc ccc atc gcc aca ggc aac gac atc cta tcg atg ctg 595
Thr Ser Pro Phe Pro Ile Ala Thr Gly Asn Asp Ile Leu Ser Met Leu
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gtt tac cga gcc aac ttg ctg ggt aaa ttc ttc ggt cgc atg gct gat 643
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tcg atg agc cca cgc agg cac ttg gtc agc ctc atc gtg ctg ctc tgg 691
Ser Met Ser Pro Arg Arg His Leu Val Ser Leu Ile Val Leu Leu Trp
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gcg ctg gct gct ttt gcc acc att cac ccc tcg gtt cag ctt gca cca 739
Ala Leu Ala Ala Phe Ala Thr Ile His Pro Ser Val Gln Leu Ala Pro
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gca gcc gtg ctt gtg ggt acc gtt ggt gtg ggt gtt tcc ttc cag atg Ala Ala Val Leu Val Gly Thr Val Gly Val Gly Val Ser Phe Gln Met 250 255 260	883
cta ctt ctg ggc gct ccc gat gtt gca ctt acc cag ttc ctg gta gaa Leu Leu Leu Gly Ala Pro Asp Val Ala Leu Thr Gln Phe Leu Val Glu 265 270 275	931
ggc ctc gtc gtg gta atc atc atg atg gtt gtc cgg cac cag cct gcc Gly Leu Val Val Val Ile Ile Met Met Val Val Arg His Gln Pro Ala 280 285 290	979
aac ttc aag cgc atc aag ccc agc aga agg cgc agc acc gtt ctt gtc Asn Phe Lys Arg Ile Lys Pro Ser Arg Arg Arg Ser Thr Val Leu Val 295 300 305	1027
gcc gtc ctt gct gcc ttc gcc gca ttc atg gcg gtg tgg gga ttg ctt Ala Val Leu Ala Ala Phe Ala Ala Phe Met Ala Val Trp Gly Leu Leu 310 315 320 325	1075
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cca gag atc acc tct ggc gcc aac gtg gtg aac acc atc ctc gtg gaa Pro Glu Ile Thr Ser Gly Ala Asn Val Val Asn Thr Ile Leu Val Glu 345 350 355	1171
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Ser Lys Ala Lys Asp Gly Arg Ile Phe Arg Pro Asn Val Pro Phe Ile
 455 460 465

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 470 475 480 485

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 Leu Thr His Gly Ser Phe Leu Tyr Ala Ile His Phe Asn Phe Val Gly
 490 495 500

cag cac tgg acc acc tcg atg atc ttc gac ctc ggc gtg tac ctg gcc 1651
 Gln His Trp Thr Ser Met Ile Phe Asp Leu Gly Val Tyr Leu Ala
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Ala Lys Leu Val Leu Gly Ala Phe Val Asp Gly Pro Arg Asp Met Ser
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His Val Lys Glu Ala Pro Val Ser Leu Trp Leu Pro Ala Ala Leu Pro
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Gly Leu Met Ser Leu Pro Leu Val Leu Val Leu Ser Leu Phe Asp Ala
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Pro Val Ser Ala Ala Ala Thr Ser Ala Ala Gly Glu Ala Ala His Met

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Ser	Gln	Leu	Asn	Ser	Ile	Pro	Leu	Arg	Met	Leu	Leu	Lys	Val	Leu	Val	
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Pro	Ala	Leu	Cys	Phe	Leu	Ser	Phe	Met	Val	Phe	Met	Arg	Gly	His	Asn	
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Asp Pro Gly Gly Gly Phe Ile Ala Ala Leu Ile Ala Gly Gly Ala Leu
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 Asn Val Pro Phe Ile Leu Thr Gly Ala Gly Ile Leu Met Ala Val Phe
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 Ser Gly Val Leu Gly Leu Thr His Gly Ser Phe Leu Tyr Ala Ile His
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 Met Ala Met Asp Val
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 Val Leu Leu Pro Trp Arg Leu Ile Arg Asp Ile Leu His Ile Ile Val
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 Pro Phe Ala Gly Ile Phe Ala Gly Ile Trp Leu Phe Ala His Thr Ala
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 Glu His Gly Pro Ile Ala His Asn Val Gly Leu Tyr Val Gly Gly Val
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 Thr Ser Ile Val Ala Val Ala Ala Asn Trp Phe Ala Thr Ile Val Gly
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gaa acc cgc gcg cgt ttc tat cca gcg ctc aca ttg atg ctg atc acg 451
 Glu Thr Arg Ala Arg Phe Tyr Pro Ala Leu Thr Leu Met Leu Ile Thr
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 Gly Val Asn Gly Ala Leu Leu Thr Ala Asp Leu Phe Asn Phe Phe Val
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 Phe Ile Glu Val Met Leu Leu Pro Ser Tyr Gly Leu Ile Ala Met Thr
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 Leu Ser Ala Ser Thr Leu Leu Val Ala Gly Val Gly Ile Val Tyr Gly
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gtc ata ggc tca gtc aac atc gca gct ctg caa gat gtc gta gag ggc 691
 Val Ile Gly Ser Val Asn Ile Ala Ala Leu Gln Asp Val Val Glu Gly
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 Asn Pro Leu Val Ala Ser Ala Met Gly Ile Val Val Ile Ala Ile Ala
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 Pro Gly Thr Ser Ala Ala Val Met Gly Leu Phe Ser Gly Leu His Thr
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 Lys Val Ala Val Tyr Met Leu Tyr Arg Ile Trp Val His Ile Phe Asn
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Lys	Ala	Leu	Ile	Leu	Leu	Glu	Ile	Ala	Arg	Val	Gly	Asn	Ile	Ala	Ala		
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Trp	Ile	Ala	Ile	Ala	Ala	Ile	Ile	Ile	Ala	Ser	Leu	Gly	Ala	Leu	Leu		
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Gln	Arg	Gly	Val	Ser	Pro	Gln	Leu	Arg	Ile	Ser	Pro	Ala	Lys	Ile	Ala		
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Pro	Ala	Leu	Ser	Leu	Ile	Ile	Leu	Ser	Val	Gly	Met	Phe	Ile	Phe	Ala		
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Gly	Pro	Leu	Ile	Asp	Ala	Thr	Leu	Thr	Ala	Thr	Asp	Gly	Leu	Leu	Asn		
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<213> *Corynebacterium glutamicum*

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Leu His Ile Ile Val Pro Phe Ala Gly Ile Phe Ala Gly Ile Trp Leu
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Phe Ala His Thr Ala Glu His Gly Pro Ile Ala His Asn Val Gly Leu
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Tyr Val Gly Gly Val Ala Ile Pro Phe Ala Ala Asp Thr Phe Ser Ala
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Ile Met Leu Ile Thr Thr Ser Ile Val Ala Val Ala Ala Asn Trp Phe
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Ala Thr Ile Val Gly Glu Thr Arg Ala Arg Phe Tyr Pro Ala Leu Thr
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Leu Met Leu Ile Thr Gly Val Asn Gly Ala Leu Leu Thr Ala Asp Leu
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Phe Asn Phe Phe Val Phe Ile Glu Val Met Leu Leu Pro Ser Tyr Gly
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Leu Ile Ala Met Thr Gly Thr Trp Ala Arg Leu Ala Ser Gly Arg Ile
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Phe Val Leu Val Asn Leu Ser Ala Ser Thr Leu Leu Val Ala Gly Val
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Gly Ile Val Tyr Gly Val Ile Gly Ser Val Asn Ile Ala Ala Leu Gln
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Asp Val Val Glu Gly Asn Pro Leu Val Ala Ser Ala Met Gly Ile Val
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Val Ile Ala Ile Ala Val Lys Ala Gly Val Phe Pro Val His Thr Trp
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Leu Pro Arg Thr Tyr Pro Gly Thr Ser Ala Ala Val Met Gly Leu Phe
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Ser Gly Leu His Thr Lys Val Ala Val Tyr Met Leu Tyr Arg Ile Trp
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Val His Ile Phe Asn Met Asp Pro Thr Trp Asn Trp Leu Ile Val Ala
      260           265           270

Phe Met Val Ile Ser Met Leu Val Gly Gly Phe Ala Gly Leu Ala Glu
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Asn Ser Ile Arg Arg Val Leu Ala Tyr Gln Met Val Asn Gly Met Pro
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Phe Ile Leu Ile Met Met Ala Phe Thr Ser Asp Asp Pro Gln Arg Ala

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 Ala Leu Val Leu Thr Ser Gly Ala Ile Glu Glu Thr Tyr Gly Thr Gly
 340 345 350
 Met Leu Ser Lys Leu Ser Gly Leu Ala Arg Arg Glu Pro Val Val Ala
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 Ala Val Phe Ala Ala Gly Ala Phe Ser Val Val Gly Phe Pro Pro Phe
 370 375 380
 Ser Gly Met Trp Gly Lys Ala Leu Ile Leu Leu Glu Ile Ala Arg Val
 385 390 395 400
 Gly Asn Ile Ala Ala Trp Ile Ala Ile Ala Ala Ile Ile Ile Ala Ser
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 Leu Gly Ala Leu Leu Ser Met Ile Arg Val Trp Arg Glu Val Phe Trp
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 Gly Gly Ala Met His Gln Arg Gly Val Ser Pro Gln Leu Arg Ile Ser
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 Pro Ala Lys Ile Ala Pro Ala Leu Ser Leu Ile Ile Leu Ser Val Gly
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 Met Phe Ile Phe Ala Gly Pro Leu Ile Asp Ala Thr Leu Thr Ala Thr
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Pro	Phe	Ala	Gly	Ile	Phe	Ala	Gly	Ile	Trp	Leu	Phe	Ala	His	Thr	Ala		
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Glu	His	Gly	Pro	Ile	Ala	His	Asn	Val	Gly	Leu	Tyr	Val	Gly	Gly	Val		
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Ala	Ile	Pro	Phe	Ala	Ala	Asp	Thr	Phe	Ser	Ala	Ile	Met	Leu	Ile	Thr		
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Thr	Ser	Ile	Val	Ala	Val	Ala	Ala	Asn	Trp	Phe	Ala	Thr	Ile	Val	Gly		
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Glu	Thr	Arg	Ala	Arg	Phe	Tyr	Pro	Ala	Leu	Thr	Leu	Met	Leu	Ile	Thr		
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Val	Ile	Gly	Ser	Val	Asn	Ile	Ala	Ala	Leu	Gln	Asp	Val	Val	Glu	Gly		
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Asn	Pro	Leu	Val	Ala	Ser	Ala	Met	Gly	Ile	Val	Val	Ile	Ala	Ile	Ala		
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Leu His Ile Ile Val Pro Phe Ala Gly Ile Phe Ala Gly Ile Trp Leu
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Phe Ala His Thr Ala Glu His Gly Pro Ile Ala His Asn Val Gly Leu
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Tyr Val Gly Gly Val Ala Ile Pro Phe Ala Ala Asp Thr Phe Ser Ala
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Ile Met Leu Ile Thr Thr Ser Ile Val Ala Val Ala Ala Asn Trp Phe
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Ala Thr Ile Val Gly Glu Thr Arg Ala Arg Phe Tyr Pro Ala Leu Thr
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Leu Met Leu Ile Thr Gly Val Asn Gly Ala Leu Leu Thr Ala Asp Leu
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Phe Asn Phe Phe Val Phe Ile Glu Val Met Leu Leu Pro Ser Tyr Gly
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Leu Ile Ala Met Thr Gly Thr Trp Ala Arg Leu Ala Ser Gly Arg Ile
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Phe Val Leu Val Asn Leu Ser Ala Ser Thr Leu Leu Val Ala Gly Val
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Gly Ile Val Tyr Gly Val Ile Gly Ser Val Asn Ile Ala Ala Leu Gln
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Asp Val Val Glu Gly Asn Pro Leu Val Ala Ser Ala Met Gly Ile Val
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Val Ile Ala Ile Ala Val Lys Ala Gly Val Phe Pro Val His Thr Trp
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Thr Val Gly Ala Ile Asp His Thr Thr Gly Thr Arg Asp Ile Arg Lys	
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Phe Thr Met Ala Tyr Ser Cys Tyr Phe Leu Tyr Glu Ala Phe Ala Thr	
115 120 125	
aag cac tcc aaa ttc cca gag gcc aac ggt gtc tca cct gca gtg gag	432
Lys His Ser Lys Phe Pro Glu Ala Asn Gly Val Ser Pro Ala Val Glu	
130 135 140	
gca atg cat ccg gtg aag ttt aag ctg tgg atc gca cct gtc atc ctg	480
Ala Met His Pro Val Lys Phe Lys Leu Trp Ile Ala Pro Val Ile Leu	
145 150 155 160	
gct att ttg acc gta gtg ttt ggt gtt ttc ccc aag cca gtg tgc gaa	528
Ala Ile Leu Thr Val Val Phe Gly Val Phe Pro Lys Pro Val Ser Glu	
165 170 175	
gca att gtc acg cat ctt gat aac gtc acg cca tgc ctt gat gat gtc	576
Ala Ile Val Thr His Leu Asp Asn Val Thr Pro Ser Leu Asp Asp Val	
180 185 190	
cac acc aaa ctg gcc ttg tgg cat ggt ctg aat cta ccg ctg ctg ctg	624
His Thr Lys Leu Ala Leu Trp His Gly Leu Asn Leu Pro Leu Leu Leu	
195 200 205	
tct gtg gtg atc atc att tcc gga ttc atc atc ttc tgg gag cga gac	672
Ser Val Val Ile Ile Ile Ser Gly Phe Ile Ile Phe Trp Glu Arg Asp	
210 215 220	
acc gtc gaa cgt ttg cgc cct aac acc gca gcg ttt ggc agt gcc gat	720

Thr Val Glu Arg Leu Arg Pro Asn Thr Ala Ala Phe Gly Ser Ala Asp	
225 230 235 240	
acc gcc tac gac gcc att ctt gat gca ctg cgt gtg ctc tcc cac cgc	768
Thr Ala Tyr Asp Ala Ile Leu Asp Ala Leu Arg Val Leu Ser His Arg	
245 250 255	
ctg act gca tcc acc cag cgt ggt tct ttg acc ctg aac gtc ggt gtg	816
Leu Thr Ala Ser Thr Gln Arg Gly Ser Leu Thr Leu Asn Val Gly Val	
260 265 270	
atc ttc ttc gtc ctc acg att gtt ccg ctg atc gct ttg atc act ggc	864
Ile Phe Phe Val Leu Thr Ile Val Pro Leu Ile Ala Leu Ile Thr Gly	
275 280 285	
gaa caa agc gat gtc cgc atg gag ctg tgg gat agc cct att cag ggc	912
Glu Gln Ser Asp Val Arg Met Glu Leu Trp Asp Ser Pro Ile Gln Gly	
290 295 300	
ttc atc gcg gcc atc att atc gtc gtt gcg att gtg gca acc acc atg	960
Phe Ile Ala Ala Ile Ile Ile Val Val Ala Ile Val Ala Thr Thr Met	
305 310 315 320	
gat aac cgt ttg tct gcg ctg att ttg gtg ggt gtg aca ggt tat ggc	1008
Asp Asn Arg Leu Ser Ala Leu Ile Leu Val Gly Val Thr Gly Tyr Gly	
325 330 335	
att gcc gtt atc ttc gcg cta cat ggc gca ccg gac ttg gcg cta acc	1056
Ile Ala Val Ile Phe Ala Leu His Gly Ala Pro Asp Leu Ala Leu Thr	
340 345 350	
cag gtg ctg gtg gag acc atc gtc atg gtg gta ttc atg ctg gtg ctg	1104
Gln Val Leu Val Glu Thr Ile Val Met Val Val Phe Met Leu Val Leu	
355 360 365	
cgt aaa atg ccg aca gaa gtt gcg tgg aag gca gaa cct aaa cag tct	1152
Arg Lys Met Pro Thr Glu Val Ala Trp Lys Ala Glu Pro Lys Gln Ser	
370 375 380	
cgc gtg cga gcg tgg ctt gct ggc gcc acc gga ttg tcc gtt gtt att	1200
Arg Val Arg Ala Trp Leu Ala Gly Ala Thr Gly Leu Ser Val Val Ile	
385 390 395 400	
gtc acc att ttt gcc atg aat gct cgc acc act gaa ccg atc tct gta	1248
Val Thr Ile Phe Ala Met Asn Ala Arg Thr Thr Glu Pro Ile Ser Val	
405 410 415	
tac atg cag gat ctg gcc tat gag atc gga cat ggc gca aac acc gtc	1296
Tyr Met Gln Asp Leu Ala Tyr Glu Ile Gly His Gly Ala Asn Thr Val	
420 425 430	
aac gta ctg ctc gta gac ctg cgt ggt ttt gat acc ttc ggt gaa att	1344
Asn Val Leu Leu Val Asp Leu Arg Gly Phe Asp Thr Phe Gly Glu Ile	
435 440 445	
tcc gtc ctt gtg atc gcg gca acc ggt atc gcc tcc ctg gtc tac cga	1392
Ser Val Leu Val Ile Ala Ala Thr Gly Ile Ala Ser Leu Val Tyr Arg	
450 455 460	
aac cgc agc ttc cgc aag gat tct cgc aga cca acc ctg gct acc act	1440
Asn Arg Ser Phe Arg Lys Asp Ser Arg Arg Pro Thr Leu Ala Thr Thr	

465	470	475	480	
ggt cgc cgt tgg ttg gct gct gct gtt gat acc gaa agg gcg cag aac				1488
Gly Arg Arg Trp Leu Ala Ala Ala Val Asp Thr Glu Arg Ala Gln Asn	485	490	495	
cgc tcg ctg atg gtt gat gtg gca acg cgc atc ctc ttc cct gcc atg				1536
Arg Ser Leu Met Val Asp Val Ala Thr Arg Ile Leu Phe Pro Ala Met	500	505	510	
atc atg ttg tct gtg tac ttc ttc ttc gcc gga cac aac gcg ccg ggc				1584
Ile Met Leu Ser Val Tyr Phe Phe Phe Ala Gly His Asn Ala Pro Gly	515	520	525	
ggc gga ttc gcc ggc ggc ctt gtt gcc tcc ttg gcg ttc gcc ttg cgc				1632
Gly Gly Phe Ala Gly Gly Leu Val Ala Ser Leu Ala Phe Ala Leu Arg	530	535	540	
tac ctt gcc ggt gga cgt gaa gaa ctt gaa gaa gcg ttg cct atc gac				1680
Tyr Leu Ala Gly Gly Arg Glu Glu Leu Glu Glu Ala Leu Pro Ile Asp	545	550	555	560
gcc ggc cgt atc ttg gga act gga cta ttt gtt tct gca act gca gtg				1728
Ala Gly Arg Ile Leu Gly Thr Gly Leu Phe Val Ser Ala Thr Ala Val	565	570	575	
ctg tgg ccc atg gtt ctt ctt ggt gaa cca ccg ctg acc tcc cat att				1776
Leu Trp Pro Met Val Leu Leu Gly Glu Pro Pro Leu Thr Ser His Ile	580	585	590	
tgg gat ctc aca ctg cca ctt atc ggt gag att cac att gca tcc gcg				1824
Trp Asp Leu Thr Leu Pro Leu Ile Gly Glu Ile His Ile Ala Ser Ala	595	600	605	
ctg ctc ttt gac ctt ggt gtc tac ctg atc gtc atc ggt ttg acc atg				1872
Leu Leu Phe Asp Leu Gly Val Tyr Leu Ile Val Ile Gly Leu Thr Met	610	615	620	
cac att ctc aac agt ttg ggc ggc cag ctc gac cgc gat gag gaa atg				1920
His Ile Leu Asn Ser Leu Gly Gly Gln Leu Asp Arg Asp Glu Glu Met	625	630	635	640
cgt aag cag cgt gcg cgc gac cga gct cga cgc ttg gcg cgc aac cag				1968
Arg Lys Gln Arg Ala Arg Asp Arg Ala Arg Arg Leu Ala Arg Asn Gln	645	650	655	
cgt cga gaa gca gca acc gtc ggc gca cgc agg tcg aac gag aaa tcg				2016
Arg Arg Glu Ala Ala Thr Val Gly Ala Arg Arg Ser Asn Glu Lys Ser	660	665	670	
aca cgc caa atg ccg acg att cgg cct cca ggg gca gac aca gaa tcg				2064
Thr Arg Gln Met Pro Thr Ile Arg Pro Pro Gly Ala Asp Thr Glu Ser	675	680	685	
gtg gag cag aac ggt gag aac cag acg tcg ata agc aca aag cgt tta				2112
Val Glu Gln Asn Gly Glu Asn Gln Thr Ser Ile Ser Thr Lys Arg Leu	690	695	700	
aag cag				2118
Lys Gln				
705				

<210> 692
 <211> 706
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 692

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Leu Ala Leu Thr Val Ala His Ser Leu Phe Lys Ala Thr Leu Phe Met
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Thr Val Gly Ala Ile Asp His Thr Thr Gly Thr Arg Asp Ile Arg Lys
 35 40 45

Leu Ser Gly Leu Trp Arg Lys Gln Pro Ile Leu Phe Ala Val Ala Ala
 50 55 60

Val Ser Ala Ala Ser Met Ala Gly Ile Pro Pro Leu Phe Gly Phe Ile
 65 70 75 80

Ala Lys Glu Thr Ala Leu Asp Thr Val Leu Asn Glu Gln Met Leu His
 85 90 95

Gly Met Pro Gly Arg Leu Met Leu Ala Gly Ile Val Leu Gly Ser Ile
 100 105 110

Phe Thr Met Ala Tyr Ser Cys Tyr Phe Leu Tyr Glu Ala Phe Ala Thr
 115 120 125

Lys His Ser Lys Phe Pro Glu Ala Asn Gly Val Ser Pro Ala Val Glu
 130 135 140

Ala Met His Pro Val Lys Phe Lys Leu Trp Ile Ala Pro Val Ile Leu
 145 150 155 160

Ala Ile Leu Thr Val Val Phe Gly Val Phe Pro Lys Pro Val Ser Glu
 165 170 175

Ala Ile Val Thr His Leu Asp Asn Val Thr Pro Ser Leu Asp Asp Val
 180 185 190

His Thr Lys Leu Ala Leu Trp His Gly Leu Asn Leu Pro Leu Leu Leu
 195 200 205

Ser Val Val Ile Ile Ile Ser Gly Phe Ile Ile Phe Trp Glu Arg Asp
 210 215 220

Thr Val Glu Arg Leu Arg Pro Asn Thr Ala Ala Phe Gly Ser Ala Asp
 225 230 235 240

Thr Ala Tyr Asp Ala Ile Leu Asp Ala Leu Arg Val Leu Ser His Arg
 245 250 255

Leu Thr Ala Ser Thr Gln Arg Gly Ser Leu Thr Leu Asn Val Gly Val
 260 265 270

Ile Phe Phe Val Leu Thr Ile Val Pro Leu Ile Ala Leu Ile Thr Gly
 275 280 285

Glu Gln Ser Asp Val Arg Met Glu Leu Trp Asp Ser Pro Ile Gln Gly
 290 295 300
 Phe Ile Ala Ala Ile Ile Ile Val Val Ala Ile Val Ala Thr Thr Met
 305 310 315 320
 Asp Asn Arg Leu Ser Ala Leu Ile Leu Val Gly Val Thr Gly Tyr Gly
 325 330 335
 Ile Ala Val Ile Phe Ala Leu His Gly Ala Pro Asp Leu Ala Leu Thr
 340 345 350
 Gln Val Leu Val Glu Thr Ile Val Met Val Val Phe Met Leu Val Leu
 355 360 365
 Arg Lys Met Pro Thr Glu Val Ala Trp Lys Ala Glu Pro Lys Gln Ser
 370 375 380
 Arg Val Arg Ala Trp Leu Ala Gly Ala Thr Gly Leu Ser Val Val Ile
 385 390 395 400
 Val Thr Ile Phe Ala Met Asn Ala Arg Thr Thr Glu Pro Ile Ser Val
 405 410 415
 Tyr Met Gln Asp Leu Ala Tyr Glu Ile Gly His Gly Ala Asn Thr Val
 420 425 430
 Asn Val Leu Leu Val Asp Leu Arg Gly Phe Asp Thr Phe Gly Glu Ile
 435 440 445
 Ser Val Leu Val Ile Ala Ala Thr Gly Ile Ala Ser Leu Val Tyr Arg
 450 455 460
 Asn Arg Ser Phe Arg Lys Asp Ser Arg Arg Pro Thr Leu Ala Thr Thr
 465 470 475 480
 Gly Arg Arg Trp Leu Ala Ala Ala Val Asp Thr Glu Arg Ala Gln Asn
 485 490 495
 Arg Ser Leu Met Val Asp Val Ala Thr Arg Ile Leu Phe Pro Ala Met
 500 505 510
 Ile Met Leu Ser Val Tyr Phe Phe Phe Ala Gly His Asn Ala Pro Gly
 515 520 525
 Gly Gly Phe Ala Gly Gly Leu Val Ala Ser Leu Ala Phe Ala Leu Arg
 530 535 540
 Tyr Leu Ala Gly Gly Arg Glu Glu Leu Glu Glu Ala Leu Pro Ile Asp
 545 550 555 560
 Ala Gly Arg Ile Leu Gly Thr Gly Leu Phe Val Ser Ala Thr Ala Val
 565 570 575
 Leu Trp Pro Met Val Leu Leu Gly Glu Pro Pro Leu Thr Ser His Ile
 580 585 590
 Trp Asp Leu Thr Leu Pro Leu Ile Gly Glu Ile His Ile Ala Ser Ala
 595 600 605

Leu Leu Phe Asp Leu Gly Val Tyr Leu Ile Val Ile Gly Leu Thr Met
 610 615 620
 His Ile Leu Asn Ser Leu Gly Gly Gln Leu Asp Arg Asp Glu Glu Met
 625 630 635 640
 Arg Lys Gln Arg Ala Arg Asp Arg Ala Arg Arg Leu Ala Arg Asn Gln
 645 650 655
 Arg Arg Glu Ala Ala Thr Val Gly Ala Arg Arg Ser Asn Glu Lys Ser
 660 665 670
 Thr Arg Gln Met Pro Thr Ile Arg Pro Pro Gly Ala Asp Thr Glu Ser
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 Val Glu Gln Asn Gly Glu Asn Gln Thr Ser Ile Ser Thr Lys Arg Leu
 690 695 700
 Lys Gln
 705

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 <212> DNA
 <213> Corynebacterium glutamicum

<220>
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 <222> (101)..(955)
 <223> RXA00909

<400> 693

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 Val Leu Ile Leu Phe
 1 5
 ctc gcg ctc act gca gcc gca gta gtc gcc ccc atc ctg atc cga act 163
 Leu Ala Leu Thr Ala Ala Ala Val Val Ala Pro Ile Leu Ile Arg Thr
 10 15 20
 ctc ggt cga cca gct ttt ggt ctg ctg gcg ctt gta cct ggc att ggt 211
 Leu Gly Arg Pro Ala Phe Gly Leu Leu Ala Leu Val Pro Gly Ile Gly
 25 30 35
 ttt ttc tgg gtg ctt tcg gag ttc atc aaa ggc act ttc aag gat gga 259
 Phe Phe Trp Val Leu Ser Glu Phe Ile Lys Gly Thr Phe Lys Asp Gly
 40 45 50
 ggt gaa ctc ctc ctc cac tat gcc tgg atg cct tcg gct cac ctc aat 307
 Gly Glu Leu Leu Leu His Tyr Ala Trp Met Pro Ser Ala His Leu Asn
 55 60 65
 atc gat ttc cgt atg gat tcc ctc gcg gcg ctg ttc tca ctc atc gtc 355
 Ile Asp Phe Arg Met Asp Ser Leu Ala Ala Leu Phe Ser Leu Ile Val
 70 75 80 85
 tta ggc gtg ggc gcc cta gtg ctg ctg tac tgc tgg gga tat ttt gat 403
 Leu Gly Val Gly Ala Leu Val Leu Leu Tyr Cys Trp Gly Tyr Phe Asp

90	95	100	
tcc aac gcg ggt cgc ctc agt gcc ttt ggt gct gaa ctg gtg gcc ttc			451
Ser Asn Ala Gly Arg Leu Ser Ala Phe Gly Ala Glu Leu Val Ala Phe			
105	110	115	
gcc atg gcg atg ttt ggt ctt gtc att tca gac aac atc ctg ctg atg			499
Ala Met Ala Met Phe Gly Leu Val Ile Ser Asp Asn Ile Leu Leu Met			
120	125	130	
tac gtc ttc tgg gaa atc acc tcc gtt tta tcc ttc ctc ctg gtt ggt			547
Tyr Val Phe Trp Glu Ile Thr Ser Val Leu Ser Phe Leu Leu Val Gly			
135	140	145	
tat tac ggc gaa cgc gca tct tca cgt cgc tct gca ggt caa gcc ttg			595
Tyr Tyr Gly Glu Arg Ala Ser Ser Arg Arg Ser Ala Gly Gln Ala Leu			
150	155	160	165
atg gtg acc acc ctg ggt gga ttg gcc atg ctg gtg ggc atc att ttg			643
Met Val Thr Thr Leu Gly Gly Leu Ala Met Leu Val Gly Ile Ile Leu			
170	175	180	
atg ggt acc caa act ggc gtg tgg cga ttc tct gag atc cct gcc tac			691
Met Gly Thr Gln Thr Gly Val Trp Arg Phe Ser Glu Ile Pro Ala Tyr			
185	190	195	
tca agc tcc tgg gca gat gtg ccg tat att tcc gct gct gct gcc ctt			739
Ser Ser Ser Trp Ala Asp Val Pro Tyr Ile Ser Ala Ala Ala Ala Leu			
200	205	210	
atc ttg gct ggc gca cta tcc aaa tcg gct atc gca cca acc cac ttc			787
Ile Leu Ala Gly Ala Leu Ser Lys Ser Ala Ile Ala Pro Thr His Phe			
215	220	225	
tgg ctt ccc ggc gcg atg gcc gca cca acg ccg gtg tct gct tac ctg			835
Trp Leu Pro Gly Ala Met Ala Ala Pro Thr Pro Val Ser Ala Tyr Leu			
230	235	240	245
cac tcc gca gcg atg gtg aag gcg ggt att tac ctt gtg gct cgc ctc			883
His Ser Ala Ala Met Val Lys Ala Gly Ile Tyr Leu Val Ala Arg Leu			
250	255	260	
tct cca gac ctc aac gta gtt ggt tcg tgg tac ctg atc atc atc ccg			931
Ser Pro Asp Leu Asn Val Val Gly Ser Trp Tyr Leu Ile Ile Ile Pro			
265	270	275	
ttg ggc atg ttg acc atg ctc atg			955
Leu Gly Met Leu Thr Met Leu Met			
280	285		

<210> 694

<211> 285

<212> PRT

<213> Corynebacterium glutamicum

<400> 694

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Ile Leu Ile Arg Thr Leu Gly Arg Pro Ala Phe Gly Leu Leu Ala Leu

20										25										30										
Val	Pro	Gly	Ile	Gly	Phe	Phe	Trp	Val	Leu	Ser	Glu	Phe	Ile	Lys	Gly															
		35					40					45																		
Thr	Phe	Lys	Asp	Gly	Gly	Glu	Leu	Leu	Leu	His	Tyr	Ala	Trp	Met	Pro															
	50				55						60																			
Ser	Ala	His	Leu	Asn	Ile	Asp	Phe	Arg	Met	Asp	Ser	Leu	Ala	Ala	Leu															
	65			70					75						80															
Phe	Ser	Leu	Ile	Val	Leu	Gly	Val	Gly	Ala	Leu	Val	Leu	Leu	Tyr	Cys															
			85					90						95																
Trp	Gly	Tyr	Phe	Asp	Ser	Asn	Ala	Gly	Arg	Leu	Ser	Ala	Phe	Gly	Ala															
			100					105						110																
Glu	Leu	Val	Ala	Phe	Ala	Met	Ala	Met	Phe	Gly	Leu	Val	Ile	Ser	Asp															
		115					120						125																	
Asn	Ile	Leu	Leu	Met	Tyr	Val	Phe	Trp	Glu	Ile	Thr	Ser	Val	Leu	Ser															
		130				135								140																
Phe	Leu	Leu	Val	Gly	Tyr	Tyr	Gly	Glu	Arg	Ala	Ser	Ser	Arg	Arg	Ser															
	145				150					155				160																
Ala	Gly	Gln	Ala	Leu	Met	Val	Thr	Thr	Leu	Gly	Gly	Leu	Ala	Met	Leu															
			165						170					175																
Val	Gly	Ile	Ile	Leu	Met	Gly	Thr	Gln	Thr	Gly	Val	Trp	Arg	Phe	Ser															
			180					185						190																
Glu	Ile	Pro	Ala	Tyr	Ser	Ser	Ser	Trp	Ala	Asp	Val	Pro	Tyr	Ile	Ser															
		195					200					205																		
Ala	Ala	Ala	Ala	Leu	Ile	Leu	Ala	Gly	Ala	Leu	Ser	Lys	Ser	Ala	Ile															
		210				215					220																			
Ala	Pro	Thr	His	Phe	Trp	Leu	Pro	Gly	Ala	Met	Ala	Ala	Pro	Thr	Pro															
	225				230					235				240																
Val	Ser	Ala	Tyr	Leu	His	Ser	Ala	Ala	Met	Val	Lys	Ala	Gly	Ile	Tyr															
			245						250					255																
Leu	Val	Ala	Arg	Leu	Ser	Pro	Asp	Leu	Asn	Val	Val	Gly	Ser	Trp	Tyr															
		260						265					270																	
Leu	Ile	Ile	Ile	Pro	Leu	Gly	Met	Leu	Thr	Met	Leu	Met																		
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<211> 927

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(904)

<223> RXA00700

<400> 695

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                                         Met Ile Asn Ala Ile
                                         1 5
aca ctc aag ccc aaa acc ttc ctc acc tta agc ttc ctt gcg gtt ttg 163
Thr Leu Lys Pro Lys Thr Phe Leu Thr Leu Ser Phe Leu Ala Val Leu
                        10 15 20
agc atc gtg att ttc ttc tgg ccg ctg atc gtc aac ccg gaa tcc ttc 211
Ser Ile Val Ile Phe Phe Trp Pro Leu Ile Val Asn Pro Glu Ser Phe
                        25 30 35
ctg tcc gac aaa gcc caa gcg ccc ctc tac atc gcg atc gtc att ccc 259
Leu Ser Asp Lys Ala Gln Ala Pro Leu Tyr Ile Ala Ile Val Ile Pro
                        40 45 50
ctc gtg ctg gcc gct gtc atc gcc gaa atc agt gaa aac gga ttc gac 307
Leu Val Leu Ala Ala Val Ile Ala Glu Ile Ser Glu Asn Gly Phe Asp
                        55 60 65
gtt aaa gcc gta gcc atg ctc ggc gtc ctc acc gcc atg gtt gcc gta 355
Val Lys Ala Val Ala Met Leu Gly Val Leu Thr Ala Met Val Ala Val
                        70 75 80 85
gtc cga cca ttc ggt gcc ggc gca gca ggc ttt gaa gca gtc ttc ttt 403
Val Arg Pro Phe Gly Ala Gly Ala Ala Gly Phe Glu Ala Val Phe Phe
                        90 95 100
gtc ctc atc ctc ggc gga cga gcc ttc gga ccc ggc ttc gga ttc atc 451
Val Leu Ile Leu Gly Gly Arg Ala Phe Gly Pro Gly Phe Gly Phe Ile
                        105 110 115
ctc ggc aac acc gga ctg ttc gca tcc gcg ctg ctc acc gca gga atc 499
Leu Gly Asn Thr Gly Leu Phe Ala Ser Ala Leu Leu Thr Ala Gly Ile
                        120 125 130
gga ccg tgg ctc ccc tac caa atg ctc gca gcc gcc tgg gtc agc ttc 547
Gly Pro Trp Leu Pro Tyr Gln Met Leu Ala Ala Ala Trp Val Ser Phe
                        135 140 145
ggc gcc ggc cta ctc ccc caa gta cgc ggc aaa aag gaa atg ctc atc 595
Gly Ala Gly Leu Leu Pro Gln Val Arg Gly Lys Lys Glu Met Leu Ile
                        150 155 160 165
atc gtc cta tac gcc atc gtc tct tca ctc ggc tac gga acc atg atg 643
Ile Val Leu Tyr Ala Ile Val Ser Ser Leu Gly Tyr Gly Thr Met Met
                        170 175 180
aac atg agc ttc tgg ccc tac gcc atc ggt gtc acc agc ggg ctt tcc 691
Asn Met Ser Phe Trp Pro Tyr Ala Ile Gly Val Thr Ser Gly Leu Ser
                        185 190 195
ttc aca ccc ggc gcg ccc gtc ctg gaa aac ctc cac acc ttc atg ctg 739
Phe Thr Pro Gly Ala Pro Val Leu Glu Asn Leu His Thr Phe Met Leu
                        200 205 210
ttc tgc ctc acc aca tcc atg ggt tgg gat ctc ggc cgc gcc ttc ttc 787
Phe Cys Leu Thr Thr Ser Met Gly Trp Asp Leu Gly Arg Ala Phe Phe

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215

220

225

acc tca gtg cta tta ctg ctc aca gcc aaa ccc gtt tta ggt gct tta 835
 Thr Ser Val Leu Leu Leu Thr Ala Lys Pro Val Leu Gly Ala Leu
 230 235 240 245

cga cgc gcc agc cgc cgc gcc gct ttc ggc gtc gag cgt gac ttc ggg 883
 Arg Arg Ala Ser Arg Arg Ala Ala Phe Gly Val Glu Arg Asp Phe Gly
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gag gcc ggg gtg cct cgg gtc taaagatttt gttggcttgc ttc 927
 Glu Ala Gly Val Pro Arg Val
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<210> 696

<211> 268

<212> PRT

<213> Corynebacterium glutamicum

<400> 696

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Phe Leu Ala Val Leu Ser Ile Val Ile Phe Phe Trp Pro Leu Ile Val
 20 25 30

Asn Pro Glu Ser Phe Leu Ser Asp Lys Ala Gln Ala Pro Leu Tyr Ile
 35 40 45

Ala Ile Val Ile Pro Leu Val Leu Ala Ala Val Ile Ala Glu Ile Ser
 50 55 60

Glu Asn Gly Phe Asp Val Lys Ala Val Ala Met Leu Gly Val Leu Thr
 65 70 75 80

Ala Met Val Ala Val Val Arg Pro Phe Gly Ala Gly Ala Ala Gly Phe
 85 90 95

Glu Ala Val Phe Phe Val Leu Ile Leu Gly Gly Arg Ala Phe Gly Pro
 100 105 110

Gly Phe Gly Phe Ile Leu Gly Asn Thr Gly Leu Phe Ala Ser Ala Leu
 115 120 125

Leu Thr Ala Gly Ile Gly Pro Trp Leu Pro Tyr Gln Met Leu Ala Ala
 130 135 140

Ala Trp Val Ser Phe Gly Ala Gly Leu Leu Pro Gln Val Arg Gly Lys
 145 150 155 160

Lys Glu Met Leu Ile Ile Val Leu Tyr Ala Ile Val Ser Ser Leu Gly
 165 170 175

Tyr Gly Thr Met Met Asn Met Ser Phe Trp Pro Tyr Ala Ile Gly Val
 180 185 190

Thr Ser Gly Leu Ser Phe Thr Pro Gly Ala Pro Val Leu Glu Asn Leu
 195 200 205

His Thr Phe Met Leu Phe Cys Leu Thr Thr Ser Met Gly Trp Asp Leu

210

215

220

Gly Arg Ala Phe Phe Thr Ser Val Leu Leu Leu Thr Ala Lys Pro
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Val Leu Gly Ala Leu Arg Arg Ala Ser Arg Arg Ala Ala Phe Gly Val
 245 250 255

Glu Arg Asp Phe Gly Glu Ala Gly Val Pro Arg Val
 260 265

<210> 697

<211> 1587

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1564)

<223> RXN00483

<400> 697

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 Val Leu Val Thr Gly
 1 5

gcg aca ggc tac att ggc ggc agg ttg att act gag tta ctt gct gcc 163
 Ala Thr Gly Tyr Ile Gly Gly Arg Leu Ile Thr Glu Leu Leu Ala Ala
 10 15 20

ggt ttc caa gtt cgg gcc acc tcg agg aaa aaa aca agt ctt cag cgc 211
 Gly Phe Gln Val Arg Ala Thr Ser Arg Lys Lys Thr Ser Leu Gln Arg
 25 30 35

ttt gac tgg tac gag gac gtc gag gca gtg gaa gcg gat ctg act gac 259
 Phe Asp Trp Tyr Glu Asp Val Glu Ala Val Glu Ala Asp Leu Thr Asp
 40 45 50

gcg act gag tta gat acg tta ttt aag gat gta gac gtt gtt tac tat 307
 Ala Thr Glu Leu Asp Thr Leu Phe Lys Asp Val Asp Val Val Tyr Tyr
 55 60 65

cta gtg cat tcc atg gga ggt aag aat gtt gat ttt gaa gag caa gag 355
 Leu Val His Ser Met Gly Gly Lys Asn Val Asp Phe Glu Glu Gln Glu
 70 75 80 85

caa cgc act gct gaa aat gta att caa gct gct gat caa gcc ggg ata 403
 Gln Arg Thr Ala Glu Asn Val Ile Gln Ala Ala Asp Gln Ala Gly Ile
 90 95 100

aaa cag att gtc tac ctt tcc ggc tta cac ccg cgt aat cga aaa ata 451
 Lys Gln Ile Val Tyr Leu Ser Gly Leu His Pro Arg Asn Arg Lys Ile
 105 110 115

gaa gaa cta tct aag cac atg cgc tca cgg gaa aag gtc gcc cag att 499
 Glu Glu Leu Ser Lys His Met Arg Ser Arg Glu Lys Val Ala Gln Ile
 120 125 130

ttg ctg gca ggc cag aca cca gct tta att tta agg gct gcc aca att	547
Leu Leu Ala Gly Gln Thr Pro Ala Leu Ile Leu Arg Ala Ala Thr Ile	
135 140 145	
att ggt tcc ggc tct gca tca ttt gaa ata atc cgt cat ctc acg gag	595
Ile Gly Ser Gly Ser Ala Ser Phe Glu Ile Ile Arg His Leu Thr Glu	
150 155 160 165	
cgt ttg cct aga atg ata gcg cct cag tgg att act aat cag att gag	643
Arg Leu Pro Arg Met Ile Ala Pro Gln Trp Ile Thr Asn Gln Ile Glu	
170 175 180	
cct tta gca ata cgg gat gtt ttg cat tac cta atc tcg gcg gct gat	691
Pro Leu Ala Ile Arg Asp Val Leu His Tyr Leu Ile Ser Ala Ala Asp	
185 190 195	
tta aag gat cca gtc aac cgc tcc tgc gat att ggg tgt gga aag tcg	739
Leu Lys Asp Pro Val Asn Arg Ser Cys Asp Ile Gly Cys Gly Lys Ser	
200 205 210	
tat gaa ttt gcg gat cta ttg cgt atc tat gcc gat gtt cgg gga ctg	787
Tyr Glu Phe Ala Asp Leu Leu Arg Ile Tyr Ala Asp Val Arg Gly Leu	
215 220 225	
aaa cgt cat gta aat tcc gta cct ctc aat ttg ccc atg gac aag cta	835
Lys Arg His Val Asn Ser Val Pro Leu Asn Leu Pro Met Asp Lys Leu	
230 235 240 245	
tcc ggt ctt tgg att agt cta gtg aca cct gtt cca ttt caa ttg tct	883
Ser Gly Leu Trp Ile Ser Leu Val Thr Pro Val Pro Phe Gln Leu Ser	
250 255 260	
ttc cct tta gct caa tca atg gct gag gat gcc gtc act gaa gag cac	931
Phe Pro Leu Ala Gln Ser Met Ala Glu Asp Ala Val Thr Glu Glu His	
265 270 275	
agc att aaa gat att att tca gat cca ccc gat ggt ttt att gag tat	979
Ser Ile Lys Asp Ile Ile Ser Asp Pro Pro Asp Gly Phe Ile Glu Tyr	
280 285 290	
cgg gaa gca gtg gag ctg gca tta gct gca gaa ttt gat cgt gga gtt	1027
Arg Glu Ala Val Glu Leu Ala Leu Ala Ala Glu Phe Asp Arg Gly Val	
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Pro Thr Ser Trp Asp Arg Ser Trp Thr Val Gln Gln Pro Trp Ala Gly	
310 315 320 325	
cag cct acc gat cca gag tgg gcg ggc aaa gct gta tat gaa gac gtc	1123
Gln Pro Thr Asp Pro Glu Trp Ala Gly Lys Ala Val Tyr Glu Asp Val	
330 335 340	
cgc aca gaa gat act gat ctc cga gca gcg cag gtc tgg ccg atc att	1171
Arg Thr Glu Asp Thr Asp Leu Arg Ala Ala Gln Val Trp Pro Ile Ile	
345 350 355	
gaa ggt ttg ggt ggc gtg aac ggc tgg tat tct gca cca ctg cta tgg	1219
Glu Gly Leu Gly Gly Val Asn Gly Trp Tyr Ser Ala Pro Leu Leu Trp	
360 365 370	
cga ttg cgg ggt atc gct gac aga ctc atc ggc ggt cca ggt ttg ggc	1267

Arg Leu Arg Gly Ile Ala Asp Arg Leu Ile Gly Gly Pro Gly Leu Gly
 375 380 385

gga cgg cgg gat ccc cgt cat ttg aaa ctt ggg gat cgc att gat tgg 1315
 Gly Arg Arg Asp Pro Arg His Leu Lys Leu Gly Asp Arg Ile Asp Trp
 390 395 400 405

tgg cgg gtt act gag atc gat cca cca cat aga tta gtg ctc acc gca 1363
 Trp Arg Val Thr Glu Ile Asp Pro Pro His Arg Leu Val Leu Thr Ala
 410 415 420

gag atg aaa gta gat ggt ggc gct tgg ctg atc ctg gaa gtt gcg gac 1411
 Glu Met Lys Val Asp Gly Gly Ala Trp Leu Ile Leu Glu Val Ala Asp
 425 430 435

aag gaa aat ggc gga tgt act tat acc cag cgc gca ata ttt gag ccg 1459
 Lys Glu Asn Gly Gly Cys Thr Tyr Thr Gln Arg Ala Ile Phe Glu Pro
 440 445 450

aag ggt ttg ccc ggt tat ctc tat tgg tgg gtt gtt tca ccg ttc cat 1507
 Lys Gly Leu Pro Gly Tyr Leu Tyr Trp Trp Val Val Ser Pro Phe His
 455 460 465

gcg att att ttt cct tat atg cgt tcg aat att tta aaa gct gcg cgt 1555
 Ala Ile Ile Phe Pro Tyr Met Arg Ser Asn Ile Leu Lys Ala Ala Arg
 470 475 480 485

aaa ctc act taatcgacaga gtaggcgtct aaa 1587
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<210> 698

<211> 488

<212> PRT

<213> Corynebacterium glutamicum

<400> 698

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Thr Ser Leu Gln Arg Phe Asp Trp Tyr Glu Asp Val Glu Ala Val Glu
 35 40 45

Ala Asp Leu Thr Asp Ala Thr Glu Leu Asp Thr Leu Phe Lys Asp Val
 50 55 60

Asp Val Val Tyr Tyr Leu Val His Ser Met Gly Gly Lys Asn Val Asp
 65 70 75 80

Phe Glu Glu Gln Glu Gln Arg Thr Ala Glu Asn Val Ile Gln Ala Ala
 85 90 95

Asp Gln Ala Gly Ile Lys Gln Ile Val Tyr Leu Ser Gly Leu His Pro
 100 105 110

Arg Asn Arg Lys Ile Glu Glu Leu Ser Lys His Met Arg Ser Arg Glu
 115 120 125

Lys Val Ala Gln Ile Leu Leu Ala Gly Gln Thr Pro Ala Leu Ile Leu
 130 135 140
 Arg Ala Ala Thr Ile Ile Gly Ser Gly Ser Ala Ser Phe Glu Ile Ile
 145 150 155 160
 Arg His Leu Thr Glu Arg Leu Pro Arg Met Ile Ala Pro Gln Trp Ile
 165 170 175
 Thr Asn Gln Ile Glu Pro Leu Ala Ile Arg Asp Val Leu His Tyr Leu
 180 185 190
 Ile Ser Ala Ala Asp Leu Lys Asp Pro Val Asn Arg Ser Cys Asp Ile
 195 200 205
 Gly Cys Gly Lys Ser Tyr Glu Phe Ala Asp Leu Leu Arg Ile Tyr Ala
 210 215 220
 Asp Val Arg Gly Leu Lys Arg His Val Asn Ser Val Pro Leu Asn Leu
 225 230 235 240
 Pro Met Asp Lys Leu Ser Gly Leu Trp Ile Ser Leu Val Thr Pro Val
 245 250 255
 Pro Phe Gln Leu Ser Phe Pro Leu Ala Gln Ser Met Ala Glu Asp Ala
 260 265 270
 Val Thr Glu Glu His Ser Ile Lys Asp Ile Ile Ser Asp Pro Pro Asp
 275 280 285
 Gly Phe Ile Glu Tyr Arg Glu Ala Val Glu Leu Ala Leu Ala Ala Glu
 290 295 300
 Phe Asp Arg Gly Val Pro Thr Ser Trp Asp Arg Ser Trp Thr Val Gln
 305 310 315 320
 Gln Pro Trp Ala Gly Gln Pro Thr Asp Pro Glu Trp Ala Gly Lys Ala
 325 330 335
 Val Tyr Glu Asp Val Arg Thr Glu Asp Thr Asp Leu Arg Ala Ala Gln
 340 345 350
 Val Trp Pro Ile Ile Glu Gly Leu Gly Gly Val Asn Gly Trp Tyr Ser
 355 360 365
 Ala Pro Leu Leu Trp Arg Leu Arg Gly Ile Ala Asp Arg Leu Ile Gly
 370 375 380
 Gly Pro Gly Leu Gly Gly Arg Arg Asp Pro Arg His Leu Lys Leu Gly
 385 390 395 400
 Asp Arg Ile Asp Trp Trp Arg Val Thr Glu Ile Asp Pro Pro His Arg
 405 410 415
 Leu Val Leu Thr Ala Glu Met Lys Val Asp Gly Gly Ala Trp Leu Ile
 420 425 430
 Leu Glu Val Ala Asp Lys Glu Asn Gly Gly Cys Thr Tyr Thr Gln Arg
 435 440 445

Ala Ile Phe Glu Pro Lys Gly Leu Pro Gly Tyr Leu Tyr Trp Trp Val
 450 455 460

Val Ser Pro Phe His Ala Ile Ile Phe Pro Tyr Met Arg Ser Asn Ile
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Leu Lys Ala Ala Arg Lys Leu Thr
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<210> 699

<211> 1587

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1564)

<223> FRXA00483

<400> 699

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 Val Leu Val Thr Gly
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gcg aca ggc tac att ggc ggc agg ttg att act gag tta ctt gct gcc 163
 Ala Thr Gly Tyr Ile Gly Gly Arg Leu Ile Thr Glu Leu Leu Ala Ala
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ggt ttc caa gtt cgg gcc acc tcg agg aaa aaa aca agt ctt cag cgc 211
 Gly Phe Gln Val Arg Ala Thr Ser Arg Lys Lys Thr Ser Leu Gln Arg
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ttt gac tgg tac gag gac gtc gag gca gtg gaa gcg gat ctg act gac 259
 Phe Asp Trp Tyr Glu Asp Val Glu Ala Val Glu Ala Asp Leu Thr Asp
 40 45 50

gcg act gag tta gat acg tta ttt aag gat gta gac gtt gtt tac tat 307
 Ala Thr Glu Leu Asp Thr Leu Phe Lys Asp Val Asp Val Val Tyr Tyr
 55 60 65

cta gtg cat tcc atg gga ggt aag aat gtt gat ttt gaa gag caa gag 355
 Leu Val His Ser Met Gly Gly Lys Asn Val Asp Phe Glu Glu Gln Glu
 70 75 80 85

caa cgc act gct gaa aat gta att caa gct gct gat caa gcc ggg ata 403
 Gln Arg Thr Ala Glu Asn Val Ile Gln Ala Ala Asp Gln Ala Gly Ile
 90 95 100

aaa cag att gtc tac ctt tcc ggc tta cac ccg cgt aat cga aaa ata 451
 Lys Gln Ile Val Tyr Leu Ser Gly Leu His Pro Arg Asn Arg Lys Ile
 105 110 115

gaa gaa cta tct aag cac atg cgc tca cgg gaa aag gtc gcc cag att 499
 Glu Glu Leu Ser Lys His Met Arg Ser Arg Glu Lys Val Ala Gln Ile
 120 125 130

ttg ctg gca ggc cag aca cca gct tta att tta agg gct gcc aca att 547
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cgt ttg cct aga atg ata gcg cct cag tgg att act aat cag att gag Arg Leu Pro Arg Met Ile Ala Pro Gln Trp Ile Thr Asn Gln Ile Glu 170 175 180			643
cct tta gca ata cgg gat gtt ttg cat tac cta atc tcg gcg gct gat Pro Leu Ala Ile Arg Asp Val Leu His Tyr Leu Ile Ser Ala Ala Asp 185 190 195			691
tta aag gat cca gtc aac cgc tcc tgc gat att ggg tgt gga aag tcg Leu Lys Asp Pro Val Asn Arg Ser Cys Asp Ile Gly Cys Gly Lys Ser 200 205 210			739
tat gaa ttt gcg gat cta ttg cgt atc tat gcc gat gtt cgg gga ctg Tyr Glu Phe Ala Asp Leu Leu Arg Ile Tyr Ala Asp Val Arg Gly Leu 215 220 225			787
aaa cgt cat gta aat tcc gta cct ctc aat ttg ccc atg gac aag cta Lys Arg His Val Asn Ser Val Pro Leu Asn Leu Pro Met Asp Lys Leu 230 235 240 245			835
tcc ggt ctt tgg att agt cta gtg aca cct gtt cca ttt caa ttg tct Ser Gly Leu Trp Ile Ser Leu Val Thr Pro Val Pro Phe Gln Leu Ser 250 255 260			883
ttc cct tta gct caa tca atg gct gag gat gcc gtc act gaa gag cac Phe Pro Leu Ala Gln Ser Met Ala Glu Asp Ala Val Thr Glu Glu His 265 270 275			931
agc att aaa gat att att tca gat cca ccc gat ggt ttt att gag tat Ser Ile Lys Asp Ile Ile Ser Asp Pro Pro Asp Gly Phe Ile Glu Tyr 280 285 290			979
cgg gaa gca gtg gag ctg gca tta gct gca gaa ttt gat cgt gga gtt Arg Glu Ala Val Glu Leu Ala Leu Ala Ala Glu Phe Asp Arg Gly Val 295 300 305			1027
cca acg tca tgg gat cga agc tgg act gta caa caa ccg tgg gct ggc Pro Thr Ser Trp Asp Arg Ser Trp Thr Val Gln Gln Pro Trp Ala Gly 310 315 320 325			1075
cag cct acc gat cca gag tgg gcg ggc aaa gct gta tat gaa gac gtc Gln Pro Thr Asp Pro Glu Trp Ala Gly Lys Ala Val Tyr Glu Asp Val 330 335 340			1123
cgc aca gaa gat act gat ctc cga gca gcg cag gtc tgg ccg atc att Arg Thr Glu Asp Thr Asp Leu Arg Ala Ala Gln Val Trp Pro Ile Ile 345 350 355			1171
gaa ggt ttg ggt ggc gtg aac ggc tgg tat tct gca cca ctg cta tgg Glu Gly Leu Gly Gly Val Asn Gly Trp Tyr Ser Ala Pro Leu Leu Trp 360 365 370			1219
cga ttg cgg ggt atc gct gac aga ctc atc ggc ggt cca ggt ttg ggc Arg Leu Arg Gly Ile Ala Asp Arg Leu Ile Gly Gly Pro Gly Leu Gly 375 380 385			1267

gga cgg cgg gat ccc cgt cat ttg aaa ctt ggg gat cgc att gat tgg 1315
 Gly Arg Arg Asp Pro Arg His Leu Lys Leu Gly Asp Arg Ile Asp Trp
 390 395 400 405

 tgg cgg gtt act gag atc gat cca cca cat aga tta gtg ctc acc gca 1363
 Trp Arg Val Thr Glu Ile Asp Pro Pro His Arg Leu Val Leu Thr Ala
 410 415 420

 gag atg aaa gta gat ggt ggc gct tgg ctg atc ctg gaa gtt gcg gac 1411
 Glu Met Lys Val Asp Gly Gly Ala Trp Leu Ile Leu Glu Val Ala Asp
 425 430 435

 aag gaa aat ggc gga tgt act tat acc cag cgc gca ata ttt gag ccg 1459
 Lys Glu Asn Gly Gly Cys Thr Tyr Thr Gln Arg Ala Ile Phe Glu Pro
 440 445 450

 aag ggt ttg ccc ggt tat ctc tat tgg tgg gtt gtt tca ccg ttc cat 1507
 Lys Gly Leu Pro Gly Tyr Leu Tyr Trp Trp Val Val Ser Pro Phe His
 455 460 465

 gcg att att ttt cct tat atg cgt tcg aat att tta aaa gct gcg cgt 1555
 Ala Ile Ile Phe Pro Tyr Met Arg Ser Asn Ile Leu Lys Ala Ala Arg
 470 475 480 485

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 Lys Leu Thr

<210> 700

<211> 488

<212> PRT

<213> Corynebacterium glutamicum

<400> 700

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 20 25 30

 Thr Ser Leu Gln Arg Phe Asp Trp Tyr Glu Asp Val Glu Ala Val Glu
 35 40 45

 Ala Asp Leu Thr Asp Ala Thr Glu Leu Asp Thr Leu Phe Lys Asp Val
 50 55 60

 Asp Val Val Tyr Tyr Leu Val His Ser Met Gly Gly Lys Asn Val Asp
 65 70 75 80

 Phe Glu Glu Gln Glu Gln Arg Thr Ala Glu Asn Val Ile Gln Ala Ala
 85 90 95

 Asp Gln Ala Gly Ile Lys Gln Ile Val Tyr Leu Ser Gly Leu His Pro
 100 105 110

 Arg Asn Arg Lys Ile Glu Glu Leu Ser Lys His Met Arg Ser Arg Glu
 115 120 125

 Lys Val Ala Gln Ile Leu Leu Ala Gly Gln Thr Pro Ala Leu Ile Leu

130	135	140
Arg Ala Ala Thr Ile Ile Gly Ser Gly Ser Ala Ser Phe Glu Ile Ile 145 150 155 160		
Arg His Leu Thr Glu Arg Leu Pro Arg Met Ile Ala Pro Gln Trp Ile 165 170 175		
Thr Asn Gln Ile Glu Pro Leu Ala Ile Arg Asp Val Leu His Tyr Leu 180 185 190		
Ile Ser Ala Ala Asp Leu Lys Asp Pro Val Asn Arg Ser Cys Asp Ile 195 200 205		
Gly Cys Gly Lys Ser Tyr Glu Phe Ala Asp Leu Leu Arg Ile Tyr Ala 210 215 220		
Asp Val Arg Gly Leu Lys Arg His Val Asn Ser Val Pro Leu Asn Leu 225 230 235 240		
Pro Met Asp Lys Leu Ser Gly Leu Trp Ile Ser Leu Val Thr Pro Val 245 250 255		
Pro Phe Gln Leu Ser Phe Pro Leu Ala Gln Ser Met Ala Glu Asp Ala 260 265 270		
Val Thr Glu Glu His Ser Ile Lys Asp Ile Ile Ser Asp Pro Pro Asp 275 280 285		
Gly Phe Ile Glu Tyr Arg Glu Ala Val Glu Leu Ala Leu Ala Ala Glu 290 295 300		
Phe Asp Arg Gly Val Pro Thr Ser Trp Asp Arg Ser Trp Thr Val Gln 305 310 315 320		
Gln Pro Trp Ala Gly Gln Pro Thr Asp Pro Glu Trp Ala Gly Lys Ala 325 330 335		
Val Tyr Glu Asp Val Arg Thr Glu Asp Thr Asp Leu Arg Ala Ala Gln 340 345 350		
Val Trp Pro Ile Ile Glu Gly Leu Gly Gly Val Asn Gly Trp Tyr Ser 355 360 365		
Ala Pro Leu Leu Trp Arg Leu Arg Gly Ile Ala Asp Arg Leu Ile Gly 370 375 380		
Gly Pro Gly Leu Gly Gly Arg Arg Asp Pro Arg His Leu Lys Leu Gly 385 390 395 400		
Asp Arg Ile Asp Trp Trp Arg Val Thr Glu Ile Asp Pro Pro His Arg 405 410 415		
Leu Val Leu Thr Ala Glu Met Lys Val Asp Gly Gly Ala Trp Leu Ile 420 425 430		
Leu Glu Val Ala Asp Lys Glu Asn Gly Gly Cys Thr Tyr Thr Gln Arg 435 440 445		
Ala Ile Phe Glu Pro Lys Gly Leu Pro Gly Tyr Leu Tyr Trp Trp Val 450 455 460		

Val Ser Pro Phe His Ala Ile Ile Phe Pro Tyr Met Arg Ser Asn Ile
465 470 475 480

Leu Lys Ala Ala Arg Lys Leu Thr
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<211> 612
<212> DNA
<213> Corynebacterium glutamicum
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<222> (101)..(589)  
<223> RXA01534
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Met Thr Ser Ala Ile																115
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Thr Thr Ala Thr Asp Leu Arg Ser Val Leu Arg Asn Val Pro Thr Pro																
10 15 20																
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Ile Ser Phe Ile Ala Thr His Thr Asp Gln Pro Leu Gly Met Ile Val																
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Gly Ser Phe Val Ser Ile Ser Ala Glu Pro Pro Leu Val Gly Ile Phe																
40 45 50																
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Leu Gln Lys Ser Ser Ser Ser Trp Pro Ala Ile Glu Gln Ala Leu Val																
55 60 65																
acc ggc caa gag cta ggc att tct atc ctc ggc ggg gca cac gca gac																355
Thr Gly Gln Glu Leu Gly Ile Ser Ile Leu Gly Gly Ala His Ala Asp																
70 75 80 85																
cat gtg cgt aag ctt tct ggc cca tcc gac cag cgc ttt gaa aac ctt																403
His Val Arg Lys Leu Ser Gly Pro Ser Asp Gln Arg Phe Glu Asn Leu																
90 95 100																
ggg tgg gca tcc acc gaa aac ggt gcg att cac ctt gaa ggc gct gat																451
Gly Trp Ala Ser Thr Glu Asn Gly Ala Ile His Leu Glu Gly Ala Asp																
105 110 115																
gca caa cta acc acg aaa ctt cat gat ctc cag gaa atc ggc gat cac																499
Ala Gln Leu Thr Thr Lys Leu His Asp Leu Gln Glu Ile Gly Asp His																
120 125 130																
ttc ttt gca gtt cta gaa gtt att gac gct tcc gct gac caa gac ttc																547
Phe Phe Ala Val Leu Glu Val Ile Asp Ala Ser Ala Asp Gln Asp Phe																
135 140 145																

agc tca gcg ctg gtg tac cac cgc tca cag gtg tcc tcg ctg 589
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taggacacta aattttaaga ggg 612

<210> 702

<211> 163

<212> PRT

<213> Corynebacterium glutamicum

<400> 702

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 Leu Gly Met Ile Val Gly Ser Phe Val Ser Ile Ser Ala Glu Pro Pro
 35 40 45
 Leu Val Gly Ile Phe Leu Gln Lys Ser Ser Ser Ser Trp Pro Ala Ile
 50 55 60
 Glu Gln Ala Leu Val Thr Gly Gln Glu Leu Gly Ile Ser Ile Leu Gly
 65 70 75 80
 Gly Ala His Ala Asp His Val Arg Lys Leu Ser Gly Pro Ser Asp Gln
 85 90 95
 Arg Phe Glu Asn Leu Gly Trp Ala Ser Thr Glu Asn Gly Ala Ile His
 100 105 110
 Leu Glu Gly Ala Asp Ala Gln Leu Thr Thr Lys Leu His Asp Leu Gln
 115 120 125
 Glu Ile Gly Asp His Phe Phe Ala Val Leu Glu Val Ile Asp Ala Ser
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 Ala Asp Gln Asp Phe Ser Ser Ala Leu Val Tyr His Arg Ser Gln Val
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<210> 703

<211> 1134

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1111)

<223> RXA00288

<400> 703

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Asn	Pro	Val	Asp	Thr	Lys	Val	Arg	Met	Arg	Ala	Gly	Lys	Gln	Lys	His					
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Pro	Lys	Ile	Leu	Gly	Phe	Asp	Ala	Ala	Gly	Glu	Val	Val	Ala	Val	Gly					
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Ser	Asn	Gln	Arg	Pro	Gly	Ser	Asn	Ala	Glu	Tyr	Gln	Val	Val	Asp	Glu					
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Arg	Leu	Val	Gly	His	Ala	Pro	Gln	Ser	Leu	Gly	Ala	His	Asp	Ala	Ala					
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gct	ctc	cca	ctt	gtc	gcg	ctc	act	gca	tgg	gag	tca	ctt	ttt	gac	cga	547				
Ala	Leu	Pro	Leu	Val	Ala	Leu	Thr	Ala	Trp	Glu	Ser	Leu	Phe	Asp	Arg					
		135					140					145								
ttg	gga	gta	act	cag	tca	act	act	gga	aca	ctg	ttg	gtc	ttg	ggc	ggt	595				
Leu	Gly	Val	Thr	Gln	Ser	Thr	Thr	Gly	Thr	Leu	Leu	Val	Leu	Gly	Gly					
		150					155					160			165					
tca	gga	ggt	gtg	cct	tca	gct	ctt	att	caa	ctt	gct	cga	gct	ctc	act	643				
Ser	Gly	Gly	Val	Pro	Ser	Ala	Leu	Ile	Gln	Leu	Ala	Arg	Ala	Leu	Thr					
				170					175					180						
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Gly	Leu	Lys	Val	Val	Ala	Thr	Ala	Ser	Arg	Pro	Glu	Ser	Gln	Glu	Trp					
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gtg	aca	aag	ctc	ggt	gct	cat	gag	gtg	att	gat	cac	tcc	aag	gat	ttg	739				
Val	Thr	Lys	Leu	Gly	Ala	His	Glu	Val	Ile	Asp	His	Ser	Lys	Asp	Leu					
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Ser	Glu	Gln	Ile	Ser	Asp	Val	Asp	Phe	Val	Phe	Ser	Ser	Trp	Thr	Thr					
		215					220					225								
ggg	cgt	gaagta	gag	ctc	gcc	acg	ttg	atg	aaa	ccc	cag	tcc	cac	cta		835				
Gly	Arg	Glu	Val	Glu	Leu	Ala	Thr	Leu	Met	Lys	Pro	Gln	Ser	His	Leu					

230	235	240	245	
gtg ctc atc gat gat cca gtg gat ccc aat ttg ggc gct ttt aag caa				883
Val Leu Ile Asp Asp Pro Val Asp Pro Asn Leu Gly Ala Phe Lys Gln	250	255	260	
aaa gcg atc gct ttg cac tgg gag ttc atg ttt acc cgc gct atg ttc				931
Lys Ala Ile Ala Leu His Trp Glu Phe Met Phe Thr Arg Ala Met Phe	265	270	275	
aac act cct gat atg ggt gaa caa ggg aaa att ctg aat aag atc gcc				979
Asn Thr Pro Asp Met Gly Glu Gln Gly Lys Ile Leu Asn Lys Ile Ala	280	285	290	
gac atg gtt gat cgg ggt cag ttt gag tcc gtg aca gca acg gtg ctg				1027
Asp Met Val Asp Arg Gly Gln Phe Glu Ser Val Thr Ala Thr Val Leu	295	300	305	
gat ggg ctc aac gct gca aac atc atg gag ggg cac cgg ctc gtt gag				1075
Asp Gly Leu Asn Ala Ala Asn Ile Met Glu Gly His Arg Leu Val Glu	310	315	320	325
cag ggt aaa acc tca gga aaa att gtt gtg agg gta taaagaggac				1121
Gln Gly Lys Thr Ser Gly Lys Ile Val Val Arg Val	330	335		
ttgaaaaatg cac				1134
<210> 704				
<211> 337				
<212> PRT				
<213> Corynebacterium glutamicum				
<400> 704				
Met Ser Ala Gln Met Asp Thr Pro Asp Pro Thr Met Ser Ala Val Ala	1	5	10	15
Met Leu Asp Ser Ile Pro Ser Asp Gln Pro Asp Phe Leu Ile Asp Val	20	25	30	
Glu Val Asp Arg Pro Thr Pro Gly Pro His Asp Leu Leu Val His Ile	35	40	45	
Glu Ala Val Ser Ile Asn Pro Val Asp Thr Lys Val Arg Met Arg Ala	50	55	60	
Gly Lys Gln Lys His Pro Lys Ile Leu Gly Phe Asp Ala Ala Gly Glu	65	70	75	80
Val Val Ala Val Gly Ser Gln Val Thr Leu Phe Asn Val Gly Asp Lys	85	90	95	
Val Phe Tyr Ala Gly Ser Asn Gln Arg Pro Gly Ser Asn Ala Glu Tyr	100	105	110	
Gln Val Val Asp Glu Arg Leu Val Gly His Ala Pro Gln Ser Leu Gly	115	120	125	
Ala His Asp Ala Ala Ala Leu Pro Leu Val Ala Leu Thr Ala Trp Glu	130	135	140	

Ser Leu Phe Asp Arg Leu Gly Val Thr Gln Ser Thr Thr Gly Thr Leu
 145 150 155 160
 Leu Val Leu Gly Gly Ser Gly Gly Val Pro Ser Ala Leu Ile Gln Leu
 165 170 175
 Ala Arg Ala Leu Thr Gly Leu Lys Val Val Ala Thr Ala Ser Arg Pro
 180 185 190
 Glu Ser Gln Glu Trp Val Thr Lys Leu Gly Ala His Glu Val Ile Asp
 195 200 205
 His Ser Lys Asp Leu Ser Glu Gln Ile Ser Asp Val Asp Phe Val Phe
 210 215 220
 Ser Ser Trp Thr Thr Gly Arg Glu Val Glu Leu Ala Thr Leu Met Lys
 225 230 235 240
 Pro Gln Ser His Leu Val Leu Ile Asp Asp Pro Val Asp Pro Asn Leu
 245 250 255
 Gly Ala Phe Lys Gln Lys Ala Ile Ala Leu His Trp Glu Phe Met Phe
 260 265 270
 Thr Arg Ala Met Phe Asn Thr Pro Asp Met Gly Glu Gln Gly Lys Ile
 275 280 285
 Leu Asn Lys Ile Ala Asp Met Val Asp Arg Gly Gln Phe Glu Ser Val
 290 295 300
 Thr Ala Thr Val Leu Asp Gly Leu Asn Ala Ala Asn Ile Met Glu Gly
 305 310 315 320
 His Arg Leu Val Glu Gln Gly Lys Thr Ser Gly Lys Ile Val Val Arg
 325 330 335
 Val

<210> 705
 <211> 1089
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1066)
 <223> RXA02741

<400> 705
 actggtcacc tgggtttggtc tgcactctga ctcccctcaa aagggcacaa tttggtcaat 60
 ttcccaacct tgtctttcag tcatggttag tgtgggaacc atg aag gca atc tta 115
 Met Lys Ala Ile Leu
 1 5
 gtt tcc cgc acc ggc gga cca gag gtg ttg gag ttc acc gac act gac 163
 Val Ser Arg Thr Gly Gly Pro Glu Val Leu Glu Phe Thr Asp Thr Asp
 10 15 20

gcc cca aag ccc act gat gat cag gtt tta gtt gaa gtt gat atg gct	211
Ala Pro Lys Pro Thr Asp Asp Gln Val Leu Val Glu Val Asp Met Ala	
25 30 35	
ggc gtc aac ttt att gat act tac tat cgc cag ggt gaa tat cac gct	259
Gly Val Asn Phe Ile Asp Thr Tyr Tyr Arg Gln Gly Glu Tyr His Ala	
40 45 50	
cgc ctg ccg ttt atc cca ggt ttt gaa ggc act ggt cgg gtg ttg gag	307
Arg Leu Pro Phe Ile Pro Gly Phe Glu Gly Thr Gly Arg Val Leu Glu	
55 60 65	
gat ccg cag ggg ttg att gcg gcg ggt acc aag gtg gcg tgg tgt gat	355
Asp Pro Gln Gly Leu Ile Ala Ala Gly Thr Lys Val Ala Trp Cys Asp	
70 75 80 85	
gcc atg ggt tcg tat gct cag cag gtg tgt gtg ccg cgg gat cgc ttg	403
Ala Met Gly Ser Tyr Ala Gln Gln Val Cys Val Pro Arg Asp Arg Leu	
90 95 100	
gtg gcg gtt ccc gag ggc gtg agt tcg gaa gtg gct gcg tcg atg ttg	451
Val Ala Val Pro Glu Gly Val Ser Ser Glu Val Ala Ala Ser Met Leu	
105 110 115	
atg cag gga atc act gcg cat tat cta acc aat ggt gtg tat gag ctt	499
Met Gln Gly Ile Thr Ala His Tyr Leu Thr Asn Gly Val Tyr Glu Leu	
120 125 130	
gaa gag ggc gat tct tgc ctc atc act gct ggc gcg ggt ggt gtt gga	547
Glu Glu Gly Asp Ser Cys Leu Ile Thr Ala Gly Ala Gly Gly Val Gly	
135 140 145	
ttg ttg gct acg cag atg gcg gcg gcc aag gga gtg cgc gtg tac agc	595
Leu Leu Ala Thr Gln Met Ala Ala Ala Lys Gly Val Arg Val Tyr Ser	
150 155 160 165	
gtg gtg tcc acg gat gaa aaa gct gag ctt gct ttg gat gcc ggt gct	643
Val Val Ser Thr Asp Glu Lys Ala Glu Leu Ala Leu Asp Ala Gly Ala	
170 175 180	
tat gag gtg ttt cgt tat tcc gat aat ttg gcg gag cag gtt cgt cgg	691
Tyr Glu Val Phe Arg Tyr Ser Asp Asn Leu Ala Glu Gln Val Arg Arg	
185 190 195	
cac aac ggg ggt cgc gga gtt gat gtg gtg tat gac ggt gtc ggc cag	739
His Asn Gly Gly Arg Gly Val Asp Val Val Tyr Asp Gly Val Gly Gln	
200 205 210	
tcc acg ttc aat gag tcc tta gag gct gtt cgt ccg cgc ggc act gtg	787
Ser Thr Phe Asn Glu Ser Leu Glu Ala Val Arg Pro Arg Gly Thr Val	
215 220 225	
tgt ttg ttt ggt gcg gcg tcg ggt cct gtg gag cct ttt gat ccg cag	835
Cys Leu Phe Gly Ala Ala Ser Gly Pro Val Glu Pro Phe Asp Pro Gln	
230 235 240 245	
ctg ttg aac act cac ggt tcg atc ttc ttg acc cgc cca agc att ggc	883
Leu Leu Asn Thr His Gly Ser Ile Phe Leu Thr Arg Pro Ser Ile Gly	
250 255 260	

gcg tgg acg tct gag gag ggc gaa ttt gcc aag cgt gca cag gcg gtc 931
 Ala Trp Thr Ser Glu Glu Gly Glu Phe Ala Lys Arg Ala Gln Ala Val
 265 270 275

acg cag gcc atc gtc gaa ggc acc ttg cgg gtt cgc gtt act ggc aca 979
 Thr Gln Ala Ile Val Glu Gly Thr Leu Arg Val Arg Val Thr Gly Thr
 280 285 290

tat tcg ctt gcc gac gcc tac atc gcc cac cgc gac ctt cag gcg cgt 1027
 Tyr Ser Leu Ala Asp Ala Tyr Ile Ala His Arg Asp Leu Gln Ala Arg
 295 300 305

agc acg agc ggt tct ttg gtc ttg gaa atc ccg aag gac taaacacgca 1076
 Ser Thr Ser Gly Ser Leu Val Leu Glu Ile Pro Lys Asp
 310 315 320

taaaaagatc ctg 1089

<210> 706

<211> 322

<212> PRT

<213> Corynebacterium glutamicum

<400> 706

Met Lys Ala Ile Leu Val Ser Arg Thr Gly Gly Pro Glu Val Leu Glu
 1 5 10 15

Phe Thr Asp Thr Asp Ala Pro Lys Pro Thr Asp Asp Gln Val Leu Val
 20 25 30

Glu Val Asp Met Ala Gly Val Asn Phe Ile Asp Thr Tyr Tyr Arg Gln
 35 40 45

Gly Glu Tyr His Ala Arg Leu Pro Phe Ile Pro Gly Phe Glu Gly Thr
 50 55 60

Gly Arg Val Leu Glu Asp Pro Gln Gly Leu Ile Ala Ala Gly Thr Lys
 65 70 75 80

Val Ala Trp Cys Asp Ala Met Gly Ser Tyr Ala Gln Gln Val Cys Val
 85 90 95

Pro Arg Asp Arg Leu Val Ala Val Pro Glu Gly Val Ser Ser Glu Val
 100 105 110

Ala Ala Ser Met Leu Met Gln Gly Ile Thr Ala His Tyr Leu Thr Asn
 115 120 125

Gly Val Tyr Glu Leu Glu Glu Gly Asp Ser Cys Leu Ile Thr Ala Gly
 130 135 140

Ala Gly Gly Val Gly Leu Leu Ala Thr Gln Met Ala Ala Ala Lys Gly
 145 150 155 160

Val Arg Val Tyr Ser Val Val Ser Thr Asp Glu Lys Ala Glu Leu Ala
 165 170 175

Leu Asp Ala Gly Ala Tyr Glu Val Phe Arg Tyr Ser Asp Asn Leu Ala
 180 185 190

Glu Gln Val Arg Arg His Asn Gly Gly Arg Gly Val Asp Val Val Tyr
 195 200 205
 Asp Gly Val Gly Gln Ser Thr Phe Asn Glu Ser Leu Glu Ala Val Arg
 210 215 220
 Pro Arg Gly Thr Val Cys Leu Phe Gly Ala Ala Ser Gly Pro Val Glu
 225 230 235 240
 Pro Phe Asp Pro Gln Leu Leu Asn Thr His Gly Ser Ile Phe Leu Thr
 245 250 255
 Arg Pro Ser Ile Gly Ala Trp Thr Ser Glu Glu Gly Glu Phe Ala Lys
 260 265 270
 Arg Ala Gln Ala Val Thr Gln Ala Ile Val Glu Gly Thr Leu Arg Val
 275 280 285
 Arg Val Thr Gly Thr Tyr Ser Leu Ala Asp Ala Tyr Ile Ala His Arg
 290 295 300
 Asp Leu Gln Ala Arg Ser Thr Ser Gly Ser Leu Val Leu Glu Ile Pro
 305 310 315 320
 Lys Asp

<210> 707
 <211> 990
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(967)
 <223> RXN02560

<400> 707
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 ggaacttcta agagcagtgg aatgaaataa tccggtgctg atg cag ggc aac tcg 115
 Met Gln Gly Asn Ser
 1 5
 ctt aat ctg gca gac aac agc gag aga aag aag ccc atg ccg tca cca 163
 Leu Asn Leu Ala Asp Asn Ser Glu Arg Lys Lys Pro Met Pro Ser Pro
 10 15 20
 gga gaa ctt tta gcc gcc cgc tac gga caa cct gca acc tgg acg cca 211
 Gly Glu Leu Leu Ala Ala Arg Tyr Gly Gln Pro Ala Thr Trp Thr Pro
 25 30 35
 ccg cag tgg aat gag acg ctt gat gtc att cac cag cat cga tca gtt 259
 Pro Gln Trp Asn Glu Thr Leu Asp Val Ile His Gln His Arg Ser Val
 40 45 50
 cgc agg tgg ttg gat aaa ccg gtt gat gat gac acc atc cgc acc att 307
 Arg Arg Trp Leu Asp Lys Pro Val Asp Asp Asp Thr Ile Arg Thr Ile
 55 60 65

att tcc gcc gca caa tcg gct gga acc tct tcc aat aag cag gtc att 355
 Ile Ser Ala Ala Gln Ser Ala Gly Thr Ser Ser Asn Lys Gln Val Ile
 70 75 80 85

tct gtc atc gtg gtt aaa gat cct gag ctg agg aaa ggc ctc gcg ggg 403
 Ser Val Ile Val Val Lys Asp Pro Glu Leu Arg Lys Gly Leu Ala Gly
 90 95 100

atc act cgc cag atg ttt ccg cac ctt gag cag gtt ccc gcg gtg ctg 451
 Ile Thr Arg Gln Met Phe Pro His Leu Glu Gln Val Pro Ala Val Leu
 105 110 115

att tgg ttg att gat tat tcc cga atc agt gcg gtg gca gcc aga gaa 499
 Ile Trp Leu Ile Asp Tyr Ser Arg Ile Ser Ala Val Ala Ala Arg Glu
 120 125 130

gat ctc cca aca ggg gct ctt gat tat ctc gat gag gcc gcg tgg ggg 547
 Asp Leu Pro Thr Gly Ala Leu Asp Tyr Leu Asp Glu Ala Ala Trp Gly
 135 140 145

ttc ctc gac gcc gga atc gca gct caa aac gct gca att gct gcg gag 595
 Phe Leu Asp Ala Gly Ile Ala Ala Gln Asn Ala Ala Ile Ala Ala Glu
 150 155 160 165

tca ctt gga ttg gga acg ctc tat ttg ggt tcg gtg cgc aac gat gcg 643
 Ser Leu Gly Leu Gly Thr Leu Tyr Leu Gly Ser Val Arg Asn Asp Ala
 170 175 180

gaa gcc gtg cac aaa ttg ctt ggc ctt cca cct gag atc gtg cct gtc 691
 Glu Ala Val His Lys Leu Leu Gly Leu Pro Pro Glu Ile Val Pro Val
 185 190 195

gtg ggc ttg gaa atg ggg cat gcg gat ccg cct gaa cct gcc gga att 739
 Val Gly Leu Glu Met Gly His Ala Asp Pro Pro Glu Pro Ala Gly Ile
 200 205 210

aaa cct ccc ctg cca caa gaa gcc att gtt cac tgg gat acc tac acc 787
 Lys Pro Pro Leu Pro Gln Glu Ala Ile Val His Trp Asp Thr Tyr Thr
 215 220 225

gag aaa aac ctc gaa ctt atc gat tcc tac gac cgc gcc ctc gac act 835
 Glu Lys Asn Leu Glu Leu Ile Asp Ser Tyr Asp Arg Ala Leu Asp Thr
 230 235 240 245

tac tat tct cgc tac ggc cag cac cag ctc tgg tcg aag cag acg gcg 883
 Tyr Tyr Ser Arg Tyr Gly Gln His Gln Leu Trp Ser Lys Gln Thr Ala
 250 255 260

cat agg gcg gcg tcg aaa agc ttt tca aaa acc aac agg cag ttc ctt 931
 His Arg Ala Ala Ser Lys Ser Phe Ser Lys Thr Asn Arg Gln Phe Leu
 265 270 275

agg ggc gtg ttt gag cgc gcc ggg ttt ggg ctg aga taaaagcatg 977
 Arg Gly Val Phe Glu Arg Ala Gly Phe Gly Leu Arg
 280 285

attatggacg cct 990

<210> 708

<211> 289

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 708

Met Gln Gly Asn Ser Leu Asn Leu Ala Asp Asn Ser Glu Arg Lys Lys
 1 5 10 15
 Pro Met Pro Ser Pro Gly Glu Leu Leu Ala Ala Arg Tyr Gly Gln Pro
 20 25 30
 Ala Thr Trp Thr Pro Pro Gln Trp Asn Glu Thr Leu Asp Val Ile His
 35 40 45
 Gln His Arg Ser Val Arg Arg Trp Leu Asp Lys Pro Val Asp Asp Asp
 50 55 60
 Thr Ile Arg Thr Ile Ile Ser Ala Ala Gln Ser Ala Gly Thr Ser Ser
 65 70 75 80
 Asn Lys Gln Val Ile Ser Val Ile Val Val Lys Asp Pro Glu Leu Arg
 85 90 95
 Lys Gly Leu Ala Gly Ile Thr Arg Gln Met Phe Pro His Leu Glu Gln
 100 105 110
 Val Pro Ala Val Leu Ile Trp Leu Ile Asp Tyr Ser Arg Ile Ser Ala
 115 120 125
 Val Ala Ala Arg Glu Asp Leu Pro Thr Gly Ala Leu Asp Tyr Leu Asp
 130 135 140
 Glu Ala Ala Trp Gly Phe Leu Asp Ala Gly Ile Ala Ala Gln Asn Ala
 145 150 155 160
 Ala Ile Ala Ala Glu Ser Leu Gly Leu Gly Thr Leu Tyr Leu Gly Ser
 165 170 175
 Val Arg Asn Asp Ala Glu Ala Val His Lys Leu Leu Gly Leu Pro Pro
 180 185 190
 Glu Ile Val Pro Val Val Gly Leu Glu Met Gly His Ala Asp Pro Pro
 195 200 205
 Glu Pro Ala Gly Ile Lys Pro Pro Leu Pro Gln Glu Ala Ile Val His
 210 215 220
 Trp Asp Thr Tyr Thr Glu Lys Asn Leu Glu Leu Ile Asp Ser Tyr Asp
 225 230 235 240
 Arg Ala Leu Asp Thr Tyr Tyr Ser Arg Tyr Gly Gln His Gln Leu Trp
 245 250 255
 Ser Lys Gln Thr Ala His Arg Ala Ala Ser Lys Ser Phe Ser Lys Thr
 260 265 270
 Asn Arg Gln Phe Leu Arg Gly Val Phe Glu Arg Ala Gly Phe Gly Leu
 275 280 285
 Arg

<210> 709
 <211> 922
 <212> DNA
 <213> *Corynebacterium glutamicum*

<220>
 <221> CDS
 <222> (101)..(922)
 <223> FRXA02560

<400> 709
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 ggaacttcta agagcagtgg aatgaaataa tccggtgctg atg cag ggc aac tcg 115
 Met Gln Gly Asn Ser
 1 5
 ctt aat ctg gca gac aac agc gag aga aag aag ccc atg ccg tca cca 163
 Leu Asn Leu Ala Asp Asn Ser Glu Arg Lys Lys Pro Met Pro Ser Pro
 10 15 20
 gga gaa ctt tta gcc gcc cgc tac gga caa cct gca acc tgg acg cca 211
 Gly Glu Leu Leu Ala Ala Arg Tyr Gly Gln Pro Ala Thr Trp Thr Pro
 25 30 35
 ccg cag tgg aat gag acg ctt gat gtc att cac cag cat cga tca gtt 259
 Pro Gln Trp Asn Glu Thr Leu Asp Val Ile His Gln His Arg Ser Val
 40 45 50
 cgc agg tgg ttg gat aaa ccg gtt gat gat gac acc atc cgc acc att 307
 Arg Arg Trp Leu Asp Lys Pro Val Asp Asp Asp Thr Ile Arg Thr Ile
 55 60 65
 att tcc gcc gca caa tcg gct gga acc tct tcc aat aag cag gtc att 355
 Ile Ser Ala Ala Gln Ser Ala Gly Thr Ser Ser Asn Lys Gln Val Ile
 70 75 80 85
 tct gtc atc gtg gtt aaa gat cct gag ctg agg aaa ggc ctc gcg ggg 403
 Ser Val Ile Val Val Lys Asp Pro Glu Leu Arg Lys Gly Leu Ala Gly
 90 95 100
 atc act cgc cag atg ttt ccg cac ctt gag cag gtt ccc gcg gtg ctg 451
 Ile Thr Arg Gln Met Phe Pro His Leu Glu Gln Val Pro Ala Val Leu
 105 110 115
 att tgg ttg att gat tat tcc cga atc agt gcg gtg gca gcc aga gaa 499
 Ile Trp Leu Ile Asp Tyr Ser Arg Ile Ser Ala Val Ala Ala Arg Glu
 120 125 130
 gat ctc cca aca ggg gct ctt gat tat ctc gat gag gcc gcg tgg ggg 547
 Asp Leu Pro Thr Gly Ala Leu Asp Tyr Leu Asp Glu Ala Ala Trp Gly
 135 140 145
 ttc ctc gac gcc gga atc gca gct caa aac gct gca att gct gcg gag 595
 Phe Leu Asp Ala Gly Ile Ala Ala Gln Asn Ala Ala Ile Ala Ala Glu
 150 155 160 165
 tca ctt gga ttg gga acg ctc tat ttg ggt tcg gtg cgc aac gat gcg 643
 Ser Leu Gly Leu Gly Thr Leu Tyr Leu Gly Ser Val Arg Asn Asp Ala
 170 175 180

gaa gcc gtg cac aaa ttg ctt ggc ctt cca cct gag atc gtg cct gtc 691
 Glu Ala Val His Lys Leu Leu Gly Leu Pro Pro Glu Ile Val Pro Val
 185 190 195
 gtg ggc ttg gaa atg ggg cat gcg gat ccg cct gaa cct gcc gga att 739
 Val Gly Leu Glu Met Gly His Ala Asp Pro Pro Glu Pro Ala Gly Ile
 200 205 210
 aaa cct ccc ctg cca caa gaa gcc att gtt cac tgg gat acc tac acc 787
 Lys Pro Pro Leu Pro Gln Glu Ala Ile Val His Trp Asp Thr Tyr Thr
 215 220 225
 gag aaa aac ctc gaa ctt atc gat tcc tac gac cgc gcc ctc gac act 835
 Glu Lys Asn Leu Glu Leu Ile Asp Ser Tyr Asp Arg Ala Leu Asp Thr
 230 235 240 245
 tac tat tct cgc tac ggc cag cac cag ctc tgg tcg aag cag acg gcg 883
 Tyr Tyr Ser Arg Tyr Gly Gln His Gln Leu Trp Ser Lys Gln Thr Ala
 250 255 260
 cat agg gcg gcg tct aaa cgc tgt tac aag aac caa gaa 922
 His Arg Ala Ala Ser Lys Arg Cys Tyr Lys Asn Gln Glu
 265 270

<210> 710
 <211> 274
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 710
 Met Gln Gly Asn Ser Leu Asn Leu Ala Asp Asn Ser Glu Arg Lys Lys
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 Pro Met Pro Ser Pro Gly Glu Leu Leu Ala Ala Arg Tyr Gly Gln Pro
 20 25 30
 Ala Thr Trp Thr Pro Pro Gln Trp Asn Glu Thr Leu Asp Val Ile His
 35 40 45
 Gln His Arg Ser Val Arg Arg Trp Leu Asp Lys Pro Val Asp Asp Asp
 50 55 60
 Thr Ile Arg Thr Ile Ile Ser Ala Ala Gln Ser Ala Gly Thr Ser Ser
 65 70 75 80
 Asn Lys Gln Val Ile Ser Val Ile Val Val Lys Asp Pro Glu Leu Arg
 85 90 95
 Lys Gly Leu Ala Gly Ile Thr Arg Gln Met Phe Pro His Leu Glu Gln
 100 105 110
 Val Pro Ala Val Leu Ile Trp Leu Ile Asp Tyr Ser Arg Ile Ser Ala
 115 120 125
 Val Ala Ala Arg Glu Asp Leu Pro Thr Gly Ala Leu Asp Tyr Leu Asp
 130 135 140
 Glu Ala Ala Trp Gly Phe Leu Asp Ala Gly Ile Ala Ala Gln Asn Ala
 145 150 155 160

Ala Ile Ala Ala Glu Ser Leu Gly Leu Gly Thr Leu Tyr Leu Gly Ser
 165 170 175

Val Arg Asn Asp Ala Glu Ala Val His Lys Leu Leu Gly Leu Pro Pro
 180 185 190

Glu Ile Val Pro Val Val Gly Leu Glu Met Gly His Ala Asp Pro Pro
 195 200 205

Glu Pro Ala Gly Ile Lys Pro Pro Leu Pro Gln Glu Ala Ile Val His
 210 215 220

Trp Asp Thr Tyr Thr Glu Lys Asn Leu Glu Leu Ile Asp Ser Tyr Asp
 225 230 235 240

Arg Ala Leu Asp Thr Tyr Tyr Ser Arg Tyr Gly Gln His Gln Leu Trp
 245 250 255

Ser Lys Gln Thr Ala His Arg Ala Ala Ser Lys Arg Cys Tyr Lys Asn
 260 265 270

Gln Glu

<210> 711
 <211> 870
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(847)
 <223> RXA01311

<400> 711
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tcttcgaatc tgtcccactg cagacaagga actacaagta atg aaa ctt aca ctt 115
 Met Lys Leu Thr Leu
 1 5

gag atc tgg cgt caa gca ggc cca act gcg gaa ggc aag ttc gaa acc 163
 Glu Ile Trp Arg Gln Ala Gly Pro Thr Ala Glu Gly Lys Phe Glu Thr
 10 15 20

gtc cag gtt gac gac gcc gtc gcg cag atg tcc atc ctg gag ctg ctt 211
 Val Gln Val Asp Asp Ala Val Ala Gln Met Ser Ile Leu Glu Leu Leu
 25 30 35

gac cac gta aac aac aag ttc atc gaa gaa ggc aaa gaa cca ttc gcg 259
 Asp His Val Asn Asn Lys Phe Ile Glu Glu Gly Lys Glu Pro Phe Ala
 40 45 50

ttc gcc tct gac tgc cgc gaa ggc att tgt ggt acc tgt ggt ctc ctc 307
 Phe Ala Ser Asp Cys Arg Glu Gly Ile Cys Gly Thr Cys Gly Leu Leu
 55 60 65

gtg aac ggt cgc cct cac ggc gcc gac cag aac aag cct gcc tgt gcg 355
 Val Asn Gly Arg Pro His Gly Ala Asp Gln Asn Lys Pro Ala Cys Ala

70	75	80	85
cag cgc ctg gtc agc tac aag gaa ggc gac acc ctc aag atc gaa cca Gln Arg Leu Val Ser Tyr Lys Glu Gly Asp Thr Leu Lys Ile Glu Pro	90	95	100 403
ctg cgt tcc gcc gca tac cca gtg atc aag gac atg gtc gtc gac cgc Leu Arg Ser Ala Ala Tyr Pro Val Ile Lys Asp Met Val Val Asp Arg	105	110	115 451
tcc gca ctg gac cgt gtc atg gaa cag ggt ggc tac gtg acc atc aac Ser Ala Leu Asp Arg Val Met Glu Gln Gly Gly Tyr Val Thr Ile Asn	120	125	130 499
gca ggt acc gca cct gac gct gat acc ctc cac gtc aac cac gaa acc Ala Gly Thr Ala Pro Asp Ala Asp Thr Leu His Val Asn His Glu Thr	135	140	145 547
gca gaa ctc gca ctt gac cac gca gcc tgc atc ggc tgt ggc gca tgt Ala Glu Leu Ala Leu Asp His Ala Ala Cys Ile Gly Cys Gly Ala Cys	150	155	160 595
gtt gct gcc tgc cct aac ggc gca gca cac ctg ttc acc ggc gca aag Val Ala Ala Cys Pro Asn Gly Ala Ala His Leu Phe Thr Gly Ala Lys	170	175	180 643
ctt gtt cac ctc tcc ctc ctc cca ctg ggt aag gaa gag cgc gga ctg Leu Val His Leu Ser Leu Leu Pro Leu Gly Lys Glu Glu Arg Gly Leu	185	190	195 691
cgt gca cgt aag atg gtt gat gaa atg gaa acc aac ttc gga cac tgc Arg Ala Arg Lys Met Val Asp Glu Met Glu Thr Asn Phe Gly His Cys	200	205	210 739
tcc ctc tac ggc gag tgc gca gat gtc tgc ccc gca ggc atc cca ctg Ser Leu Tyr Gly Glu Cys Ala Asp Val Cys Pro Ala Gly Ile Pro Leu	215	220	225 787
acc gct gtg gca gct gtc acc aag gaa cgt gcg cgt gca gct ttc cga Thr Ala Val Ala Ala Val Thr Lys Glu Arg Ala Arg Ala Ala Phe Arg	230	235	240 835
ggc aaa gac gac tagtctttaa tccaagtaag tac Gly Lys Asp Asp			870

<210> 712

<211> 249

<212> PRT

<213> Corynebacterium glutamicum

<400> 712

Met	Lys	Leu	Thr	Leu	Glu	Ile	Trp	Arg	Gln	Ala	Gly	Pro	Thr	Ala	Glu
1				5					10					15	

Gly	Lys	Phe	Glu	Thr	Val	Gln	Val	Asp	Asp	Ala	Val	Ala	Gln	Met	Ser
			20					25					30		

Ile	Leu	Glu	Leu	Leu	Asp	His	Val	Asn	Asn	Lys	Phe	Ile	Glu	Glu	Gly
		35					40					45			

Lys Glu Pro Phe Ala Phe Ala Ser Asp Cys Arg Glu Gly Ile Cys Gly
 50 55 60
 Thr Cys Gly Leu Leu Val Asn Gly Arg Pro His Gly Ala Asp Gln Asn
 65 70 75 80
 Lys Pro Ala Cys Ala Gln Arg Leu Val Ser Tyr Lys Glu Gly Asp Thr
 85 90 95
 Leu Lys Ile Glu Pro Leu Arg Ser Ala Ala Tyr Pro Val Ile Lys Asp
 100 105 110
 Met Val Val Asp Arg Ser Ala Leu Asp Arg Val Met Glu Gln Gly Gly
 115 120 125
 Tyr Val Thr Ile Asn Ala Gly Thr Ala Pro Asp Ala Asp Thr Leu His
 130 135 140
 Val Asn His Glu Thr Ala Glu Leu Ala Leu Asp His Ala Ala Cys Ile
 145 150 155 160
 Gly Cys Gly Ala Cys Val Ala Ala Cys Pro Asn Gly Ala Ala His Leu
 165 170 175
 Phe Thr Gly Ala Lys Leu Val His Leu Ser Leu Leu Pro Leu Gly Lys
 180 185 190
 Glu Glu Arg Gly Leu Arg Ala Arg Lys Met Val Asp Glu Met Glu Thr
 195 200 205
 Asn Phe Gly His Cys Ser Leu Tyr Gly Glu Cys Ala Asp Val Cys Pro
 210 215 220
 Ala Gly Ile Pro Leu Thr Ala Val Ala Ala Val Thr Lys Glu Arg Ala
 225 230 235 240
 Arg Ala Ala Phe Arg Gly Lys Asp Asp
 245

<210> 713

<211> 929

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(906)

<223> RXN03014

<400> 713

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 Tyr Val Gly Phe Glu Val Leu Leu Val Ala Ser Tyr Val Leu Leu Thr
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 ttg ggt gca tcg ccg gca cgt gta cgt tcc ggc gtg ggt tac gtg atg 96
 Leu Gly Ala Ser Pro Ala Arg Val Arg Ser Gly Val Gly Tyr Val Met
 20 25 30
 gtg tcc atg gcg tca tcg atg gtg ttc ctg ttt gga ctc gca atg gtt 144

Val	Ser	Met	Ala	Ser	Ser	Met	Val	Phe	Leu	Phe	Gly	Leu	Ala	Met	Val	
		35					40					45				
tac	gcc	tca	gtg	ggc	acg	ttg	aac	atg	gct	cac	gtt	ggc	cta	cgc	atg	192
Tyr	Ala	Ser	Val	Gly	Thr	Leu	Asn	Met	Ala	His	Val	Gly	Leu	Arg	Met	
	50					55					60					
gaa	gat	gtt	ccg	tct	gga	act	cgc	tcc	gcg	atc	ttc	gca	gtg	ttg	ctc	240
Glu	Asp	Val	Pro	Ser	Gly	Thr	Arg	Ser	Ala	Ile	Phe	Ala	Val	Leu	Leu	
65					70				75					80		
gtg	gca	ttc	ggg	att	aaa	gct	gcc	gtg	ttc	ccc	cta	gat	tcc	tgg	ctg	288
Val	Ala	Phe	Gly	Ile	Lys	Ala	Ala	Val	Phe	Pro	Leu	Asp	Ser	Trp	Leu	
				85				90						95		
ccg	gac	tcc	tac	ccc	acc	gcg	cca	tcg	ctg	gtc	acc	gcg	gtg	ttc	gca	336
Pro	Asp	Ser	Tyr	Pro	Thr	Ala	Pro	Ser	Leu	Val	Thr	Ala	Val	Phe	Ala	
			100					105					110			
ggg	ctg	ttg	acc	aag	gtg	ggg	gtg	tat	tcc	atc	att	cga	gca	cgc	tcg	384
Gly	Leu	Leu	Thr	Lys	Val	Gly	Val	Tyr	Ser	Ile	Ile	Arg	Ala	Arg	Ser	
	115						120					125				
att	att	ttc	acc	gat	gga	tcc	ctt	gac	acc	atg	ctg	atg	tgg	gtg	gca	432
Ile	Ile	Phe	Thr	Asp	Gly	Ser	Leu	Asp	Thr	Met	Leu	Met	Trp	Val	Ala	
	130					135					140					
ctc	gcc	acc	atg	ctc	att	ggg	att	ttg	ggc	gcg	atg	gcg	caa	aac	gat	480
Leu	Ala	Thr	Met	Leu	Ile	Gly	Ile	Leu	Gly	Ala	Met	Ala	Gln	Asn	Asp	
145					150				155						160	
atc	aaa	cgt	ttg	ttg	tca	ttt	act	ctg	gtc	agc	cac	atc	ggc	tac	atg	528
Ile	Lys	Arg	Leu	Leu	Ser	Phe	Thr	Leu	Val	Ser	His	Ile	Gly	Tyr	Met	
				165				170						175		
atc	ttc	ggc	gta	gcc	ctt	gga	tct	gca	cag	ggg	ttg	tct	ggg	gcg	atc	576
Ile	Phe	Gly	Val	Ala	Leu	Gly	Ser	Ala	Gln	Gly	Leu	Ser	Gly	Ala	Ile	
			180					185					190			
ttc	tac	gca	atc	cac	cac	att	ctg	gtt	cag	act	tcc	ctg	ttc	ctg	gtg	624
Phe	Tyr	Ala	Ile	His	His	Ile	Leu	Val	Gln	Thr	Ser	Leu	Phe	Leu	Val	
		195					200					205				
gtc	ggg	ctg	gtg	gaa	cgc	caa	gcc	gga	tcc	tcc	tcg	ctg	cga	cgc	ctt	672
Val	Gly	Leu	Val	Glu	Arg	Gln	Ala	Gly	Ser	Ser	Ser	Leu	Arg	Arg	Leu	
	210					215					220					
gga	tcc	ctg	gca	tat	atc	tcc	cca	ctt	ctt	gcg	att	ttg	tac	ttc	atc	720
Gly	Ser	Leu	Ala	Tyr	Ile	Ser	Pro	Leu	Leu	Ala	Ile	Leu	Tyr	Phe	Ile	
225					230					235					240	
ccc	gcc	atc	aac	ctg	ggg	ggg	atc	cca	ccg	ttc	tcc	ggc	ttc	ctg	ggc	768
Pro	Ala	Ile	Asn	Leu	Gly	Gly	Ile	Pro	Pro	Phe	Ser	Gly	Phe	Leu	Gly	
				245					250					255		
aag	atc	atg	ctc	atc	gaa	gcc	ggc	gcc	cga	aga	tgg	cag	ttg	gct	ggc	816
Lys	Ile	Met	Leu	Ile	Glu	Ala	Gly	Ala	Arg	Arg	Trp	Gln	Leu	Ala	Gly	
			260				265						270			
atg	ggg	cct	tat	cgc	agg	cgc	cgt	tgt	cac	ctc	act	gct	cac	ctt	gta	864
Met	Gly	Pro	Tyr	Arg	Arg	Arg	Arg	Cys	His	Leu	Thr	Ala	His	Leu	Val	

275

280

285

cac cat ggt tct ggt ctg gtc caa ggc ctt ctg gcg cga ccg
 His His Gly Ser Gly Leu Val Gln Gly Leu Leu Ala Arg Pro
 290 295 300

906

taaagacgcc cccgatggag caa

929

<210> 714

<211> 302

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 714

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Leu Gly Ala Ser Pro Ala Arg Val Arg Ser Gly Val Gly Tyr Val Met
 20 25 30

Val Ser Met Ala Ser Ser Met Val Phe Leu Phe Gly Leu Ala Met Val
 35 40 45

Tyr Ala Ser Val Gly Thr Leu Asn Met Ala His Val Gly Leu Arg Met
 50 55 60

Glu Asp Val Pro Ser Gly Thr Arg Ser Ala Ile Phe Ala Val Leu Leu
 65 70 75 80

Val Ala Phe Gly Ile Lys Ala Ala Val Phe Pro Leu Asp Ser Trp Leu
 85 90 95

Pro Asp Ser Tyr Pro Thr Ala Pro Ser Leu Val Thr Ala Val Phe Ala
 100 105 110

Gly Leu Leu Thr Lys Val Gly Val Tyr Ser Ile Ile Arg Ala Arg Ser
 115 120 125

Ile Ile Phe Thr Asp Gly Ser Leu Asp Thr Met Leu Met Trp Val Ala
 130 135 140

Leu Ala Thr Met Leu Ile Gly Ile Leu Gly Ala Met Ala Gln Asn Asp
 145 150 155 160

Ile Lys Arg Leu Leu Ser Phe Thr Leu Val Ser His Ile Gly Tyr Met
 165 170 175

Ile Phe Gly Val Ala Leu Gly Ser Ala Gln Gly Leu Ser Gly Ala Ile
 180 185 190

Phe Tyr Ala Ile His His Ile Leu Val Gln Thr Ser Leu Phe Leu Val
 195 200 205

Val Gly Leu Val Glu Arg Gln Ala Gly Ser Ser Ser Leu Arg Arg Leu
 210 215 220

Gly Ser Leu Ala Tyr Ile Ser Pro Leu Leu Ala Ile Leu Tyr Phe Ile
 225 230 235 240

Pro Ala Ile Asn Leu Gly Gly Ile Pro Pro Phe Ser Gly Phe Leu Gly

145	150	155	160	
atc aaa cgt ttg ttg tca ttt act ctg gtc agc cac atc ggc tac atg Ile Lys Arg Leu Leu Ser Phe Thr Leu Val Ser His Ile Gly Tyr Met	165	170	175	528
atc ttc ggc gta gcc ctt gga tct gca cag ggt ttg tct ggt gcg atc Ile Phe Gly Val Ala Leu Gly Ser Ala Gln Gly Leu Ser Gly Ala Ile	180	185	190	576
ttc tac gca atc cac cac att ctg gtt cag act tcc ctg ttc ctg gtg Phe Tyr Ala Ile His His Ile Leu Val Gln Thr Ser Leu Phe Leu Val	195	200	205	624
gtc ggt ctg gtg gaa cgc caa gcc gga tcc tcc tcg ctg cga cgc ctt Val Gly Leu Val Glu Arg Gln Ala Gly Ser Ser Ser Leu Arg Arg Leu	210	215	220	672
gga tcc ctg gca tat atc tcc cca ctt ctt gcg att ttg tac ttc atc Gly Ser Leu Ala Tyr Ile Ser Pro Leu Leu Ala Ile Leu Tyr Phe Ile	225	230	235	720
ccc gcc atc aac ctg ggt ggt atc cca ccg ttc tcc ggc ttc ctg ggc Pro Ala Ile Asn Leu Gly Gly Ile Pro Pro Phe Ser Gly Phe Leu Gly	245	250	255	768
aag atc atg ctc atc gaa gcc ggc gcc gaa gat ggc agt tgg ctg gca Lys Ile Met Leu Ile Glu Ala Gly Ala Glu Asp Gly Ser Trp Leu Ala	260	265	270	816
tgg gtc ctt atc gca ggc gcc gtt gtc acc tca ctg ctc acc ttg tac Trp Val Leu Ile Ala Gly Ala Val Val Thr Ser Leu Leu Thr Leu Tyr	275	280	285	864
acc atg gtt ctg gtc tgg tcc aag gcc ttc tgg cgc gac cgt aaa gac Thr Met Val Leu Val Trp Ser Lys Ala Phe Trp Arg Asp Arg Lys Asp	290	295	300	912
gcc ccc gat gga gca acc gca ctt gcg cga ccc gca cct ttg gta gat Ala Pro Asp Gly Ala Thr Ala Leu Ala Arg Pro Ala Pro Leu Val Asp	305	310	315	960
gtc caa gac gaa gtc gcc gtt aaa gac cgc aac gat gtc gga cgg atg Val Gln Asp Glu Val Ala Val Lys Asp Arg Asn Asp Val Gly Arg Met	325	330	335	1008
cct tgg ggc atg gtc ttc tcc act gct ctc ctg gtt tca gca tct ctt Pro Trp Gly Met Val Phe Ser Thr Ala Leu Leu Val Ser Ala Ser Leu	340	345	350	1056
gct gta tcc gtg ctc gca gga cca ctg tca tct att act gga cgc gcc Ala Val Ser Val Leu Ala Gly Pro Leu Ser Ser Ile Thr Gly Arg Ala	355	360	365	1104
gcc gaa tcc gca caa gat gtc aac atc tac cgc gcc gca gta ctc ggc Ala Glu Ser Ala Gln Asp Val Asn Ile Tyr Arg Ala Ala Val Leu Gly	370	375	380	1152
ccc aac tac ctc gac cca tca cgc aca ctc gag atg gag cgt tac gac Pro Asn Tyr Leu Asp Pro Ser Arg Thr Leu Glu Met Glu Arg Tyr Asp	385	390	395	1200
			400	

245

250

255

Lys Ile Met Leu Ile Glu Ala Gly Ala Arg Arg Trp Gln Leu Ala Gly
 260 265 270

Met Gly Pro Tyr Arg Arg Arg Arg Cys His Leu Thr Ala His Leu Val
 275 280 285

His His Gly Ser Gly Leu Val Gln Gly Leu Leu Ala Arg Pro
 290 295 300

<210> 715

<211> 1280

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(1257)

<223> FRXA00910

<400> 715

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 Tyr Val Gly Phe Glu Val Leu Leu Val Ala Ser Tyr Val Leu Leu Thr
 1 5 10 15

ttg ggt gca tcg ccg gca cgt gta cgt tcc ggc gtg ggt tac gtg atg 96
 Leu Gly Ala Ser Pro Ala Arg Val Arg Ser Gly Val Gly Tyr Val Met
 20 25 30

gtg tcc atg gcg tca tcg atg gtg ttc ctg ttt gga ctc gca atg gtt 144
 Val Ser Met Ala Ser Ser Met Val Phe Leu Phe Gly Leu Ala Met Val
 35 40 45

tac gcc tca gtg ggc acg ttg aac atg gct cac gtt ggc cta cgc atg 192
 Tyr Ala Ser Val Gly Thr Leu Asn Met Ala His Val Gly Leu Arg Met
 50 55 60

gaa gat gtt ccg tct gga act cgc tcc gcg atc ttc gca gtg ttg ctc 240
 Glu Asp Val Pro Ser Gly Thr Arg Ser Ala Ile Phe Ala Val Leu Leu
 65 70 75 80

gtg gca ttc ggt att aaa gct gcc gtg ttc ccc cta gat tcc tgg ctg 288
 Val Ala Phe Gly Ile Lys Ala Ala Val Phe Pro Leu Asp Ser Trp Leu
 85 90 95

ccg gac tcc tac ccc acc gcg cca tcg ctg gtc acc gcg gtg ttc gca 336
 Pro Asp Ser Tyr Pro Thr Ala Pro Ser Leu Val Thr Ala Val Phe Ala
 100 105 110

ggt ctg ttg acc aag gtg ggt gtg tat tcc atc att cga gca cgc tcg 384
 Gly Leu Leu Thr Lys Val Gly Val Tyr Ser Ile Ile Arg Ala Arg Ser
 115 120 125

att att ttc acc gat gga tcc ctt gac acc atg ctg atg tgg gtg gca 432
 Ile Ile Phe Thr Asp Gly Ser Leu Asp Thr Met Leu Met Trp Val Ala
 130 135 140

ctc gcc acc atg ctc att ggt att ttg ggc gcg atg gcg caa aac gat 480
 Leu Ala Thr Met Leu Ile Gly Ile Leu Gly Ala Met Ala Gln Asn Asp

gcc aac cgc gat gac atc aac cac cgc gtc gac acc aac gga acg gag 1248
 Ala Asn Arg Asp Asp Ile Asn His Arg Val Asp Thr Asn Gly Thr Glu
 405 410 415

gac caa cca tgatcagtg attcaaacga cga 1280
 Asp Gln Pro

<210> 716

<211> 419

<212> PRT

<213> Corynebacterium glutamicum

<400> 716

Tyr Val Gly Phe Glu Val Leu Leu Val Ala Ser Tyr Val Leu Leu Thr
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 Leu Gly Ala Ser Pro Ala Arg Val Arg Ser Gly Val Gly Tyr Val Met
 20 25 30
 Val Ser Met Ala Ser Ser Met Val Phe Leu Phe Gly Leu Ala Met Val
 35 40 45
 Tyr Ala Ser Val Gly Thr Leu Asn Met Ala His Val Gly Leu Arg Met
 50 55 60
 Glu Asp Val Pro Ser Gly Thr Arg Ser Ala Ile Phe Ala Val Leu Leu
 65 70 75 80
 Val Ala Phe Gly Ile Lys Ala Ala Val Phe Pro Leu Asp Ser Trp Leu
 85 90 95
 Pro Asp Ser Tyr Pro Thr Ala Pro Ser Leu Val Thr Ala Val Phe Ala
 100 105 110
 Gly Leu Leu Thr Lys Val Gly Val Tyr Ser Ile Ile Arg Ala Arg Ser
 115 120 125
 Ile Ile Phe Thr Asp Gly Ser Leu Asp Thr Met Leu Met Trp Val Ala
 130 135 140
 Leu Ala Thr Met Leu Ile Gly Ile Leu Gly Ala Met Ala Gln Asn Asp
 145 150 155 160
 Ile Lys Arg Leu Leu Ser Phe Thr Leu Val Ser His Ile Gly Tyr Met
 165 170 175
 Ile Phe Gly Val Ala Leu Gly Ser Ala Gln Gly Leu Ser Gly Ala Ile
 180 185 190
 Phe Tyr Ala Ile His His Ile Leu Val Gln Thr Ser Leu Phe Leu Val
 195 200 205
 Val Gly Leu Val Glu Arg Gln Ala Gly Ser Ser Ser Leu Arg Arg Leu
 210 215 220
 Gly Ser Leu Ala Tyr Ile Ser Pro Leu Leu Ala Ile Leu Tyr Phe Ile
 225 230 235 240

Pro	Ala	Ile	Asn	Leu	Gly	Gly	Ile	Pro	Pro	Phe	Ser	Gly	Phe	Leu	Gly	245	250	255
Lys	Ile	Met	Leu	Ile	Glu	Ala	Gly	Ala	Glu	Asp	Gly	Ser	Trp	Leu	Ala	260	265	270
Trp	Val	Leu	Ile	Ala	Gly	Ala	Val	Val	Thr	Ser	Leu	Leu	Thr	Leu	Tyr	275	280	285
Thr	Met	Val	Leu	Val	Trp	Ser	Lys	Ala	Phe	Trp	Arg	Asp	Arg	Lys	Asp	290	295	300
Ala	Pro	Asp	Gly	Ala	Thr	Ala	Leu	Ala	Arg	Pro	Ala	Pro	Leu	Val	Asp	305	310	315
Val	Gln	Asp	Glu	Val	Ala	Val	Lys	Asp	Arg	Asn	Asp	Val	Gly	Arg	Met	325	330	335
Pro	Trp	Gly	Met	Val	Phe	Ser	Thr	Ala	Leu	Leu	Val	Ser	Ala	Ser	Leu	340	345	350
Ala	Val	Ser	Val	Leu	Ala	Gly	Pro	Leu	Ser	Ser	Ile	Thr	Gly	Arg	Ala	355	360	365
Ala	Glu	Ser	Ala	Gln	Asp	Val	Asn	Ile	Tyr	Arg	Ala	Ala	Val	Leu	Gly	370	375	380
Pro	Asn	Tyr	Leu	Asp	Pro	Ser	Arg	Thr	Leu	Glu	Met	Glu	Arg	Tyr	Asp	385	390	395
Ala	Asn	Arg	Asp	Asp	Ile	Asn	His	Arg	Val	Asp	Thr	Asn	Gly	Thr	Glu	405	410	415
Asp	Gln	Pro																

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<210> 717
<211> 1051
<212> DNA
<213> Corynebacterium glutamicum
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<222> (101)..(1051)  
<223> RXN01895
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cacaagcttt aagatccacg atcaggagac tttgacaaat atg tca gtt aac cca      115
                                     Met Ser Val Asn Pro
                                           1                               5

acc cgc ccc gaa ggc ggc cgt cac cac gtc gtc gtc atc ggt tct ggt      163
Thr Arg Pro Glu Gly Gly Arg His His Val Val Val Ile Gly Ser Gly
                        10                                15                    20

ttt ggt ggc ctt ttt gct gcc aag aac ctg gcc aag gca gac gtc gat      211
Phe Gly Gly Leu Phe Ala Ala Lys Asn Leu Ala Lys Ala Asp Val Asp
                      25                                30                    35
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gtc act ctg att gac cgc acc aac cac cac ctc ttc cag cca ctg ctg	259
Val Thr Leu Ile Asp Arg Thr Asn His His Leu Phe Gln Pro Leu Leu	
40 45 50	
tac caa gtg gca acc ggt atc ctc tcc tcc ggt gaa atc gca cct tcc	307
Tyr Gln Val Ala Thr Gly Ile Leu Ser Ser Gly Glu Ile Ala Pro Ser	
55 60 65	
act cga cag atc ctg ggc tcc cag gaa aac gtc aac gtc atc aag ggc	355
Thr Arg Gln Ile Leu Gly Ser Gln Glu Asn Val Asn Val Ile Lys Gly	
70 75 80 85	
gaa gtc acc gac atc aac gtc gag tcc cag act gtg acc gcc tcc ctg	403
Glu Val Thr Asp Ile Asn Val Glu Ser Gln Thr Val Thr Ala Ser Leu	
90 95 100	
ggc gag ttc acc cgc gtt ttt gag tac gat tcc ttg gtc gtt ggt gct	451
Gly Glu Phe Thr Arg Val Phe Glu Tyr Asp Ser Leu Val Val Gly Ala	
105 110 115	
ggc gca ggt cag tcc tac ttc ggc aat gat cac ttc gct gag ttc gca	499
Gly Ala Gly Gln Ser Tyr Phe Gly Asn Asp His Phe Ala Glu Phe Ala	
120 125 130	
cct ggc atg aag tcc atc gac gat gca ctg gag att cgt gca cgc atc	547
Pro Gly Met Lys Ser Ile Asp Ala Leu Glu Ile Arg Ala Arg Ile	
135 140 145	
atc ggt gct ttc gag cgc gct gag atc tgc gag gat cca gct gag cgc	595
Ile Gly Ala Phe Glu Arg Ala Glu Ile Cys Glu Asp Pro Ala Glu Arg	
150 155 160 165	
gaa cgc ctg ctc acc ttc gtc gtt gtt ggc gct ggc cca acc ggt gtt	643
Glu Arg Leu Leu Thr Phe Val Val Val Gly Ala Gly Pro Thr Gly Val	
170 175 180	
gag ctt gct ggc cag ttg gct gag atg gct cac cgc acc ctt gct ggt	691
Glu Leu Ala Gly Gln Leu Ala Glu Met Ala His Arg Thr Leu Ala Gly	
185 190 195	
gag tac aag aac ttc aac acc aac tcc gca aag atc atc ctg ctt gat	739
Glu Tyr Lys Asn Phe Asn Thr Asn Ser Ala Lys Ile Ile Leu Leu Asp	
200 205 210	
ggt gct cca cag gtt ctt cct cca ttc ggt aag cgc cta ggc cgc aac	787
Gly Ala Pro Gln Val Leu Pro Pro Phe Gly Lys Arg Leu Gly Arg Asn	
215 220 225	
gca cag cgc acc ctg gaa aag atg ggt gtc aac gtt cgc ctg aac gct	835
Ala Gln Arg Thr Leu Glu Lys Met Gly Val Asn Val Arg Leu Asn Ala	
230 235 240 245	
atg gtc acc aac gtt gac gct acc tcg gtc acc tac aag acc aag gac	883
Met Val Thr Asn Val Asp Ala Thr Ser Val Thr Tyr Lys Thr Lys Asp	
250 255 260	
ggc gaa gag cac acc atc gaa tct ttc tgc aag att tgg tcc gct ggt	931
Gly Glu Glu His Thr Ile Glu Ser Phe Cys Lys Ile Trp Ser Ala Gly	
265 270 275	

ggt gcg gca tcc cca ctg ggc aag ctc gtc gca gag cag acc ggt gtt 979
 Val Ala Ala Ser Pro Leu Gly Lys Leu Val Ala Glu Gln Thr Gly Val
 280 285 290

gag acc gac cgc gca ggc cgc gtc atg gtt aac gat gac ctg tct gtt 1027
 Glu Thr Asp Arg Ala Gly Arg Val Met Val Asn Asp Asp Leu Ser Val
 295 300 305

ggc gat cag aag aac gtc ttc gtt 1051
 Gly Asp Gln Lys Asn Val Phe Val
 310 315

<210> 718
 <211> 317
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 718
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Val Ile Gly Ser Gly Phe Gly Gly Leu Phe Ala Ala Lys Asn Leu Ala
 20 25 30

Lys Ala Asp Val Asp Val Thr Leu Ile Asp Arg Thr Asn His His Leu
 35 40 45

Phe Gln Pro Leu Leu Tyr Gln Val Ala Thr Gly Ile Leu Ser Ser Gly
 50 55 60

Glu Ile Ala Pro Ser Thr Arg Gln Ile Leu Gly Ser Gln Glu Asn Val
 65 70 75 80

Asn Val Ile Lys Gly Glu Val Thr Asp Ile Asn Val Glu Ser Gln Thr
 85 90 95

Val Thr Ala Ser Leu Gly Glu Phe Thr Arg Val Phe Glu Tyr Asp Ser
 100 105 110

Leu Val Val Gly Ala Gly Ala Gly Gln Ser Tyr Phe Gly Asn Asp His
 115 120 125

Phe Ala Glu Phe Ala Pro Gly Met Lys Ser Ile Asp Asp Ala Leu Glu
 130 135 140

Ile Arg Ala Arg Ile Ile Gly Ala Phe Glu Arg Ala Glu Ile Cys Glu
 145 150 155 160

Asp Pro Ala Glu Arg Glu Arg Leu Leu Thr Phe Val Val Val Gly Ala
 165 170 175

Gly Pro Thr Gly Val Glu Leu Ala Gly Gln Leu Ala Glu Met Ala His
 180 185 190

Arg Thr Leu Ala Gly Glu Tyr Lys Asn Phe Asn Thr Asn Ser Ala Lys
 195 200 205

Ile Ile Leu Leu Asp Gly Ala Pro Gln Val Leu Pro Pro Phe Gly Lys
 210 215 220

Arg Leu Gly Arg Asn Ala Gln Arg Thr Leu Glu Lys Met Gly Val Asn
 225 230 235 240

Val Arg Leu Asn Ala Met Val Thr Asn Val Asp Ala Thr Ser Val Thr
 245 250 255

Tyr Lys Thr Lys Asp Gly Glu Glu His Thr Ile Glu Ser Phe Cys Lys
 260 265 270

Ile Trp Ser Ala Gly Val Ala Ala Ser Pro Leu Gly Lys Leu Val Ala
 275 280 285

Glu Gln Thr Gly Val Glu Thr Asp Arg Ala Gly Arg Val Met Val Asn
 290 295 300

Asp Asp Leu Ser Val Gly Asp Gln Lys Asn Val Phe Val
 305 310 315

<210> 719
 <211> 816
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (1)..(816)
 <223> FRXA01895

<400> 719
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 His His Leu Phe Gln Pro Leu Leu Tyr Gln Val Ala Thr Gly Ile Leu
 1 5 10 15

tcc tcc ggt gaa atc gca cct tcc act cga cag atc ctg ggc tcc cag 96
 Ser Ser Gly Glu Ile Ala Pro Ser Thr Arg Gln Ile Leu Gly Ser Gln
 20 25 30

gaa aac gtc aac gtc atc aag ggc gaa gtc acc gac atc aac gtc gag 144
 Glu Asn Val Asn Val Ile Lys Gly Glu Val Thr Asp Ile Asn Val Glu
 35 40 45

tcc cag act gtg acc gcc tcc ctg ggc gag ttc acc cgc gtt ttt gag 192
 Ser Gln Thr Val Thr Ala Ser Leu Gly Glu Phe Thr Arg Val Phe Glu
 50 55 60

tac gat tcc ttg gtc gtt ggt gct ggc gca ggt cag tcc tac ttc ggc 240
 Tyr Asp Ser Leu Val Val Gly Ala Gly Ala Gly Gln Ser Tyr Phe Gly
 65 70 75 80

aat gat cac ttc gct gag ttc gca cct ggc atg aag tcc atc gac gat 288
 Asn Asp His Phe Ala Glu Phe Ala Pro Gly Met Lys Ser Ile Asp Asp
 85 90 95

gca ctg gag att cgt gca cgc atc atc ggt gct ttc gag cgc gct gag 336
 Ala Leu Glu Ile Arg Ala Arg Ile Ile Gly Ala Phe Glu Arg Ala Glu
 100 105 110

atc tgc gag gat cca gct gag cgc gaa cgc ctg ctc acc ttc gtc gtt 384
 Ile Cys Glu Asp Pro Ala Glu Arg Glu Arg Leu Leu Thr Phe Val Val
 115 120 125

gtt ggc gct ggc cca acc ggt gtt gag ctt gct ggc cag ttg gct gag 432
 Val Gly Ala Gly Pro Thr Gly Val Glu Leu Ala Gly Gln Leu Ala Glu
 130 135 140

atg gct cac cgc acc ctt gct ggt gag tac aag aac ttc aac acc aac 480
 Met Ala His Arg Thr Leu Ala Gly Glu Tyr Lys Asn Phe Asn Thr Asn
 145 150 155 160

tcc gca aag atc atc ctg ctt gat ggt gct cca cag gtt ctt cct cca 528
 Ser Ala Lys Ile Ile Leu Leu Asp Gly Ala Pro Gln Val Leu Pro Pro
 165 170 175

ttc ggt aag cgc cta ggc cgc aac gca cag cgc acc ctg gaa aag atg 576
 Phe Gly Lys Arg Leu Gly Arg Asn Ala Gln Arg Thr Leu Glu Lys Met
 180 185 190

ggt gtc aac gtt cgc ctg aac gct atg gtc acc aac gtt gac gct acc 624
 Gly Val Asn Val Arg Leu Asn Ala Met Val Thr Asn Val Asp Ala Thr
 195 200 205

tcg gtc acc tac aag acc aag gac ggc gaa gag cac acc atc gaa tct 672
 Ser Val Thr Tyr Lys Thr Lys Asp Gly Glu Glu His Thr Ile Glu Ser
 210 215 220

ttc tgc aag att tgg tcc gct ggt gtt gcg gca tcc cca ctg ggc aag 720
 Phe Cys Lys Ile Trp Ser Ala Gly Val Ala Ala Ser Pro Leu Gly Lys
 225 230 235 240

ctc gtc gca gag cag acc ggt gtt gag acc gac cgc gca ggc cgc gtc 768
 Leu Val Ala Glu Gln Thr Gly Val Glu Thr Asp Arg Ala Gly Arg Val
 245 250 255

atg gtt aac gat gac ctg tct gtt ggc gat cag aag aac gtc ttc gtt 816
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 260 265 270

<210> 720

<211> 272

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 720

His His Leu Phe Gln Pro Leu Leu Tyr Gln Val Ala Thr Gly Ile Leu
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Ser Ser Gly Glu Ile Ala Pro Ser Thr Arg Gln Ile Leu Gly Ser Gln
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Glu Asn Val Asn Val Ile Lys Gly Glu Val Thr Asp Ile Asn Val Glu
 35 40 45

Ser Gln Thr Val Thr Ala Ser Leu Gly Glu Phe Thr Arg Val Phe Glu
 50 55 60

Tyr Asp Ser Leu Val Val Gly Ala Gly Ala Gly Gln Ser Tyr Phe Gly
 65 70 75 80

Asn Asp His Phe Ala Glu Phe Ala Pro Gly Met Lys Ser Ile Asp Asp
 85 90 95

Ala Leu Glu Ile Arg Ala Arg Ile Ile Gly Ala Phe Glu Arg Ala Glu
 100 105 110

Ile Cys Glu Asp Pro Ala Glu Arg Glu Arg Leu Leu Thr Phe Val Val
 115 120 125

Val Gly Ala Gly Pro Thr Gly Val Glu Leu Ala Gly Gln Leu Ala Glu
 130 135 140

Met Ala His Arg Thr Leu Ala Gly Glu Tyr Lys Asn Phe Asn Thr Asn
 145 150 155 160

Ser Ala Lys Ile Ile Leu Leu Asp Gly Ala Pro Gln Val Leu Pro Pro
 165 170 175

Phe Gly Lys Arg Leu Gly Arg Asn Ala Gln Arg Thr Leu Glu Lys Met
 180 185 190

Gly Val Asn Val Arg Leu Asn Ala Met Val Thr Asn Val Asp Ala Thr
 195 200 205

Ser Val Thr Tyr Lys Thr Lys Asp Gly Glu Glu His Thr Ile Glu Ser
 210 215 220

Phe Cys Lys Ile Trp Ser Ala Gly Val Ala Ala Ser Pro Leu Gly Lys
 225 230 235 240

Leu Val Ala Glu Gln Thr Gly Val Glu Thr Asp Arg Ala Gly Arg Val
 245 250 255

Met Val Asn Asp Asp Leu Ser Val Gly Asp Gln Lys Asn Val Phe Val
 260 265 270

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 <213> Corynebacterium glutamicum

<220>
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 <222> (101)..(2386)
 <223> RXA00703

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 Met Thr Thr Pro Pro
 1 5

act gag att tcg aac gtg aat ccc acc gcg aat gaa ttt gat gat ccg 163
 Thr Glu Ile Ser Asn Val Asn Pro Thr Ala Asn Glu Phe Asp Asp Pro
 10 15 20

gat gtg gga cgg cgc att act tct gct gct ggt gtg cca ggc gtt ttg 211
 Asp Val Gly Arg Arg Ile Thr Ser Ala Ala Gly Val Pro Gly Val Leu

25	30	35	
cat gcg ctc cag cat gct gtt ccg aat cgt gcc ctg ctg ccg ttg ctc			259
His Ala Leu Gln His Ala Val Pro Asn Arg Ala Leu Leu Pro Leu Leu			
40	45	50	
acc atg aat aaa cca ggc ggc atc gac tgt cct ggt tgt gct tgg cct			307
Thr Met Asn Lys Pro Gly Gly Ile Asp Cys Pro Gly Cys Ala Trp Pro			
55	60	65	
gag cct tcc act gcc aac ctt ggt gtg gtt gag ttc tgc gag aac ggt			355
Glu Pro Ser Thr Ala Asn Leu Gly Val Val Glu Phe Cys Glu Asn Gly			
70	75	80	85
gcc aag gcg gtc gcc gag gaa aca aca cct gat cgt gcc ggc aaa gag			403
Ala Lys Ala Val Ala Glu Glu Thr Thr Pro Asp Arg Ala Gly Lys Glu			
90	95	100	
ttc tgg gca gag cat tct att tat gat ctg cgg gaa aag acc gat cac			451
Phe Trp Ala Glu His Ser Ile Tyr Asp Leu Arg Glu Lys Thr Asp His			
105	110	115	
tgg ctg gga aag cgt ggc cga atc acc gag ccc atg ttt tat gat cgt			499
Trp Leu Gly Lys Arg Gly Arg Ile Thr Glu Pro Met Phe Tyr Asp Arg			
120	125	130	
tct tct ggc gat gat cac tac cgc cct att tct tgg gat cgt gca ttt			547
Ser Ser Gly Asp Asp His Tyr Arg Pro Ile Ser Trp Asp Arg Ala Phe			
135	140	145	
gcg atc att gcg tcg aag ctc cgc gag atc gag cca gat gaa gcg gtg			595
Ala Ile Ile Ala Ser Lys Leu Arg Glu Ile Glu Pro Asp Glu Ala Val			
150	155	160	165
ttt tac acc tct ggt cga gca ccc aat gag ccg gct tat atg ctg cag			643
Phe Tyr Thr Ser Gly Arg Ala Pro Asn Glu Pro Ala Tyr Met Leu Gln			
170	175	180	
ctt cta gcc cgc cga ctt ggc aca aat aat ctt cca gac tgt gga aac			691
Leu Leu Ala Arg Arg Leu Gly Thr Asn Asn Leu Pro Asp Cys Gly Asn			
185	190	195	
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Met Cys His Glu Ser Thr Gly Thr Ala Leu Gly Glu Thr Leu Gly Leu			
200	205	210	
ggc aag gga tcc gtg gtg atg gag gat ttc tac aac act gat ttg ttg			787
Gly Lys Gly Ser Val Val Met Glu Asp Phe Tyr Asn Thr Asp Leu Leu			
215	220	225	
att tcc gtg gga caa aac ccg ggc acc aac cac cca cgt gcg ttg acg			835
Ile Ser Val Gly Gln Asn Pro Gly Thr Asn His Pro Arg Ala Leu Thr			
230	235	240	245
gct ttc aaa gaa ttg aag gaa aac ggt ggc aag att ctg gcg ctg aac			883
Ala Phe Lys Glu Leu Lys Glu Asn Gly Gly Lys Ile Leu Ala Leu Asn			
250	255	260	
ccc atg cca gag acc ggt ctg atg aaa ttc cgt gag ccc caa tca gtc			931
Pro Met Pro Glu Thr Gly Leu Met Lys Phe Arg Glu Pro Gln Ser Val			
265	270	275	

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atc cgt ctt gat gga gac cgc gca ttc ttc cag gcg ctc aac aag gaa Ile Arg Leu Asp Gly Asp Arg Ala Phe Phe Gln Ala Leu Asn Lys Glu 295 300 305	1027
ctc atc cgt aga gat gcc cta gat cat gca ttc ttg gat aaa ttc tgt Leu Ile Arg Arg Asp Ala Leu Asp His Ala Phe Leu Asp Lys Phe Cys 310 315 320 325	1075
tca ggt gtg gat gaa acc atc gag cac ctc aaa tca ctc gat gat gag Ser Gly Val Asp Glu Thr Ile Glu His Leu Lys Ser Leu Asp Asp Glu 330 335 340	1123
gtt ctg ctc aag gga tgc ggt ctg acg gca gcg gag atc aac aag gcc Val Leu Leu Lys Gly Cys Gly Leu Thr Ala Ala Glu Ile Asn Lys Ala 345 350 355	1171
gct gac atg gtg gaa aag tct gac acc gtg gtg gtg tca tgg act ctc Ala Asp Met Val Glu Lys Ser Asp Thr Val Val Val Ser Trp Thr Leu 360 365 370	1219
ggg gtc acc cag cat aag aac gct gtg tac acc atc cgt gaa atg gtg Gly Val Thr Gln His Lys Asn Ala Val Tyr Thr Ile Arg Glu Met Val 375 380 385	1267
aac ttc ctg ctg ctt act gga aat att ggt aag cct ggc gca ggc act Asn Phe Leu Leu Leu Thr Gly Asn Ile Gly Lys Pro Gly Ala Gly Thr 390 395 400 405	1315
gcc ccg ctt cgt ggg cac tca aac gtc cag ggt gat cga acc atg ggt Ala Pro Leu Arg Gly His Ser Asn Val Gln Gly Asp Arg Thr Met Gly 410 415 420	1363
att tgg gag aaa atg ccg gag gca ttc ctt gct gct ctt gaa aac gag Ile Trp Glu Lys Met Pro Glu Ala Phe Leu Ala Ala Leu Glu Asn Glu 425 430 435	1411
ttt ggt ttc gat gtg ccc cgc aag cac ggc ttc gac acg gta aat tcc Phe Gly Phe Asp Val Pro Arg Lys His Gly Phe Asp Thr Val Asn Ser 440 445 450	1459
ctg cga gcc atg cgc gaa ggc aag acc aag ttc ttt ctc tcc ctc ggt Leu Arg Ala Met Arg Glu Gly Lys Thr Lys Phe Phe Leu Ser Leu Gly 455 460 465	1507
ggc aac ctt gtt cga gtg tcc tca gat acg tct gtt gtc gaa aag ggc Gly Asn Leu Val Arg Val Ser Ser Asp Thr Ser Val Val Glu Lys Gly 470 475 480 485	1555
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cga aca gat aag gat gtc caa aag tca ggc gtc cag cgt gtg aca gtt	1699
Arg Thr Asp Lys Asp Val Gln Lys Ser Gly Val Gln Arg Val Thr Val	
520 525 530	
gag gat tct gcc ggc gct gtt cac gca tcc act ggt aaa cga acc gcc	1747
Glu Asp Ser Ala Gly Ala Val His Ala Ser Thr Gly Lys Arg Thr Ala	
535 540 545	
aac aag gat ctg aat ttg aag tcc gaa tgc gac atc att gga acc atc	1795
Asn Lys Asp Leu Asn Leu Lys Ser Glu Cys Asp Ile Ile Gly Thr Ile	
550 555 560 565	
ggt aag cag acc ttc ggt gat gcc ttc tgg cag ccg atg att gat aac	1843
Gly Lys Gln Thr Phe Gly Asp Ala Phe Trp Gln Pro Met Ile Asp Asn	
570 575 580	
tac gat gtg gtc cgc gat cac atc gag gcc acc att cct ggg ttc cac	1891
Tyr Asp Val Val Arg Asp His Ile Glu Ala Thr Ile Pro Gly Phe His	
585 590 595	
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Asp Phe Asn Arg Arg Ile Asp Asn Pro Gly Gly Phe Leu Leu Pro Asn	
600 605 610	
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Gly Pro Arg Glu Arg Ile Phe Asn Thr Ser Asn Gly Lys Ala Gln Leu	
615 620 625	
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Thr Val Asn Glu Thr Asn Val Ile Glu Leu Pro Lys Asp Tyr Leu Leu	
630 635 640 645	
atg aac acg gta cgt tca cat gat caa tac aac tcc acg att tac ggt	2083
Met Asn Thr Val Arg Ser His Asp Gln Tyr Asn Ser Thr Ile Tyr Gly	
650 655 660	
ctg gat gac cgc tac cgc ggt gtt cgc aat ggt cgc cgc gta gtg ttc	2131
Leu Asp Asp Arg Tyr Arg Gly Val Arg Asn Gly Arg Arg Val Val Phe	
665 670 675	
gtc aat cct caa gat tgt aag caa cgt ggt ctc aag gat gga gac atc	2179
Val Asn Pro Gln Asp Cys Lys Gln Arg Gly Leu Lys Asp Gly Asp Ile	
680 685 690	
gtc gat atc gtc tct gtc ttt gat gat ggc gaa cgc cga gca ccg aat	2227
Val Asp Ile Val Ser Val Phe Asp Asp Gly Glu Arg Arg Ala Pro Asn	
695 700 705	
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Phe Arg Val Val Glu Tyr Asp Thr Ala Arg Asp Cys Val Thr Thr Tyr	
710 715 720 725	
ttc cct gag gcc aac gta ttg gtt cca ttg gat tca gta gct gaa aaa	2323
Phe Pro Glu Ala Asn Val Leu Val Pro Leu Asp Ser Val Ala Glu Lys	
730 735 740	
tcc aac act cca gtg tcc aag tca gtt gtg gtt cgc ctt gaa gca aca	2371
Ser Asn Thr Pro Val Ser Lys Ser Val Val Val Arg Leu Glu Ala Thr	
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Gly Arg Thr Ala Ser
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<210> 722

<211> 762

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 722

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			20					25					30		
Val	Pro	Gly	Val	Leu	His	Ala	Leu	Gln	His	Ala	Val	Pro	Asn	Arg	Ala
			35				40					45			
Leu	Leu	Pro	Leu	Leu	Thr	Met	Asn	Lys	Pro	Gly	Gly	Ile	Asp	Cys	Pro
	50					55					60				
Gly	Cys	Ala	Trp	Pro	Glu	Pro	Ser	Thr	Ala	Asn	Leu	Gly	Val	Val	Glu
65					70					75					80
Phe	Cys	Glu	Asn	Gly	Ala	Lys	Ala	Val	Ala	Glu	Glu	Thr	Thr	Pro	Asp
				85					90					95	
Arg	Ala	Gly	Lys	Glu	Phe	Trp	Ala	Glu	His	Ser	Ile	Tyr	Asp	Leu	Arg
			100					105					110		
Glu	Lys	Thr	Asp	His	Trp	Leu	Gly	Lys	Arg	Gly	Arg	Ile	Thr	Glu	Pro
		115					120					125			
Met	Phe	Tyr	Asp	Arg	Ser	Ser	Gly	Asp	Asp	His	Tyr	Arg	Pro	Ile	Ser
	130					135					140				
Trp	Asp	Arg	Ala	Phe	Ala	Ile	Ile	Ala	Ser	Lys	Leu	Arg	Glu	Ile	Glu
145					150					155					160
Pro	Asp	Glu	Ala	Val	Phe	Tyr	Thr	Ser	Gly	Arg	Ala	Pro	Asn	Glu	Pro
				165					170					175	
Ala	Tyr	Met	Leu	Gln	Leu	Leu	Ala	Arg	Arg	Leu	Gly	Thr	Asn	Asn	Leu
			180					185					190		
Pro	Asp	Cys	Gly	Asn	Met	Cys	His	Glu	Ser	Thr	Gly	Thr	Ala	Leu	Gly
		195					200					205			
Glu	Thr	Leu	Gly	Leu	Gly	Lys	Gly	Ser	Val	Val	Met	Glu	Asp	Phe	Tyr
	210					215					220				
Asn	Thr	Asp	Leu	Leu	Ile	Ser	Val	Gly	Gln	Asn	Pro	Gly	Thr	Asn	His
225					230					235					240
Pro	Arg	Ala	Leu	Thr	Ala	Phe	Lys	Glu	Leu	Lys	Glu	Asn	Gly	Gly	Lys
				245					250					255	
Ile	Leu	Ala	Leu	Asn	Pro	Met	Pro	Glu	Thr	Gly	Leu	Met	Lys	Phe	Arg
			260					265					270		

Glu Pro Gln Ser Val Lys Gly Ala Leu Ser Ile Ser Asp Lys Leu Ala
 275 280 285
 Asp Glu Tyr Leu Gln Ile Arg Leu Asp Gly Asp Arg Ala Phe Phe Gln
 290 295 300
 Ala Leu Asn Lys Glu Leu Ile Arg Arg Asp Ala Leu Asp His Ala Phe
 305 310 315 320
 Leu Asp Lys Phe Cys Ser Gly Val Asp Glu Thr Ile Glu His Leu Lys
 325 330 335
 Ser Leu Asp Asp Glu Val Leu Leu Lys Gly Cys Gly Leu Thr Ala Ala
 340 345 350
 Glu Ile Asn Lys Ala Ala Asp Met Val Glu Lys Ser Asp Thr Val Val
 355 360 365
 Val Ser Trp Thr Leu Gly Val Thr Gln His Lys Asn Ala Val Tyr Thr
 370 375 380
 Ile Arg Glu Met Val Asn Phe Leu Leu Leu Thr Gly Asn Ile Gly Lys
 385 390 395 400
 Pro Gly Ala Gly Thr Ala Pro Leu Arg Gly His Ser Asn Val Gln Gly
 405 410 415
 Asp Arg Thr Met Gly Ile Trp Glu Lys Met Pro Glu Ala Phe Leu Ala
 420 425 430
 Ala Leu Glu Asn Glu Phe Gly Phe Asp Val Pro Arg Lys His Gly Phe
 435 440 445
 Asp Thr Val Asn Ser Leu Arg Ala Met Arg Glu Gly Lys Thr Lys Phe
 450 455 460
 Phe Leu Ser Leu Gly Gly Asn Leu Val Arg Val Ser Ser Asp Thr Ser
 465 470 475 480
 Val Val Glu Lys Gly Met Glu Ser Asn Glu Leu Thr Val His Leu Ser
 485 490 495
 Thr Lys Pro Asn Gly Ser Gln Ala Trp Pro Gly Glu Gln Ser Leu Ile
 500 505 510
 Leu Pro Val Ile Ala Arg Thr Asp Lys Asp Val Gln Lys Ser Gly Val
 515 520 525
 Gln Arg Val Thr Val Glu Asp Ser Ala Gly Ala Val His Ala Ser Thr
 530 535 540
 Gly Lys Arg Thr Ala Asn Lys Asp Leu Asn Leu Lys Ser Glu Cys Asp
 545 550 555 560
 Ile Ile Gly Thr Ile Gly Lys Gln Thr Phe Gly Asp Ala Phe Trp Gln
 565 570 575
 Pro Met Ile Asp Asn Tyr Asp Val Val Arg Asp His Ile Glu Ala Thr
 580 585 590
 Ile Pro Gly Phe His Asp Phe Asn Arg Arg Ile Asp Asn Pro Gly Gly

1032

gat att gag ttg gtg cat ggc ctc ctc ttg tca gaa ggt ctg atc acg Asp Ile Glu Leu Val His Gly Leu Leu Leu Ser Glu Gly Leu Ile Thr 55 60 65	307
gat gct tct gag gtt ttt acc gcc cgc tat tgt gca gga gct gtt ggc Asp Ala Ser Glu Val Phe Thr Ala Arg Tyr Cys Ala Gly Ala Val Gly 70 75 80 85	355
cca gat aat caa aat acg tac aac gtc tta gaa ctt gat gtc atc ccc Pro Asp Asn Gln Asn Thr Tyr Asn Val Leu Glu Leu Asp Val Ile Pro 90 95 100	403
aaa gac aat ccg gcc cgg gat ccc gtc cag aat ccc tcc cat aat ccc Lys Asp Asn Pro Ala Arg Asp Pro Val Gln Asn Pro Ser His Asn Pro 105 110 115	451
gaa ggc agc caa cac gaa gca ctc cac atc cca act ttc caa ccg gta Glu Gly Ser Gln His Glu Ala Leu His Ile Pro Thr Phe Gln Pro Val 120 125 130	499
cgc gaa cta aac ctc gtg gca gcc caa cgc aat gtg ctg act acg tct Arg Glu Leu Asn Leu Val Ala Ala Gln Arg Asn Val Leu Thr Thr Ser 135 140 145	547
gct tgt ggt gtt tgt ggc acg acg tct att gag cag ttg atg aac aag Ala Cys Gly Val Cys Gly Thr Thr Ser Ile Glu Gln Leu Met Asn Lys 150 155 160 165	595
aag ggc tgg ccc att acg ccg att aca ccg gat cct cgg atg att gtg Lys Gly Trp Pro Ile Thr Pro Ile Thr Pro Asp Pro Arg Met Ile Val 170 175 180	643
tcg ttg cca gat aag ttg aag tcg aag cag aag att ttc gac aaa act Ser Leu Pro Asp Lys Leu Lys Ser Lys Gln Lys Ile Phe Asp Lys Thr 185 190 195	691
ggt ggg gtt cat gct gct ggt ttg gcc acg ctt gat ggt gag atg ttg Gly Gly Val His Ala Ala Gly Leu Ala Thr Leu Asp Gly Glu Met Leu 200 205 210	739
att att cga gag gat gtc ggt cgg cat aac gca gct gac aaa gtt ata Ile Ile Arg Glu Asp Val Gly Arg His Asn Ala Ala Asp Lys Val Ile 215 220 225	787
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gct gga att tcg ggt gta atc gct gtt ggt gct gca aca tcg ctg gca Ala Gly Ile Ser Gly Val Ile Ala Val Gly Ala Ala Thr Ser Leu Ala 265 270 275	931
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acaggtagaa cag 1038

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 <213> Corynebacterium glutamicum

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 20 25 30
 Glu Pro Leu Glu Ile Arg Val Asn Gly Thr Ala Leu Thr Thr Thr Met
 35 40 45
 Arg Thr Pro Gly His Asp Ile Glu Leu Val His Gly Leu Leu Leu Ser
 50 55 60
 Glu Gly Leu Ile Thr Asp Ala Ser Glu Val Phe Thr Ala Arg Tyr Cys
 65 70 75 80
 Ala Gly Ala Val Gly Pro Asp Asn Gln Asn Thr Tyr Asn Val Leu Glu
 85 90 95
 Leu Asp Val Ile Pro Lys Asp Asn Pro Ala Arg Asp Pro Val Gln Asn
 100 105 110
 Pro Ser His Asn Pro Glu Gly Ser Gln His Glu Ala Leu His Ile Pro
 115 120 125
 Thr Phe Gln Pro Val Arg Glu Leu Asn Leu Val Ala Ala Gln Arg Asn
 130 135 140
 Val Leu Thr Thr Ser Ala Cys Gly Val Cys Gly Thr Thr Ser Ile Glu
 145 150 155 160
 Gln Leu Met Asn Lys Lys Gly Trp Pro Ile Thr Pro Ile Thr Pro Asp
 165 170 175
 Pro Arg Met Ile Val Ser Leu Pro Asp Lys Leu Lys Ser Lys Gln Lys
 180 185 190
 Ile Phe Asp Lys Thr Gly Gly Val His Ala Ala Gly Leu Ala Thr Leu
 195 200 205
 Asp Gly Glu Met Leu Ile Ile Arg Glu Asp Val Gly Arg His Asn Ala
 210 215 220
 Ala Asp Lys Val Ile Gly Asn Met Leu Met Ala Gly Lys Leu Pro Leu
 225 230 235 240
 Glu Asn Thr Ile Leu Val Met Ser Ser Arg Ala Ser Phe Glu Leu Val
 245 250 255

Gln Lys Ala Ala Met Ala Gly Ile Ser Gly Val Ile Ala Val Gly Ala
 260 265 270

Ala Thr Ser Leu Ala Ile Glu Ala Ala Gln Asp Ser Gly Ile Phe Leu
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Ala Gly Phe Val Arg Gly Asn Lys Phe Asn His Tyr Ala Gly Glu Leu
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Gly
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 <222> (1)..(885)
 <223> FRXA00705

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gat act gtt gcg gtg gag gag cct cta gaa att cgg gtt aat ggc act 96
 Asp Thr Val Ala Val Glu Glu Pro Leu Glu Ile Arg Val Asn Gly Thr
 20 25 30

gcg ctt acc acc act atg cgc acg ccc ggc cat gat att gag ttg gtg 144
 Ala Leu Thr Thr Thr Met Arg Thr Pro Gly His Asp Ile Glu Leu Val
 35 40 45

cat ggc ctc ctc ttg tca gaa ggt ctg atc acg gat gct tct gag gtt 192
 His Gly Leu Leu Leu Ser Glu Gly Leu Ile Thr Asp Ala Ser Glu Val
 50 55 60

ttt acc gcc cgc tat tgt gca gga gct gtt ggc cca gat aat caa aat 240
 Phe Thr Ala Arg Tyr Cys Ala Gly Ala Val Gly Pro Asp Asn Gln Asn
 65 70 75 80

acg tac aac gtc tta gaa ctt gat gtc atc ccc aaa gac aat ccg gcc 288
 Thr Tyr Asn Val Leu Glu Leu Asp Val Ile Pro Lys Asp Asn Pro Ala
 85 90 95

cgg gat ccc gtc cag aat ccc tcc cat aat ccc gaa ggc agc caa cac 336
 Arg Asp Pro Val Gln Asn Pro Ser His Asn Pro Glu Gly Ser Gln His
 100 105 110

gaa gca ctc cac atc cca act ttc caa ccg gta cgc gaa cta aac ctc 384
 Glu Ala Leu His Ile Pro Thr Phe Gln Pro Val Arg Glu Leu Asn Leu
 115 120 125

gtg gca gcc caa cgc aat gtg ctg act acg tct gct tgt ggt gtt tgt 432
 Val Ala Ala Gln Arg Asn Val Leu Thr Thr Ser Ala Cys Gly Val Cys
 130 135 140

ggc acg acg tct att gag cag ttg atg aac aag aag ggc tgg ccc att 480

Gly Thr Thr Ser Ile Glu Gln Leu Met Asn Lys Lys Gly Trp Pro Ile
 145 150 155 160
 acg ccg att aca ccg gat cct cgg atg att gtg tcg ttg cca gat aag 528
 Thr Pro Ile Thr Pro Asp Pro Arg Met Ile Val Ser Leu Pro Asp Lys
 165 170 175
 ttg aag tcg aag cag aag att ttc gac aaa act ggt ggg gtt cat gct 576
 Leu Lys Ser Lys Gln Lys Ile Phe Asp Lys Thr Gly Gly Val His Ala
 180 185 190
 gct ggt ttg gcc acg ctt gat ggt gag atg ttg att att cga gag gat 624
 Ala Gly Leu Ala Thr Leu Asp Gly Glu Met Leu Ile Ile Arg Glu Asp
 195 200 205
 gtc ggt ccg cat aac gca gct gac aaa gtt ata gga aac atg ctg atg 672
 Val Gly Arg His Asn Ala Ala Asp Lys Val Ile Gly Asn Met Leu Met
 210 215 220
 gcg gga aag ctc ccc ttg gaa aac act att ttg gtg atg agt tct agg 720
 Ala Gly Lys Leu Pro Leu Glu Asn Thr Ile Leu Val Met Ser Ser Arg
 225 230 235 240
 gcg tct ttt gag ctt gtc caa aag gct gcc atg gct gga att tcg ggt 768
 Ala Ser Phe Glu Leu Val Gln Lys Ala Ala Met Ala Gly Ile Ser Gly
 245 250 255
 gta atc gct gtt ggt gct gca aca tcg ctg gca atc gag gcg gcg cag 816
 Val Ile Ala Val Gly Ala Ala Thr Ser Leu Ala Ile Glu Ala Ala Gln
 260 265 270
 gat tca ggt att ttc ctt gct ggt ttt gtt cgg ggc aac aag ttt aac 864
 Asp Ser Gly Ile Phe Leu Ala Gly Phe Val Arg Gly Asn Lys Phe Asn
 275 280 285
 cac tat gcg ggc gag ctc gga taatgccaga acaggtagaa cag 908
 His Tyr Ala Gly Glu Leu Gly
 290 295

<210> 726

<211> 295

<212> PRT

<213> Corynebacterium glutamicum

<400> 726

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 20 25 30
 Ala Leu Thr Thr Thr Met Arg Thr Pro Gly His Asp Ile Glu Leu Val
 35 40 45
 His Gly Leu Leu Leu Ser Glu Gly Leu Ile Thr Asp Ala Ser Glu Val
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 Phe Thr Ala Arg Tyr Cys Ala Gly Ala Val Gly Pro Asp Asn Gln Asn
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<400> 727
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                                         Met Leu Pro Val Asn
                                         1             5
caa acg tat gcg cag ttc tca gac act gcc ttc gta tcg gca tac atc 163

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Gln	Thr	Tyr	Ala	Gln	Phe	Ser	Asp	Thr	Ala	Phe	Val	Ser	Ala	Tyr	Ile	
				10					15					20		
atc	tac	gtt	ctg	gca	ctc	atc	ctc	tcc	ctc	gtc	tac	tac	gta	aaa	caa	211
Ile	Tyr	Val	Leu	Ala	Leu	Ile	Leu	Ser	Leu	Val	Tyr	Tyr	Val	Lys	Gln	
			25					30					35			
caa	ggc	att	atc	gac	gcc	cgc	cgc	gag	caa	acc	cgc	gtc	agc	gaa	ctc	259
Gln	Gly	Ile	Ile	Asp	Ala	Arg	Arg	Glu	Gln	Thr	Arg	Val	Ser	Glu	Leu	
		40					45					50				
gtt	ggt	gca	ggc	ggc	agc	gct	gat	gtt	gat	act	gac	ctg	cct	gat	gac	307
Val	Gly	Ala	Gly	Gly	Ser	Ala	Asp	Val	Asp	Thr	Asp	Leu	Pro	Asp	Asp	
	55					60					65					
atc	gcc	gac	ggt	gtc	ctc	gcc	gac	gaa	gac	ctt	gca	aaa	cgc	gaa	gaa	355
Ile	Ala	Asp	Gly	Val	Leu	Ala	Asp	Glu	Asp	Leu	Ala	Lys	Arg	Glu	Glu	
	70				75					80					85	
acc	gca	cgc	aaa	cta	gcc	aac	atg	acc	caa	tct	ctc	atg	tgg	ctc	ggc	403
Thr	Ala	Arg	Lys	Leu	Ala	Asn	Met	Thr	Gln	Ser	Leu	Met	Trp	Leu	Gly	
				90					95					100		
gtc	atg	gtg	cac	ctc	gta	tcc	gtc	gtg	atg	cgc	gcg	ctg	tct	gcc	agc	451
Val	Met	Val	His	Leu	Val	Ser	Val	Val	Met	Arg	Ala	Leu	Ser	Ala	Ser	
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cga	ttc	ccc	ttc	ggc	aac	ctg	tat	gaa	tac	atc	ctc	atg	gtc	acc	ctc	499
Arg	Phe	Pro	Phe	Gly	Asn	Leu	Tyr	Glu	Tyr	Ile	Leu	Met	Val	Thr	Leu	
		120					125					130				
ttc	gcc	atg	atc	gga	gcc	gta	ctc	atc	ctg	cag	cgc	cca	caa	ttc	cgc	547
Phe	Ala	Met	Ile	Gly	Ala	Val	Leu	Ile	Leu	Gln	Arg	Pro	Gln	Phe	Arg	
	135					140					145					
gtg	gta	tgg	cca	tgg	atc	ctc	acc	cca	atg	ctg	gca	ctg	ctc	ttc	tac	595
Val	Val	Trp	Pro	Trp	Ile	Leu	Thr	Pro	Met	Leu	Ala	Leu	Leu	Phe	Tyr	
	150				155					160					165	
ggt	ggc	acc	cag	ctg	tac	tcc	gac	gca	gca	cca	gtc	gtt	cca	gca	ctg	643
Gly	Gly	Thr	Gln	Leu	Tyr	Ser	Asp	Ala	Ala	Pro	Val	Val	Pro	Ala	Leu	
				170				175						180		
cag	tcc	ttc	tgg	ttc	ccg	atc	cac	gtt	tcc	tcc	gtc	tcc	atc	ggc	gca	691
Gln	Ser	Phe	Trp	Phe	Pro	Ile	His	Val	Ser	Ser	Val	Ser	Ile	Gly	Ala	
			185					190					195			
tcc	atc	ggt	atc	gtc	tcc	ggt	att	gca	tcc	ctg	ctg	tac	ata	ctg	cgc	739
Ser	Ile	Gly	Ile	Val	Ser	Gly	Ile	Ala	Ser	Leu	Leu	Tyr	Ile	Leu	Arg	
		200					205					210				
atg	tgg	caa	cca	aag	ggt	aaa	gaa	aag	ggc	ttc	ttc	ggc	gca	gta	gca	787
Met	Trp	Gln	Pro	Lys	Gly	Lys	Glu	Lys	Gly	Phe	Phe	Gly	Ala	Val	Ala	
	215					220					225					
aaa	cca	ctc	cca	tcc	gga	aaa	acc	ctg	gat	aac	ctg	gca	tac	aag	acc	835
Lys	Pro	Leu	Pro	Ser	Gly	Lys	Thr	Leu	Asp	Asn	Leu	Ala	Tyr	Lys	Thr	
	230				235					240					245	
gcg	atc	tgg	act	gtc	cca	atc	ttc	ggc	ctg	ggc	atc	atc	ttg	ggt	gcc	883
Ala	Ile	Trp	Thr	Val	Pro	Ile	Phe	Gly	Leu	Gly	Ile	Ile	Leu	Gly	Ala	

250										255					260					
atc	tgg	gca	gaa	gca	gcc	tgg	ggg	cgt	ttc	tgg	gga	tgg	gat	cct	aag	931				
Ile	Trp	Ala	Glu	Ala	Ala	Trp	Gly	Arg	Phe	Trp	Gly	Trp	Asp	Pro	Lys					
			265					270					275							
gaa	aca	gtc	tcc	ttc	atc	acc	tgg	gtt	ctc	tac	gct	ggg	tac	ctc	cac	979				
Glu	Thr	Val	Ser	Phe	Ile	Thr	Trp	Val	Leu	Tyr	Ala	Gly	Tyr	Leu	His					
		280					285					290								
gca	cgt	gca	act	gct	ggg	tgg	cgc	aac	acc	aac	gct	gca	tgg	atc	aac	1027				
Ala	Arg	Ala	Thr	Ala	Gly	Trp	Arg	Asn	Thr	Asn	Ala	Ala	Trp	Ile	Asn					
	295					300					305									
atc	ctg	gcg	ctg	gtc	acg	atg	att	ttt	aat	ctg	ttc	ttc	atc	aac	atg	1075				
Ile	Leu	Ala	Leu	Val	Thr	Met	Ile	Phe	Asn	Leu	Phe	Phe	Ile	Asn	Met					
310					315					320				325						
gtc	gta	tct	ggg	ctg	cac	tct	tac	gcc	gga	ctg	aac	taagcacttt				1121				
Val	Val	Ser	Gly	Leu	His	Ser	Tyr	Ala	Gly	Leu	Asn									
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<211> 337																				
<212> PRT																				
<213> Corynebacterium glutamicum																				
<400> 728																				
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1				5					10					15						
Val	Ser	Ala	Tyr	Ile	Ile	Tyr	Val	Leu	Ala	Leu	Ile	Leu	Ser	Leu	Val					
			20					25					30							
Tyr	Tyr	Val	Lys	Gln	Gln	Gly	Ile	Ile	Asp	Ala	Arg	Arg	Glu	Gln	Thr					
		35				40						45								
Arg	Val	Ser	Glu	Leu	Val	Gly	Ala	Gly	Gly	Ser	Ala	Asp	Val	Asp	Thr					
	50					55					60									
Asp	Leu	Pro	Asp	Asp	Ile	Ala	Asp	Gly	Val	Leu	Ala	Asp	Glu	Asp	Leu					
65					70					75					80					
Ala	Lys	Arg	Glu	Glu	Thr	Ala	Arg	Lys	Leu	Ala	Asn	Met	Thr	Gln	Ser					
				85					90					95						
Leu	Met	Trp	Leu	Gly	Val	Met	Val	His	Leu	Val	Ser	Val	Val	Met	Arg					
			100					105					110							
Ala	Leu	Ser	Ala	Ser	Arg	Phe	Pro	Phe	Gly	Asn	Leu	Tyr	Glu	Tyr	Ile					
		115					120					125								
Leu	Met	Val	Thr	Leu	Phe	Ala	Met	Ile	Gly	Ala	Val	Leu	Ile	Leu	Gln					
	130					135					140									
Arg	Pro	Gln	Phe	Arg	Val	Val	Trp	Pro	Trp	Ile	Leu	Thr	Pro	Met	Leu					
145					150					155					160					

Asn

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<222> (1)..(303)
<223> FRXA00388
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Thr	Leu	Asp	Asn	Leu	Ala	Tyr	Lys	Thr	Ala	Ile	Trp	Thr	Val	Pro	Ile	
1				5					10					15		
ttc	ggc	ctg	ggc	atc	atc	ttg	ggt	gcc	atc	tgg	gca	gaa	gca	gcc	tgg	96
Phe	Gly	Leu	Gly	Ile	Ile	Leu	Gly	Ala	Ile	Trp	Ala	Glu	Ala	Ala	Trp	
			20					25					30			
ggt	cgt	ttc	tgg	gga	tgg	gat	cct	aag	gaa	aca	gtc	tcc	ttc	atc	acc	144
Gly	Arg	Phe	Trp	Gly	Trp	Asp	Pro	Lys	Glu	Thr	Val	Ser	Phe	Ile	Thr	
		35					40					45				
tgg	gtt	ctc	tac	gct	ggt	tac	ctc	cac	gca	cgt	gca	act	gct	ggt	tgg	192

Trp Val Leu Tyr Ala Gly Tyr Leu His Ala Arg Ala Thr Ala Gly Trp
 50 55 60

cgc aac acc aac gct gca tgg atc aac atc ctg gcg ctg gtc acg atg 240
 Arg Asn Thr Asn Ala Ala Trp Ile Asn Ile Leu Ala Leu Val Thr Met
 65 70 75 80

att ttt aat ctg ttc ttc atc aac atg gtc gta tct ggt ctg cac tct 288
 Ile Phe Asn Leu Phe Phe Ile Asn Met Val Val Ser Gly Leu His Ser
 85 90 95

tac gcc gga ctg aac taagcacttt tgggtggcgg ggt 326
 Tyr Ala Gly Leu Asn
 100

<210> 730
 <211> 101
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 730
 Thr Leu Asp Asn Leu Ala Tyr Lys Thr Ala Ile Trp Thr Val Pro Ile
 1 5 10 15

Phe Gly Leu Gly Ile Ile Leu Gly Ala Ile Trp Ala Glu Ala Ala Trp
 20 25 30

Gly Arg Phe Trp Gly Trp Asp Pro Lys Glu Thr Val Ser Phe Ile Thr
 35 40 45

Trp Val Leu Tyr Ala Gly Tyr Leu His Ala Arg Ala Thr Ala Gly Trp
 50 55 60

Arg Asn Thr Asn Ala Ala Trp Ile Asn Ile Leu Ala Leu Val Thr Met
 65 70 75 80

Ile Phe Asn Leu Phe Phe Ile Asn Met Val Val Ser Gly Leu His Ser
 85 90 95

Tyr Ala Gly Leu Asn
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<210> 731
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 <212> DNA
 <213> Corynebacterium glutamicum

<220>
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 <223> FRXA00386

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 acatcgaagc agttttcaca aagaataagg ttggaaaatt atg ttg ccc gtc aac 115
 Met Leu Pro Val Asn
 1 5

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caa acg tat gcg cag ttc tca gac act gcc ttc gta tcg gca tac atc 163
Gln Thr Tyr Ala Gln Phe Ser Asp Thr Ala Phe Val Ser Ala Tyr Ile
      10              15              20

atc tac gtt ctg gca ctc atc ctc tcc ctc gtc tac tac gta aaa caa 211
Ile Tyr Val Leu Ala Leu Ile Leu Ser Leu Val Tyr Tyr Val Lys Gln
      25              30              35

caa ggc att atc gac gcc cgc cgc gag caa acc cgc gtc agc gaa ctc 259
Gln Gly Ile Ile Asp Ala Arg Arg Glu Gln Thr Arg Val Ser Glu Leu
      40              45              50

gtt ggt gca ggc ggc agc gct gat gtt gat act gac ctg cct gat gac 307
Val Gly Ala Gly Gly Ser Ala Asp Val Asp Thr Asp Leu Pro Asp Asp
      55              60              65

atc gcc gac ggt gtc ctc gcc gac gaa gac ctt gca aaa cgc gaa gaa 355
Ile Ala Asp Gly Val Leu Ala Asp Glu Asp Leu Ala Lys Arg Glu Glu
      70              75              80              85

acc gca cgc aaa cta gcc aac atg acc caa tct ctc atg tgg ctc ggc 403
Thr Ala Arg Lys Leu Ala Asn Met Thr Gln Ser Leu Met Trp Leu Gly
      90              95              100

gtc atg gtg cac ctc gta tcc gtc gtg atg cgc gcg ctg tct gcc agc 451
Val Met Val His Leu Val Ser Val Val Met Arg Ala Leu Ser Ala Ser
      105              110              115

cga ttc ccc ttc ggc aac ctg tat gaa tac atc ctc atg gtc acc ctc 499
Arg Phe Pro Phe Gly Asn Leu Tyr Glu Tyr Ile Leu Met Val Thr Leu
      120              125              130

ttc gcc atg atc gga gcc gta ctc atc ctg cag cgc cca caa ttc cgc 547
Phe Ala Met Ile Gly Ala Val Leu Ile Leu Gln Arg Pro Gln Phe Arg
      135              140              145

gtg gta tgg cca tgg atc ctc acc cca atg gct ggc act tgg ttt tct 595
Val Val Trp Pro Trp Ile Leu Thr Pro Met Ala Gly Thr Trp Phe Ser
      150              155              160              165

acg gtg gca ccc agc
Thr Val Ala Pro Ser
      170

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<210> 732

<211> 170

<212> PRT

<213> Corynebacterium glutamicum

<400> 732

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Met Leu Pro Val Asn Gln Thr Tyr Ala Gln Phe Ser Asp Thr Ala Phe
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Val Ser Ala Tyr Ile Ile Tyr Val Leu Ala Leu Ile Leu Ser Leu Val
      20              25              30

Tyr Tyr Val Lys Gln Gln Gly Ile Ile Asp Ala Arg Arg Glu Gln Thr
      35              40              45

Arg Val Ser Glu Leu Val Gly Ala Gly Gly Ser Ala Asp Val Asp Thr

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50	55	60
Asp Leu Pro Asp Asp Ile Ala Asp Gly Val Leu Ala Asp Glu Asp Leu		
65	70	75
Ala Lys Arg Glu Glu Thr Ala Arg Lys Leu Ala Asn Met Thr Gln Ser		
	85	90
Leu Met Trp Leu Gly Val Met Val His Leu Val Ser Val Val Met Arg		
	100	105
Ala Leu Ser Ala Ser Arg Phe Pro Phe Gly Asn Leu Tyr Glu Tyr Ile		
	115	120
Leu Met Val Thr Leu Phe Ala Met Ile Gly Ala Val Leu Ile Leu Gln		
	130	135
Arg Pro Gln Phe Arg Val Val Trp Pro Trp Ile Leu Thr Pro Met Ala		
	145	150
Gly Thr Trp Phe Ser Thr Val Ala Pro Ser		
	165	170

<210> 733

<211> 1095

<212> DNA

<213> Corynebacterium glutamicum

<220>

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<222> (101)..(1072)

<223> RXA00945

<400> 733

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ttcccgtgtg	ttgagggc	gat tgcaccgtac	actaatgtgc	atg ctt gaa cgc ctc	115
				Met Leu Glu Arg Leu	
				1	5

aaa cgc cta gat ccg ctc att gtc ctc att gtg ctg gct gtc att gtg	163
Lys Arg Leu Asp Pro Leu Ile Val Leu Ile Val Leu Ala Val Ile Val	
	10
	15
	20

gcg atc atc att cca gtt cgc ggg gtt gct gcg gat tgg ttt gat gtc	211
Ala Ile Ile Ile Pro Val Arg Gly Val Ala Ala Asp Trp Phe Asp Val	
	25
	30
	35

gcc gtc aag att gcc att gcg ctg ctg ttt ttt ctt tat ggt gcc cgc	259
Ala Val Lys Ile Ala Ile Ala Leu Leu Phe Phe Leu Tyr Gly Ala Arg	
	40
	45
	50

cta tcc acc caa gag gcg ctg aat ggt ctg aag cac tgg agg ctt cac	307
Leu Ser Thr Gln Glu Ala Leu Asn Gly Leu Lys His Trp Arg Leu His	
	55
	60
	65

ctg act att ttg gcg atc act ttc gga ata ttc cca ctt atc ggc att	355
Leu Thr Ile Leu Ala Ile Thr Phe Gly Ile Phe Pro Leu Ile Gly Ile	
	70
	75
	80
	85

ggg ctc gag ccg atg act gca ttt gtg tcg gaa gat att tat cgg gga	403
Gly Leu Glu Pro Met Thr Ala Phe Val Ser Glu Asp Ile Tyr Arg Gly	
90 95 100	
att ttg ttc ctc acg ctc gtt ccg tcc acc gtg cag tca tcg gtg gcg	451
Ile Leu Phe Leu Thr Leu Val Pro Ser Thr Val Gln Ser Ser Val Ala	
105 110 115	
ttt acc tcg atc gct aaa ggc aac gta gct ggt gcg att gtg tcg gca	499
Phe Thr Ser Ile Ala Lys Gly Asn Val Ala Gly Ala Ile Val Ser Ala	
120 125 130	
tcg ctc tcc aac ctt gcg ggt gtt ttc ctc act ccg ctg ctg gtc atg	547
Ser Leu Ser Asn Leu Ala Gly Val Phe Leu Thr Pro Leu Leu Val Met	
135 140 145	
ctc atc atg tct gcg ggc ggg gga gtt cac gtg gat tcc cag gtc ttc	595
Leu Ile Met Ser Ala Gly Gly Val His Val Asp Ser Gln Val Phe	
150 155 160 165	
ctc gac att gcg att cag ctt ctg ctg ccg ttc atc ctc ggc cag gta	643
Leu Asp Ile Ala Ile Gln Leu Leu Leu Pro Phe Ile Leu Gly Gln Val	
170 175 180	
tgt agg cgt tgg gtg aag aat ttt gcg gcc aac aaa gca aca aaa atc	691
Cys Arg Arg Trp Val Lys Asn Phe Ala Ala Asn Lys Ala Thr Lys Ile	
185 190 195	
gtg gac cgc ggc tcg atc gcg atg gtc gtg tac tcc gcg ttt tct gcc	739
Val Asp Arg Gly Ser Ile Ala Met Val Val Tyr Ser Ala Phe Ser Ala	
200 205 210	
ggc atg gtg gct ggc att tgg tcc act gtg agc gtt cta gag att atc	787
Gly Met Val Ala Gly Ile Trp Ser Thr Val Ser Val Leu Glu Ile Ile	
215 220 225	
tac ctc att gtt ttc gct att ctg ctg gtg atg gcc atg ctg tgg ttc	835
Tyr Leu Ile Val Phe Ala Ile Leu Leu Val Met Ala Met Leu Trp Phe	
230 235 240 245	
acg ctg ttc atg gct aca cgc ctt gga ttt aac cgg gca gat tcc atc	883
Thr Leu Phe Met Ala Thr Arg Leu Gly Phe Asn Arg Ala Asp Ser Ile	
250 255 260	
gct att cag ttc tgc gga acc aag aaa tcc ctg gcc aca ggc ctc cca	931
Ala Ile Gln Phe Cys Gly Thr Lys Lys Ser Leu Ala Thr Gly Leu Pro	
265 270 275	
atg gcg gca gtc atc ttc ggt ggc gcc aat atc ggc ctg ctc atc ttg	979
Met Ala Ala Val Ile Phe Gly Gly Ala Asn Ile Gly Leu Leu Ile Leu	
280 285 290	
ccg ttg atg atc ttc cac caa gtc cag ctg atg att tgt gca tgg ctt	1027
Pro Leu Met Ile Phe His Gln Val Gln Leu Met Ile Cys Ala Trp Leu	
295 300 305	
gca gct cgt tat ggt cgt gat gcg cag gaa cag aaa gcc aac gcc	1072
Ala Ala Arg Tyr Gly Arg Asp Ala Gln Glu Gln Lys Ala Asn Ala	
310 315 320	
taaaagtcct cagtagctag cca	1095

<210> 734

<211> 324

<212> PRT

<213> Corynebacterium glutamicum

<400> 734

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Met Leu Glu Arg Leu Lys Arg Leu Asp Pro Leu Ile Val Leu Ile Val
 1           5           10           15

Leu Ala Val Ile Val Ala Ile Ile Ile Pro Val Arg Gly Val Ala Ala
      20           25           30

Asp Trp Phe Asp Val Ala Val Lys Ile Ala Ile Ala Leu Leu Phe Phe
      35           40           45

Leu Tyr Gly Ala Arg Leu Ser Thr Gln Glu Ala Leu Asn Gly Leu Lys
      50           55           60

His Trp Arg Leu His Leu Thr Ile Leu Ala Ile Thr Phe Gly Ile Phe
      65           70           75           80

Pro Leu Ile Gly Ile Gly Leu Glu Pro Met Thr Ala Phe Val Ser Glu
      85           90           95

Asp Ile Tyr Arg Gly Ile Leu Phe Leu Thr Leu Val Pro Ser Thr Val
      100          105          110

Gln Ser Ser Val Ala Phe Thr Ser Ile Ala Lys Gly Asn Val Ala Gly
      115          120          125

Ala Ile Val Ser Ala Ser Leu Ser Asn Leu Ala Gly Val Phe Leu Thr
      130          135          140

Pro Leu Leu Val Met Leu Ile Met Ser Ala Gly Gly Gly Val His Val
      145          150          155          160

Asp Ser Gln Val Phe Leu Asp Ile Ala Ile Gln Leu Leu Leu Pro Phe
      165          170          175

Ile Leu Gly Gln Val Cys Arg Arg Trp Val Lys Asn Phe Ala Ala Asn
      180          185          190

Lys Ala Thr Lys Ile Val Asp Arg Gly Ser Ile Ala Met Val Val Tyr
      195          200          205

Ser Ala Phe Ser Ala Gly Met Val Ala Gly Ile Trp Ser Thr Val Ser
      210          215          220

Val Leu Glu Ile Ile Tyr Leu Ile Val Phe Ala Ile Leu Leu Val Met
      225          230          235          240

Ala Met Leu Trp Phe Thr Leu Phe Met Ala Thr Arg Leu Gly Phe Asn
      245          250          255

Arg Ala Asp Ser Ile Ala Ile Gln Phe Cys Gly Thr Lys Lys Ser Leu
      260          265          270

Ala Thr Gly Leu Pro Met Ala Ala Val Ile Phe Gly Gly Ala Asn Ile
      275          280          285

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Gly Leu Leu Ile Leu Pro Leu Met Ile Phe His Gln Val Gln Leu Met
 290 295 300

Ile Cys Ala Trp Leu Ala Ala Arg Tyr Gly Arg Asp Ala Gln Glu Gln
 305 310 315 320

Lys Ala Asn Ala

<210> 735

<211> 1281

<212> DNA

<213> Corynebacterium glutamicum

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<221> CDS

<222> (101)..(1258)

<223> RXN02556

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gtagaaatta gcccatgaag catggaaagg cgaaaacccc ttg atc gtt tcc acc 115
 Leu Ile Val Ser Thr
 1 5

cag ccc att act gat cgc agc gca ctc tcg gca gaa cac gca gag gtg 163
 Gln Pro Ile Thr Asp Arg Ser Ala Leu Ser Ala Glu His Ala Glu Val
 10 15 20

atc aaa gca acg ctt cct ctc gtg ggc ggc aag att aat gag atc acg 211
 Ile Lys Ala Thr Leu Pro Leu Val Gly Gly Lys Ile Asn Glu Ile Thr
 25 30 35

ccg gtt ttc tac aac aag atg ttt gcg gct cac cca gaa ttg atc gct 259
 Pro Val Phe Tyr Asn Lys Met Phe Ala Ala His Pro Glu Leu Ile Ala
 40 45 50

aac acc ttc aac cgt ggc aat cag aag caa ggc gat cag cag aag gcg 307
 Asn Thr Phe Asn Arg Gly Asn Gln Lys Gln Gly Asp Gln Gln Lys Ala
 55 60 65

ctg gcg gct tcg att gca acg ttt gcc acc atg ctc gtt act cct gat 355
 Leu Ala Ala Ser Ile Ala Thr Phe Ala Thr Met Leu Val Thr Pro Asp
 70 75 80 85

gct cct gac cca gtt cag ctg ctg tcc cgc att ggc cac aag cac gtg 403
 Ala Pro Asp Pro Val Gln Leu Leu Ser Arg Ile Gly His Lys His Val
 90 95 100

tcc ctc ggc att act gct gat cag tac gac att gtt cac gag cac ctg 451
 Ser Leu Gly Ile Thr Ala Asp Gln Tyr Asp Ile Val His Glu His Leu
 105 110 115

ttc gcc gca atc gtt gag gtt ttg gga gcg gaa act gtc acc gca cct 499
 Phe Ala Ala Ile Val Glu Val Leu Gly Ala Glu Thr Val Thr Ala Pro
 120 125 130

gtc gct gaa gcc tgg gat gct gtc tac tgg atc atg gca aat gtg ctg 547

Val	Ala	Glu	Ala	Trp	Asp	Ala	Val	Tyr	Trp	Ile	Met	Ala	Asn	Val	Leu		
135						140					145						
atc	ggt	ttt	gag	aac	aac	ctt	tat	gct	tcc	aac	gat	ctg	gag	cct	ggc	595	
Ile	Gly	Phe	Glu	Asn	Asn	Leu	Tyr	Ala	Ser	Asn	Asp	Leu	Glu	Pro	Gly		
150				155						160					165		
gac	gtc	ttc	cgc	gaa	gtc	acc	gtg	acc	gcg	aag	aag	cag	ctc	agc	gca	643	
Asp	Val	Phe	Arg	Glu	Val	Thr	Val	Thr	Ala	Lys	Lys	Gln	Leu	Ser	Ala		
				170					175					180			
acc	gtc	tgg	gaa	tac	acc	ctg	gca	ggt	gag	ctg	gtt	gcc	cca	gag	cca	691	
Thr	Val	Trp	Glu	Tyr	Thr	Leu	Ala	Gly	Glu	Leu	Val	Ala	Pro	Glu	Pro		
			185					190					195				
ggt	cag	tac	acc	tcc	atc	gga	gta	gtg	ctt	gac	gac	ggc	gcc	cgc	cag	739	
Gly	Gln	Tyr	Thr	Ser	Ile	Gly	Val	Val	Leu	Asp	Asp	Gly	Ala	Arg	Gln		
		200					205					210					
ctg	cgc	cag	tac	agc	ttg	ctc	ggc	ggc	tcc	gac	acc	gag	tac	cgc	att	787	
Leu	Arg	Gln	Tyr	Ser	Leu	Leu	Gly	Gly	Ser	Asp	Thr	Glu	Tyr	Arg	Ile		
	215					220					225						
gcg	gtt	gag	gat	aac	ggc	gag	gtt	tct	gga	ttc	ctg	cgt	gat	cgc	gta	835	
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Ser	Val	Gly	Asp	Lys	Ile	Glu	Ala	Thr	Ile	Ala	Ala	Gly	Asp	Leu	Val		
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ctt	aac	aag	gac	acc	aat	cca	gtt	gtg	ctg	att	tcc	cag	ggc	atc	ggc	931	
Leu	Asn	Lys	Asp	Thr	Asn	Pro	Val	Val	Leu	Ile	Ser	Gln	Gly	Ile	Gly		
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Ser	Thr	Pro	Met	Val	Gly	Met	Leu	Ala	Gly	Met	Asn	Pro	Glu	Arg	Asp		
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Glu	Glu	Val	Gln	Gly	Leu	Val	Glu	Lys	Leu	Pro	Lys	Ala	Ala	Phe	Glu		
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Ile	Phe	Tyr	Arg	Asp	Asn	Asp	Gln	Trp	Leu	Glu	Val	Ala	Gly	Arg	Ile		
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Pro	Ser	Gly	Ala	Ser	Val	Tyr	Leu	Cys	Gly	Gly	Val	Glu	Phe	Leu	Lys		
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Asn	Val	Arg	Glu	Gln	Ile	Glu	Ala	Leu	Asp	Glu	Gln	Pro	Arg	Asp	Val		
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aac	ttc	gag	ctc	ttc	gca	cca	aac	gac	tgg	ctg	att	tcc	taagccca			1268	
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 <212> PRT
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 Pro Glu Leu Ile Ala Asn Thr Phe Asn Arg Gly Asn Gln Lys Gln Gly
 50 55 60
 Asp Gln Gln Lys Ala Leu Ala Ala Ser Ile Ala Thr Phe Ala Thr Met
 65 70 75 80
 Leu Val Thr Pro Asp Ala Pro Asp Pro Val Gln Leu Leu Ser Arg Ile
 85 90 95
 Gly His Lys His Val Ser Leu Gly Ile Thr Ala Asp Gln Tyr Asp Ile
 100 105 110
 Val His Glu His Leu Phe Ala Ala Ile Val Glu Val Leu Gly Ala Glu
 115 120 125
 Thr Val Thr Ala Pro Val Ala Glu Ala Trp Asp Ala Val Tyr Trp Ile
 130 135 140
 Met Ala Asn Val Leu Ile Gly Phe Glu Asn Asn Leu Tyr Ala Ser Asn
 145 150 155 160
 Asp Leu Glu Pro Gly Asp Val Phe Arg Glu Val Thr Val Thr Ala Lys
 165 170 175
 Lys Gln Leu Ser Ala Thr Val Trp Glu Tyr Thr Leu Ala Gly Glu Leu
 180 185 190
 Val Ala Pro Glu Pro Gly Gln Tyr Thr Ser Ile Gly Val Val Leu Asp
 195 200 205
 Asp Gly Ala Arg Gln Leu Arg Gln Tyr Ser Leu Leu Gly Gly Ser Asp
 210 215 220
 Thr Glu Tyr Arg Ile Ala Val Glu Asp Asn Gly Glu Val Ser Gly Phe
 225 230 235 240
 Leu Arg Asp Arg Val Ser Val Gly Asp Lys Ile Glu Ala Thr Ile Ala
 245 250 255
 Ala Gly Asp Leu Val Leu Asn Lys Asp Thr Asn Pro Val Val Leu Ile
 260 265 270

Ser Gln Gly Ile Gly Ser Thr Pro Met Val Gly Met Leu Ala Gly Met
 275 280 285

Asn Pro Glu Arg Asp Val Val Val Leu His Ala Asp Gln Ala Glu Ser
 290 295 300

Thr Tyr Ala Gln Val Glu Glu Val Gln Gly Leu Val Glu Lys Leu Pro
 305 310 315 320

Lys Ala Ala Phe Glu Ile Phe Tyr Arg Asp Asn Asp Gln Trp Leu Glu
 325 330 335

Val Ala Gly Arg Ile Pro Ser Gly Ala Ser Val Tyr Leu Cys Gly Gly
 340 345 350

Val Glu Phe Leu Lys Asn Val Arg Glu Gln Ile Glu Ala Leu Asp Glu
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Gln Pro Arg Asp Val Asn Phe Glu Leu Phe Ala Pro Asn Asp Trp Leu
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Ile Ser
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<211> 1281

<212> DNA

<213> Corynebacterium glutamicum

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<223> FRXA02556

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cag ccc att act gat cgc agc gca ctc tcg gca gaa cac gca gag gtg 163
 Gln Pro Ile Thr Asp Arg Ser Ala Leu Ser Ala Glu His Ala Glu Val
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atc aaa gca acg ctt cct ctc gtg ggc ggc aag att aat gag atc acg 211
 Ile Lys Ala Thr Leu Pro Leu Val Gly Gly Lys Ile Asn Glu Ile Thr
 25 30 35

ccg gtt ttc tac aac aag atg ttt gcg gct cac cca gaa ttg atc gct 259
 Pro Val Phe Tyr Asn Lys Met Phe Ala Ala His Pro Glu Leu Ile Ala
 40 45 50

aac acc ttc aac ggt ggc aat cag aag caa ggc gat cag cag aag gcg 307
 Asn Thr Phe Asn Gly Gly Asn Gln Lys Gln Gly Asp Gln Gln Lys Ala
 55 60 65

ctg gcg gct tcg att gca acg ttt gcc acc atg ctc gtt act cct gat 355
 Leu Ala Ala Ser Ile Ala Thr Phe Ala Thr Met Leu Val Thr Pro Asp

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Ala Pro Asp Pro Val Gln Leu Leu Ser Arg Ile Gly His Lys His Val													
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Ser Leu Gly Ile Thr Ala Asp Gln Tyr Asp Ile Val His Glu His Leu													
	105				110				115				
ttc gcc gca atc gtt gag gtt ttg gga gcg gaa act gtc acc gca cct	499												
Phe Ala Ala Ile Val Glu Val Leu Gly Ala Glu Thr Val Thr Ala Pro													
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gtc gct gaa gcc tgg gat gct gtc tac tgg atc atg gca aat gtg ctg	547												
Val Ala Glu Ala Trp Asp Ala Val Tyr Trp Ile Met Ala Asn Val Leu													
	135				140				145				
atc ggt ttt gag aac aac ctt tat gct tcc aac gat ctg gag cct ggc	595												
Ile Gly Phe Glu Asn Asn Leu Tyr Ala Ser Asn Asp Leu Glu Pro Gly													
	150				155				160				165
gac gtc ttc cgc gaa gtc acc gtg acc gcg aag aag cag ctc agc gca	643												
Asp Val Phe Arg Glu Val Thr Val Thr Ala Lys Lys Gln Leu Ser Ala													
	170				175				180				
acc gtc tgg gaa tac acc ctg gca ggt gag ctg gtt gcc cca gag cca	691												
Thr Val Trp Glu Tyr Thr Leu Ala Gly Glu Leu Val Ala Pro Glu Pro													
	185				190				195				
ggt cag tac acc tcc atc gga gta gtg ctt gac gac ggc gcc cgc cag	739												
Gly Gln Tyr Thr Ser Ile Gly Val Val Leu Asp Asp Gly Ala Arg Gln													
	200				205				210				
ctg cgc cag tac agc ttg ctc ggc ggc tcc gac acc gag tac cgc att	787												
Leu Arg Gln Tyr Ser Leu Leu Gly Gly Ser Asp Thr Glu Tyr Arg Ile													
	215				220				225				
gcg gtt gag gat aac ggc gag gtt tct gga ttc ctg cgt gat cgc gta	835												
Ala Val Glu Asp Asn Gly Glu Val Ser Gly Phe Leu Arg Asp Arg Val													
	230				235				240				245
tcc gtt ggt gac aag att gaa gcc acc atc gcg gcc ggc gac ctg gtt	883												
Ser Val Gly Asp Lys Ile Glu Ala Thr Ile Ala Ala Gly Asp Leu Val													
	250				255				260				
ctt aac aag gac acc aat cca gtt gtg ctg att tcc cag ggc atc ggc	931												
Leu Asn Lys Asp Thr Asn Pro Val Val Leu Ile Ser Gln Gly Ile Gly													
	265				270				275				
tcc acc cca atg gtg ggc atg ctc gca ggt atg aac cct gaa cgt gac	979												
Ser Thr Pro Met Val Gly Met Leu Ala Gly Met Asn Pro Glu Arg Asp													
	280				285				290				
gtt gtg gtt ttg cat gct gac cag gcc gag tcc acc tac gcg cag gtg	1027												
Val Val Val Leu His Ala Asp Gln Ala Glu Ser Thr Tyr Ala Gln Val													
	295				300				305				
gag gaa gtg cag ggg ctc gtc gaa aag ctc cct aag gct gcg ttt gaa	1075												
Glu Glu Val Gln Gly Leu Val Glu Lys Leu Pro Lys Ala Ala Phe Glu													
	310				315				320				325

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 Ile Phe Tyr Arg Asp Asn Asp Gln Trp Leu Glu Val Ala Gly Arg Ile
 330 335 340

cca tca ggt gcg tcc gtg tac ctg tgc ggt ggc gtg gaa ttc ttg aag 1171
 Pro Ser Gly Ala Ser Val Tyr Leu Cys Gly Gly Val Glu Phe Leu Lys
 345 350 355

aac gtg cgt gag cag atc gag gcg ctc gat gag cag cct cgc gac gta 1219
 Asn Val Arg Glu Gln Ile Glu Ala Leu Asp Glu Gln Pro Arg Asp Val
 360 365 370

aac ttc gag ctc ttc gca cca aac gac tgg ctg att tcc taagcccaca 1268
 Asn Phe Glu Leu Phe Ala Pro Asn Asp Trp Leu Ile Ser
 375 380 385

ccccagaact tcc 1281

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 <212> PRT
 <213> Corynebacterium glutamicum

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 35 40 45

Pro Glu Leu Ile Ala Asn Thr Phe Asn Gly Gly Asn Gln Lys Gln Gly
 50 55 60

Asp Gln Gln Lys Ala Leu Ala Ala Ser Ile Ala Thr Phe Ala Thr Met
 65 70 75 80

Leu Val Thr Pro Asp Ala Pro Asp Pro Val Gln Leu Leu Ser Arg Ile
 85 90 95

Gly His Lys His Val Ser Leu Gly Ile Thr Ala Asp Gln Tyr Asp Ile
 100 105 110

Val His Glu His Leu Phe Ala Ala Ile Val Glu Val Leu Gly Ala Glu
 115 120 125

Thr Val Thr Ala Pro Val Ala Glu Ala Trp Asp Ala Val Tyr Trp Ile
 130 135 140

Met Ala Asn Val Leu Ile Gly Phe Glu Asn Asn Leu Tyr Ala Ser Asn
 145 150 155 160

Asp Leu Glu Pro Gly Asp Val Phe Arg Glu Val Thr Val Thr Ala Lys
 165 170 175

Lys Gln Leu Ser Ala Thr Val Trp Glu Tyr Thr Leu Ala Gly Glu Leu
 180 185 190

Val Ala Pro Glu Pro Gly Gln Tyr Thr Ser Ile Gly Val Val Leu Asp
 195 200 205

Asp Gly Ala Arg Gln Leu Arg Gln Tyr Ser Leu Leu Gly Gly Ser Asp
 210 215 220

Thr Glu Tyr Arg Ile Ala Val Glu Asp Asn Gly Glu Val Ser Gly Phe
 225 230 235 240

Leu Arg Asp Arg Val Ser Val Gly Asp Lys Ile Glu Ala Thr Ile Ala
 245 250 255

Ala Gly Asp Leu Val Leu Asn Lys Asp Thr Asn Pro Val Val Leu Ile
 260 265 270

Ser Gln Gly Ile Gly Ser Thr Pro Met Val Gly Met Leu Ala Gly Met
 275 280 285

Asn Pro Glu Arg Asp Val Val Val Leu His Ala Asp Gln Ala Glu Ser
 290 295 300

Thr Tyr Ala Gln Val Glu Glu Val Gln Gly Leu Val Glu Lys Leu Pro
 305 310 315 320

Lys Ala Ala Phe Glu Ile Phe Tyr Arg Asp Asn Asp Gln Trp Leu Glu
 325 330 335

Val Ala Gly Arg Ile Pro Ser Gly Ala Ser Val Tyr Leu Cys Gly Gly
 340 345 350

Val Glu Phe Leu Lys Asn Val Arg Glu Gln Ile Glu Ala Leu Asp Glu
 355 360 365

Gln Pro Arg Asp Val Asn Phe Glu Leu Phe Ala Pro Asn Asp Trp Leu
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Ile Ser
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 Val Ala Asn Thr Ser
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 Ser Asp Trp Ala Gly Ala Pro Gln Asn Ala Ser Ala Asp Gly Glu Phe
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Val Arg Asp Thr Asn Tyr Ile Asp Asp Arg Ile Val Ala Asp Val Pro	
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Ala Gly Ser Glu Pro Ile Ala Gln Glu Asp Gly Thr Phe His Trp Pro	
40 45 50	
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Val Glu Ala Gly Arg Tyr Arg Leu Val Ala Ala Arg Ala Cys Pro Trp	
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gca cac cgc act gtt atc acc cgt cgt ctt ctc ggc ctg gag aac gtg	355
Ala His Arg Thr Val Ile Thr Arg Arg Leu Leu Gly Leu Glu Asn Val	
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Ile Ser Leu Gly Leu Thr Gly Pro Thr His Asp Val Arg Ser Trp Thr	
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ttc gat tta gat cca aac cat ctt gat ccc gtg ctg cag att cct cgt	451
Phe Asp Leu Asp Pro Asn His Leu Asp Pro Val Leu Gln Ile Pro Arg	
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cta cag gac gcg tat ttc aac cgc ttc ccc gat tac ccg cgc ggc att	499
Leu Gln Asp Ala Tyr Phe Asn Arg Phe Pro Asp Tyr Pro Arg Gly Ile	
120 125 130	
act gtc cca gcg ctc gtg gag gaa tcg tct aag aag gtc gtc acc aac	547
Thr Val Pro Ala Leu Val Glu Glu Ser Ser Lys Lys Val Val Thr Asn	
135 140 145	
gat tac cct tcc atc acc atc gat ttc aat ctt gag tgg aag cag ttc	595
Asp Tyr Pro Ser Ile Thr Ile Asp Phe Asn Leu Glu Trp Lys Gln Phe	
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cac cgt gag ggt gcg cct aac ctc tac ccc gcg gag ctg cgc gag gag	643
His Arg Glu Gly Ala Pro Asn Leu Tyr Pro Ala Glu Leu Arg Glu Glu	
170 175 180	
atg gcg ccg gtg atg aag cgc atc ttc act gag gtc aac aac ggc gta	691
Met Ala Pro Val Met Lys Arg Ile Phe Thr Glu Val Asn Asn Gly Val	
185 190 195	
tac agg acc ggc ttt gcc ggt agc cag gaa gcg cac aac gag gcg tac	739
Tyr Arg Thr Gly Phe Ala Gly Ser Gln Glu Ala His Asn Glu Ala Tyr	
200 205 210	
aag cgg ctt tgg gtt gcg ttg gac tgg cta gaa gat cgc tta tcg acg	787
Lys Arg Leu Trp Val Ala Leu Asp Trp Leu Glu Asp Arg Leu Ser Thr	
215 220 225	
cga cgt tac ctc atg ggg gat cac atc acc gag gcg gat atc cgc ctc	835
Arg Arg Tyr Leu Met Gly Asp His Ile Thr Glu Ala Asp Ile Arg Leu	
230 235 240 245	
tac cca acc ctc gtg cgt ttc gat gcc gtc tac cac gga cac ttc aag	883
Tyr Pro Thr Leu Val Arg Phe Asp Ala Val Tyr His Gly His Phe Lys	
250 255 260	

tgt ggc cgc aac aag atc acc gaa atg ccg aat cta tgg ggc tac ctg 931
 Cys Gly Arg Asn Lys Ile Thr Glu Met Pro Asn Leu Trp Gly Tyr Leu
 265 270 275

 cgg gat ctt ttc cag acc cca ggc ttt ggc gac acc acc gat ttc acc 979
 Arg Asp Leu Phe Gln Thr Pro Gly Phe Gly Asp Thr Thr Asp Phe Thr
 280 285 290

 gaa atc aag cag cac tac tac atc acc cac gcg gag att aac ccc acc 1027
 Glu Ile Lys Gln His Tyr Tyr Ile Thr His Ala Glu Ile Asn Pro Thr
 295 300 305

 cgg atc gtt cca gtc gga cca gat ctg tct ggt ttc gcg aca cca cac 1075
 Arg Ile Val Pro Val Gly Pro Asp Leu Ser Gly Phe Ala Thr Pro His
 310 315 320 325

 ggc cgt gaa aag ctc ggc gga tcc cca ttt gct gaa ggt gtt act ctg 1123
 Gly Arg Glu Lys Leu Gly Gly Ser Pro Phe Ala Glu Gly Val Thr Leu
 330 335 340

 cct ggc cca att cct gcg ggc gaa gaa gtg aaa aac cct gaa cct ttt 1171
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<211> 359

<212> PRT

<213> Corynebacterium glutamicum

<400> 740

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 20 25 30

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 35 40 45

 Thr Phe His Trp Pro Val Glu Ala Gly Arg Tyr Arg Leu Val Ala Ala
 50 55 60

 Arg Ala Cys Pro Trp Ala His Arg Thr Val Ile Thr Arg Arg Leu Leu
 65 70 75 80

 Gly Leu Glu Asn Val Ile Ser Leu Gly Leu Thr Gly Pro Thr His Asp
 85 90 95

 Val Arg Ser Trp Thr Phe Asp Leu Asp Pro Asn His Leu Asp Pro Val
 100 105 110

 Leu Gln Ile Pro Arg Leu Gln Asp Ala Tyr Phe Asn Arg Phe Pro Asp
 115 120 125

 Tyr Pro Arg Gly Ile Thr Val Pro Ala Leu Val Glu Glu Ser Ser Lys
 130 135 140

Lys Val Val Thr Asn Asp Tyr Pro Ser Ile Thr Ile Asp Phe Asn Leu
 145 150 155 160
 Glu Trp Lys Gln Phe His Arg Glu Gly Ala Pro Asn Leu Tyr Pro Ala
 165 170 175
 Glu Leu Arg Glu Glu Met Ala Pro Val Met Lys Arg Ile Phe Thr Glu
 180 185 190
 Val Asn Asn Gly Val Tyr Arg Thr Gly Phe Ala Gly Ser Gln Glu Ala
 195 200 205
 His Asn Glu Ala Tyr Lys Arg Leu Trp Val Ala Leu Asp Trp Leu Glu
 210 215 220
 Asp Arg Leu Ser Thr Arg Arg Tyr Leu Met Gly Asp His Ile Thr Glu
 225 230 235 240
 Ala Asp Ile Arg Leu Tyr Pro Thr Leu Val Arg Phe Asp Ala Val Tyr
 245 250 255
 His Gly His Phe Lys Cys Gly Arg Asn Lys Ile Thr Glu Met Pro Asn
 260 265 270
 Leu Trp Gly Tyr Leu Arg Asp Leu Phe Gln Thr Pro Gly Phe Gly Asp
 275 280 285
 Thr Thr Asp Phe Thr Glu Ile Lys Gln His Tyr Tyr Ile Thr His Ala
 290 295 300
 Glu Ile Asn Pro Thr Arg Ile Val Pro Val Gly Pro Asp Leu Ser Gly
 305 310 315 320
 Phe Ala Thr Pro His Gly Arg Glu Lys Leu Gly Gly Ser Pro Phe Ala
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 Asn Pro Glu Pro Phe Gln Lys
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 <212> DNA
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 <222> (101)..(1204)
 <223> RXA00800

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 Met Ser Thr Val Val
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cct gga att gtc gca ctg tcc aag ggt gca ccg gta gaa aaa gta aac	163
Pro Gly Ile Val Ala Leu Ser Lys Gly Ala Pro Val Glu Lys Val Asn	
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gtt gtt gtc cct gat cca ggt gct aac gat gtc atc gtc aag att cag	211
Val Val Val Pro Asp Pro Gly Ala Asn Asp Val Ile Val Lys Ile Gln	
25 30 35	
gcc tgc ggt gtg tgc cac acc gac ttg gcc tac cgc gat ggc gat att	259
Ala Cys Gly Val Cys His Thr Asp Leu Ala Tyr Arg Asp Gly Asp Ile	
40 45 50	
tca gat gag ttc cct tac ctg ctg ggc cac gag gca gca ggc att gtt	307
Ser Asp Glu Phe Pro Tyr Leu Leu Gly His Glu Ala Ala Gly Ile Val	
55 60 65	
gag gag gta ggc gag tcc gtc acc cac gtt gag gtc ggc gat ttc gtc	355
Glu Glu Val Gly Glu Ser Val Thr His Val Glu Val Gly Asp Phe Val	
70 75 80 85	
atc ttg aac tgg cgt gca gtg tgc ggc gag tgc cgt gca tgt aag aag	403
Ile Leu Asn Trp Arg Ala Val Cys Gly Glu Cys Arg Ala Cys Lys Lys	
90 95 100	
ggc gag cca aag tac tgc ttt aac acc cac aac gcc tct aag aag atg	451
Gly Glu Pro Lys Tyr Cys Phe Asn Thr His Asn Ala Ser Lys Lys Met	
105 110 115	
acc ctg gaa gac ggc acc gag ctg tcc cca gca ctg ggt att ggc gcg	499
Thr Leu Glu Asp Gly Thr Glu Leu Ser Pro Ala Leu Gly Ile Gly Ala	
120 125 130	
ttc ttg gaa aag acc ctg gtc cac gaa ggc cag tgc acc aag gtt aac	547
Phe Leu Glu Lys Thr Leu Val His Glu Gly Gln Cys Thr Lys Val Asn	
135 140 145	
cct gag gaa gat cca gca gca gct ggc ctt ctg ggt tgt ggc atc atg	595
Pro Glu Glu Asp Pro Ala Ala Ala Gly Leu Leu Gly Cys Gly Ile Met	
150 155 160 165	
gca ggc ctt ggc gct gcg gtg aac acc ggt gat att aag cgt ggc gag	643
Ala Gly Leu Gly Ala Ala Val Asn Thr Gly Asp Ile Lys Arg Gly Glu	
170 175 180	
tcc gta gca gtc ttc ggc ctt ggt ggc gtg ggc atg gca gct att gct	691
Ser Val Ala Val Phe Gly Leu Gly Gly Val Gly Met Ala Ala Ile Ala	
185 190 195	
ggc gcc aag att gct ggc gct tcc aag atc att gct gtt gat atc gat	739
Gly Ala Lys Ile Ala Gly Ala Ser Lys Ile Ile Ala Val Asp Ile Asp	
200 205 210	
gag aag aag ctg gag tgg gcg aag gaa ttc ggc gca acc cac acc att	787
Glu Lys Lys Leu Glu Trp Ala Lys Glu Phe Gly Ala Thr His Thr Ile	
215 220 225	
aat tcc tct ggt ctt ggt ggc gaa ggt gat gcc tct gag gtc gtg gca	835
Asn Ser Ser Gly Leu Gly Gly Glu Gly Asp Ala Ser Glu Val Val Ala	
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aag gtt cgt gag ctg acc gat ggt ttc ggc acc gat gtc tcc atc gat	883

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<212> PRT
<213> Corynebacterium glutamicum

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Val Glu Lys Val Asn Val Val Val Pro Asp Pro Gly Ala Asn Asp Val
 20          25          30
Ile Val Lys Ile Gln Ala Cys Gly Val Cys His Thr Asp Leu Ala Tyr
 35          40          45
Arg Asp Gly Asp Ile Ser Asp Glu Phe Pro Tyr Leu Leu Gly His Glu
 50          55          60
Ala Ala Gly Ile Val Glu Glu Val Gly Glu Ser Val Thr His Val Glu
 65          70          75          80
Val Gly Asp Phe Val Ile Leu Asn Trp Arg Ala Val Cys Gly Glu Cys
 85          90          95
Arg Ala Cys Lys Lys Gly Glu Pro Lys Tyr Cys Phe Asn Thr His Asn
100          105          110

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Ala Ser Lys Lys Met Thr Leu Glu Asp Gly Thr Glu Leu Ser Pro Ala
 115 120 125
 Leu Gly Ile Gly Ala Phe Leu Glu Lys Thr Leu Val His Glu Gly Gln
 130 135 140
 Cys Thr Lys Val Asn Pro Glu Glu Asp Pro Ala Ala Ala Gly Leu Leu
 145 150 155 160
 Gly Cys Gly Ile Met Ala Gly Leu Gly Ala Ala Val Asn Thr Gly Asp
 165 170 175
 Ile Lys Arg Gly Glu Ser Val Ala Val Phe Gly Leu Gly Gly Val Gly
 180 185 190
 Met Ala Ala Ile Ala Gly Ala Lys Ile Ala Gly Ala Ser Lys Ile Ile
 195 200 205
 Ala Val Asp Ile Asp Glu Lys Lys Leu Glu Trp Ala Lys Glu Phe Gly
 210 215 220
 Ala Thr His Thr Ile Asn Ser Ser Gly Leu Gly Gly Glu Gly Asp Ala
 225 230 235 240
 Ser Glu Val Val Ala Lys Val Arg Glu Leu Thr Asp Gly Phe Gly Thr
 245 250 255
 Asp Val Ser Ile Asp Ala Val Gly Ile Met Pro Thr Trp Gln Gln Ala
 260 265 270
 Phe Tyr Ser Arg Asp His Ala Gly Arg Met Val Met Val Gly Val Pro
 275 280 285
 Asn Leu Thr Ser Arg Val Asp Val Pro Ala Ile Asp Phe Tyr Gly Arg
 290 295 300
 Gly Gly Ser Val Arg Pro Ala Trp Tyr Gly Asp Cys Leu Pro Glu Arg
 305 310 315 320
 Asp Phe Pro Thr Tyr Val Asp Leu His Leu Gln Gly Arg Phe Pro Leu
 325 330 335
 Asp Lys Phe Val Ser Glu Arg Ile Gly Leu Asp Asp Val Glu Glu Ala
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 Phe Asn Thr Met Lys Ala Gly Asp Val Leu Arg Ser Val Val Glu Ile
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<211> 1011

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(988)

<223> RXA02143

<400> 743

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Met Met Glu Thr Asn
1 5

ccg cag acc cca gag gga aat agc atg gct aaa ccc tct gct aag aag 163
Pro Gln Thr Pro Glu Gly Asn Ser Met Ala Lys Pro Ser Ala Lys Lys
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gtc aag aat cgc cgc aag gtc cgg cgc acc gtc gca ggt gca ttg gct 211
Val Lys Asn Arg Arg Lys Val Arg Arg Thr Val Ala Gly Ala Leu Ala
25 30 35

ctg acc att gga ctg agc gga gca gga atc ctc gca acc gcg atc act 259
Leu Thr Ile Gly Leu Ser Gly Ala Gly Ile Leu Ala Thr Ala Ile Thr
40 45 50

cca gat gct caa gtt gct acc gct cag cgt gac gat cag gca ctt atc 307
Pro Asp Ala Gln Val Ala Thr Ala Gln Arg Asp Asp Gln Ala Leu Ile
55 60 65

tcc gag ggt aaa gac ctc tac gat gtc gcc tgc atc acc tgc cac ggc 355
Ser Glu Gly Lys Asp Leu Tyr Asp Val Ala Cys Ile Thr Cys His Gly
70 75 80 85

gta aac ctc caa ggt gtt gag gac cgc ggt cct tcc ctc gta ggt gtt 403
Val Asn Leu Gln Gly Val Glu Asp Arg Gly Pro Ser Leu Val Gly Val
90 95 100

ggc gaa ggc gca gtg tac ttc caa gtt cac tcc ggc cgt atg cca ata 451
Gly Glu Gly Ala Val Tyr Phe Gln Val His Ser Gly Arg Met Pro Ile
105 110 115

ctg cgt aac gag gct cag gct gag cgc aag gct cct cgt tac acc gag 499
Leu Arg Asn Glu Ala Gln Ala Glu Arg Lys Ala Pro Arg Tyr Thr Glu
120 125 130

gca cag acc ctt gcg atc gct gca tat gtt gca gct aat ggc ggt ggc 547
Ala Gln Thr Leu Ala Ile Ala Ala Tyr Val Ala Ala Asn Gly Gly Gly
135 140 145

cca gga ctc gtt tac aac gag gac ggc acc ctc gcc atg gag gag ctc 595
Pro Gly Leu Val Tyr Asn Glu Asp Gly Thr Leu Ala Met Glu Glu Leu
150 155 160 165

cgt ggc gaa aac tac gac gga cag att acc tcc gcc gac gtc gct cgc 643
Arg Gly Glu Asn Tyr Asp Gly Gln Ile Thr Ser Ala Asp Val Ala Arg
170 175 180

ggc gga gat ctg ttc cgc ctg aac tgt gca tcc tgc cac aac ttc act 691
Gly Gly Asp Leu Phe Arg Leu Asn Cys Ala Ser Cys His Asn Phe Thr
185 190 195

ggg cgt ggt ggc gca ctg tcc tct ggt aag tac gca cca aac ctg gat 739
Gly Arg Gly Gly Ala Leu Ser Ser Gly Lys Tyr Ala Pro Asn Leu Asp
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gct gca aac gag cag gaa atc tac cag gct atg ctt acc ggt cct cag 787

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Ala Ala Asn Glu Gln Glu Ile Tyr Gln Ala Met Leu Thr Gly Pro Gln
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aac atg cct aag ttc tcc gat cgt cag ctc tcc gca gat gag aag aag 835
 Asn Met Pro Lys Phe Ser Asp Arg Gln Leu Ser Ala Asp Glu Lys Lys
 230 235 240 245

gac atc atc gcc ttc atc aag tcc acc aag gag act cca tca cct ggt 883
 Asp Ile Ile Ala Phe Ile Lys Ser Thr Lys Glu Thr Pro Ser Pro Gly
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ggt tac tca ctc ggt agc ttg ggc cca gtg gct gag ggt ctg ttc atg 931
 Gly Tyr Ser Leu Gly Ser Leu Gly Pro Val Ala Glu Gly Leu Phe Met
 265 270 275

tgg gta ttc ggc atc ttg gtc ctc gtg gcc gcc gct atg tgg att gga 979
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 Ser Arg Ser
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<210> 744
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 <213> Corynebacterium glutamicum

<400> 744
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Ala Gly Ala Leu Ala Leu Thr Ile Gly Leu Ser Gly Ala Gly Ile Leu
 35 40 45

Ala Thr Ala Ile Thr Pro Asp Ala Gln Val Ala Thr Ala Gln Arg Asp
 50 55 60

Asp Gln Ala Leu Ile Ser Glu Gly Lys Asp Leu Tyr Asp Val Ala Cys
 65 70 75 80

Ile Thr Cys His Gly Val Asn Leu Gln Gly Val Glu Asp Arg Gly Pro
 85 90 95

Ser Leu Val Gly Val Gly Glu Gly Ala Val Tyr Phe Gln Val His Ser
 100 105 110

Gly Arg Met Pro Ile Leu Arg Asn Glu Ala Gln Ala Glu Arg Lys Ala
 115 120 125

Pro Arg Tyr Thr Glu Ala Gln Thr Leu Ala Ile Ala Ala Tyr Val Ala
 130 135 140

Ala Asn Gly Gly Gly Pro Gly Leu Val Tyr Asn Glu Asp Gly Thr Leu
 145 150 155 160

Ala Met Glu Glu Leu Arg Gly Glu Asn Tyr Asp Gly Gln Ile Thr Ser

165					170					175					
Ala	Asp	Val	Ala	Arg	Gly	Gly	Asp	Leu	Phe	Arg	Leu	Asn	Cys	Ala	Ser
			180					185					190		
Cys	His	Asn	Phe	Thr	Gly	Arg	Gly	Gly	Ala	Leu	Ser	Ser	Gly	Lys	Tyr
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Leu	Thr	Gly	Pro	Gln	Asn	Met	Pro	Lys	Phe	Ser	Asp	Arg	Gln	Leu	Ser
225						230					235				240
Ala	Asp	Glu	Lys	Lys	Asp	Ile	Ile	Ala	Phe	Ile	Lys	Ser	Thr	Lys	Glu
				245					250					255	
Thr	Pro	Ser	Pro	Gly	Gly	Tyr	Ser	Leu	Gly	Ser	Leu	Gly	Pro	Val	Ala
			260					265					270		
Glu	Gly	Leu	Phe	Met	Trp	Val	Phe	Gly	Ile	Leu	Val	Leu	Val	Ala	Ala
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Ala	Met	Trp	Ile	Gly	Ser	Arg	Ser								
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 <212> DNA
 <213> Corynebacterium glutamicum

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 <222> (101)..(502)
 <223> RXN03096

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 Met Val Leu Val Trp
 1 5
 tcc aag gcc ttc tgg cgc gac cgt aaa gac gcc ccc gat gga gca acc 163
 Ser Lys Ala Phe Trp Arg Asp Arg Lys Asp Ala Pro Asp Gly Ala Thr
 10 15 20
 gca cta gca aga ccc gca cct ttg gta gat atc caa gac gaa gtc gcc 211
 Ala Leu Ala Arg Pro Ala Pro Leu Val Asp Ile Gln Asp Glu Val Ala
 25 30 35
 gtt aaa gac cgc aac gat gtc gga cgg atg cct tgg ggc atg gtc ttc 259
 Val Lys Asp Arg Asn Asp Val Gly Arg Met Pro Trp Gly Met Val Phe
 40 45 50
 tcc act gcc ctg ttg gtt tcc gca tcc ctt gct gta tcc gtg ctc gca 307
 Ser Thr Ala Leu Leu Val Ser Ala Ser Leu Ala Val Ser Val Leu Ala
 55 60 65
 gga cca ctg tca tct att act gga cgc gcc gcc gaa tcc gca caa gat 355

Gly Pro Leu Ser Ser Ile Thr Gly Arg Ala Ala Glu Ser Ala Gln Asp
 70 75 80 85
 gtc aac atc tac cgc gcc gca gta ctc ggc cca act acc tcg acc cat 403
 Val Asn Ile Tyr Arg Ala Ala Val Leu Gly Pro Thr Thr Ser Thr His
 90 95 100
 cac gca cac tcg aga tgg agc gtt acg acg cca acc gcg atg aca tca 451
 His Ala His Ser Arg Trp Ser Val Thr Thr Pro Thr Ala Met Thr Ser
 105 110 115
 acc acc gcg tcg aca cca atg gaa cgg agg acc aac cat gat cag tgg 499
 Thr Thr Ala Ser Thr Pro Met Glu Arg Arg Thr Asn His Asp Gln Trp
 120 125 130
 att 502
 Ile

<210> 746
 <211> 134
 <212> PRT
 <213> *Corynebacterium glutamicum*

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 35 40 45
 Trp Gly Met Val Phe Ser Thr Ala Leu Leu Val Ser Ala Ser Leu Ala
 50 55 60
 Val Ser Val Leu Ala Gly Pro Leu Ser Ser Ile Thr Gly Arg Ala Ala
 65 70 75 80
 Glu Ser Ala Gln Asp Val Asn Ile Tyr Arg Ala Ala Val Leu Gly Pro
 85 90 95
 Thr Thr Ser Thr His His Ala His Ser Arg Trp Ser Val Thr Thr Pro
 100 105 110
 Thr Ala Met Thr Ser Thr Thr Ala Ser Thr Pro Met Glu Arg Arg Thr
 115 120 125
 Asn His Asp Gln Trp Ile
 130

<210> 747
 <211> 504
 <212> DNA
 <213> *Corynebacterium glutamicum*

<220>
 <221> CDS

<222> (101)..(481)

<223> RXN02036

<400> 747

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 Val His Ile Pro Phe
 1 5

ggg cac ctc gcc gac acc gtc tcc tgg gac tgc ggg gga ggc agc tgc 163
 Gly His Leu Ala Asp Thr Val Ser Trp Asp Cys Gly Gly Gly Ser Cys
 10 15 20

gcc acc aac gat ttg gta tcc ctg ttc atg ccg gcc gcc ttc atg agt 211
 Ala Thr Asn Asp Leu Val Ser Leu Phe Met Pro Ala Ala Phe Met Ser
 25 30 35

acc ctc gcc gcc tgc gta ttt ggc gcg tgg gcc ata ggt ttg atc gct 259
 Thr Leu Ala Ala Cys Val Phe Gly Ala Trp Ala Ile Gly Leu Ile Ala
 40 45 50

ccc gca cta ttc atc gcg gtg act gcc tgg gca ttt cgc tcc ggc gtg 307
 Pro Ala Leu Phe Ile Ala Val Thr Ala Trp Ala Phe Arg Ser Gly Val
 55 60 65

cag gct gcg att gcc gac ggc tac acg tcc gcg act tcc gtc ggc ttc 355
 Gln Ala Ala Ile Ala Asp Gly Tyr Thr Ser Ala Thr Ser Val Gly Phe
 70 75 80 85

gaa atg act gtc tcg ctc att ctt ttc atc atc gca ggt ctg tgc ttt 403
 Glu Met Thr Val Ser Leu Ile Leu Phe Ile Ile Ala Gly Leu Cys Phe
 90 95 100

ctg ggc tgg atc ccc atg ttc atc aac aac cgc caa gtc gcg cgc aag 451
 Leu Gly Trp Ile Pro Met Phe Ile Asn Asn Arg Gln Val Ala Arg Lys
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ttt 504

<210> 748

<211> 127

<212> PRT

<213> Corynebacterium glutamicum

<400> 748

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 20 25 30

Ala Ala Phe Met Ser Thr Leu Ala Ala Cys Val Phe Gly Ala Trp Ala
 35 40 45

Ile Gly Leu Ile Ala Pro Ala Leu Phe Ile Ala Val Thr Ala Trp Ala

1064

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 Gly Arg Ile Gly Glu Leu Leu Glu Pro Ile Asn Arg Val Asn Gln Val
 135 140 145
 ggt cat gcg gat atg ttg gcg aca acg ctg tat gcg gga act cag cca 595
 Gly His Ala Asp Met Leu Ala Thr Thr Leu Tyr Ala Gly Thr Gln Pro
 150 155 160 165
 cct gca gtg acg gat ttg gtg cca gtg ctg cgt ccg cat ggt ttc act 643
 Pro Ala Val Thr Asp Leu Val Pro Val Leu Arg Pro His Gly Phe Thr
 170 175 180
 gcg gca ttg gtg atc gtt gat ggg ttg ctg ctg ggt gcg gtt gat gag 691
 Ala Ala Leu Val Ile Val Asp Gly Leu Leu Leu Gly Ala Val Asp Glu
 185 190 195
 gga att ctg cgg agg ttt tcg cat ttg ccg gaa att gag cag ctg gtt 739
 Gly Ile Leu Arg Arg Phe Ser His Leu Pro Glu Ile Glu Gln Leu Val
 200 205 210
 ttg agg gca ttt ttg ttc cgt cga aac ttg cag gag ttc tct gag aac 787
 Leu Arg Ala Phe Leu Phe Arg Arg Asn Leu Gln Phe Ser Glu Asn
 215 220 225
 aac gat ccg aat gtt att tcg aac cta aac agg gtg gaa tcg aca ctc 835
 Asn Asp Pro Asn Val Ile Ser Asn Leu Asn Arg Val Glu Ser Thr Leu
 230 235 240 245
 gtg tcg tat gtt tct gac aag att tgaggtatgt cggaatacaa acc 882
 Val Ser Tyr Val Ser Asp Lys Ile
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<210> 750

<211> 253

<212> PRT

<213> Corynebacterium glutamicum

<400> 750

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 35 40 45
 Trp Ser Ser Lys Thr Arg Glu Thr Leu Lys Pro Glu Gly Val Arg Val
 50 55 60
 Val Arg Pro Ile Arg Ser Thr Asp Gly Arg Phe Val Val Ala Gly Trp
 65 70 75 80
 Arg Ala Ser Val Phe Ser Thr Gly Thr Ile Ser Lys Arg Val Asp Glu
 85 90 95
 Thr Val Val Ala Gly Leu Arg Leu Ala Asp Ala Leu Val Asp Thr His

100					105					110					
Ala	Pro	Glu	Pro	Val	Asp	Asn	Val	Phe	Asn	Arg	Ala	Asp	Val	Gln	Ala
		115					120					125			
Trp	Glu	Glu	Gln	Pro	Gly	Arg	Ile	Gly	Glu	Leu	Leu	Glu	Pro	Ile	Asn
	130					135					140				
Arg	Val	Asn	Gln	Val	Gly	His	Ala	Asp	Met	Leu	Ala	Thr	Thr	Leu	Tyr
145					150					155					160
Ala	Gly	Thr	Gln	Pro	Pro	Ala	Val	Thr	Asp	Leu	Val	Pro	Val	Leu	Arg
				165					170					175	
Pro	His	Gly	Phe	Thr	Ala	Ala	Leu	Val	Ile	Val	Asp	Gly	Leu	Leu	Leu
			180					185					190		
Gly	Ala	Val	Asp	Glu	Gly	Ile	Leu	Arg	Arg	Phe	Ser	His	Leu	Pro	Glu
	195						200					205			
Ile	Glu	Gln	Leu	Val	Leu	Arg	Ala	Phe	Leu	Phe	Arg	Arg	Asn	Leu	Gln
	210					215					220				
Glu	Phe	Ser	Glu	Asn	Asn	Asp	Pro	Asn	Val	Ile	Ser	Asn	Leu	Asn	Arg
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Val	Glu	Ser	Thr	Leu	Val	Ser	Tyr	Val	Ser	Asp	Lys	Ile			
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<211> 1059

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1036)

<223> RXN02206

<400> 751

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                                     Met Val Gly Ser Ser
                                     1 5

ggt ttg cgg gta tcc agg ctc ggt ttg ggc acc tca aca tgg ggc tcg 163
Gly Leu Arg Val Ser Arg Leu Gly Leu Gly Thr Ser Thr Trp Gly Ser
                                     10 15 20

ggc acc gag ctg gct gag gca ggc gat atc ttt aag gcg ttc atc aat 211
Gly Thr Glu Leu Ala Glu Ala Gly Asp Ile Phe Lys Ala Phe Ile Asn
                                     25 30 35

tct ggt ggc acg ctt atc gac gtc tcc ccc aac tac acc acc ggc gtc 259
Ser Gly Gly Thr Leu Ile Asp Val Ser Pro Asn Tyr Thr Thr Gly Val
                                     40 45 50

gcg gaa gaa atg ctc ggc acg atg ttg gat gcg gaa gtc tct cgt tcg 307
Ala Glu Glu Met Leu Gly Thr Met Leu Asp Ala Glu Val Ser Arg Ser

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ggc cga cgt gtg gat tgc tcc cgc cgc aat ttg att gcc caa tta gat Gly Arg Arg Val Asp Cys Ser Arg Arg Asn Leu Ile Ala Gln Leu Asp 90 95 100			403
gtc acc ctg cgg gca tta aac act gac tat ttg gat ttg tgg tct gtg Val Thr Leu Arg Ala Leu Asn Thr Asp Tyr Leu Asp Leu Trp Ser Val 105 110 115			451
ggc tat tgg gat gag ggc acc cca ccg cat gag gtg gcc gat act ttg Gly Tyr Trp Asp Glu Gly Thr Pro Pro His Glu Val Ala Asp Thr Leu 120 125 130			499
gat tac gcc gtg cgc acc ggc cga gtc cga tat gcc ggt gtc cga gga Asp Tyr Ala Val Arg Thr Gly Arg Val Arg Tyr Ala Gly Val Arg Gly 135 140 145			547
tat tcc ggt tgg cag tta gcg gtc acc cac gct gca tcc aat cat gca Tyr Ser Gly Trp Gln Leu Ala Val Thr His Ala Ala Ser Asn His Ala 150 155 160 165			595
gcg gcc tcc gcc cgc ccc gtg gtc gtt gca caa aat gaa tac agc ctg Ala Ala Ser Ala Arg Pro Val Val Val Ala Gln Asn Glu Tyr Ser Leu 170 175 180			643
ctg gaa cgc cgc gca gaa caa gaa ctc ctc cct gcc acc caa cac cta Leu Glu Arg Arg Ala Glu Gln Glu Leu Leu Pro Ala Thr Gln His Leu 185 190 195			691
ggt gtc gga ttc ttt gct ggc gct ccg ctg ggg caa ggc gtg ctg act Gly Val Gly Phe Phe Ala Gly Ala Pro Leu Gly Gln Gly Val Leu Thr 200 205 210			739
gct aaa tac cgc tcc gaa att ccc cat gat tcc aga gct gca tcc aca Ala Lys Tyr Arg Ser Glu Ile Pro His Asp Ser Arg Ala Ala Ser Thr 215 220 225			787
gga cgc gac gca gaa gtc caa agc tac cta gat aat cga ggc cgc atc Gly Arg Asp Ala Glu Val Gln Ser Tyr Leu Asp Asn Arg Gly Arg Ile 230 235 240 245			835
att gtc gat gct ctt gat act gca gcc aaa gga tta ggc att agc ccc Ile Val Asp Ala Leu Asp Thr Ala Ala Lys Gly Leu Gly Ile Ser Pro 250 255 260			883
gct gtc aca gcc acc acc tgg gtg cgt gat cgt ccc gga gtg aca gct Ala Val Thr Ala Thr Thr Trp Val Arg Asp Arg Pro Gly Val Thr Ala 265 270 275			931
gtc atc gtg ggc gct cgc aca cat gaa cag ctg tca cat ctt ctc aag Val Ile Val Gly Ala Arg Thr His Glu Gln Leu Ser His Leu Leu Lys 280 285 290			979
gcg gaa tcg gtg act ttg cca aca cca atc aca caa gcc ctt gat gat Ala Glu Ser Val Thr Leu Pro Thr Pro Ile Thr Gln Ala Leu Asp Asp 295 300 305			1027

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1059

<210> 752
 <211> 312
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 752
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 Lys Ala Phe Ile Asn Ser Gly Gly Thr Leu Ile Asp Val Ser Pro Asn
 35 40 45
 Tyr Thr Thr Gly Val Ala Glu Glu Met Leu Gly Thr Met Leu Asp Ala
 50 55 60
 Glu Val Ser Arg Ser Ala Val Val Ile Ser Ser Ser Ala Gly Val Asn
 65 70 75 80
 Pro Ala Leu Pro Leu Gly Arg Arg Val Asp Cys Ser Arg Arg Asn Leu
 85 90 95
 Ile Ala Gln Leu Asp Val Thr Leu Arg Ala Leu Asn Thr Asp Tyr Leu
 100 105 110
 Asp Leu Trp Ser Val Gly Tyr Trp Asp Glu Gly Thr Pro Pro His Glu
 115 120 125
 Val Ala Asp Thr Leu Asp Tyr Ala Val Arg Thr Gly Arg Val Arg Tyr
 130 135 140
 Ala Gly Val Arg Gly Tyr Ser Gly Trp Gln Leu Ala Val Thr His Ala
 145 150 155 160
 Ala Ser Asn His Ala Ala Ala Ser Ala Arg Pro Val Val Val Ala Gln
 165 170 175
 Asn Glu Tyr Ser Leu Leu Glu Arg Arg Ala Glu Gln Glu Leu Leu Pro
 180 185 190
 Ala Thr Gln His Leu Gly Val Gly Phe Phe Ala Gly Ala Pro Leu Gly
 195 200 205
 Gln Gly Val Leu Thr Ala Lys Tyr Arg Ser Glu Ile Pro His Asp Ser
 210 215 220
 Arg Ala Ala Ser Thr Gly Arg Asp Ala Glu Val Gln Ser Tyr Leu Asp
 225 230 235 240
 Asn Arg Gly Arg Ile Ile Val Asp Ala Leu Asp Thr Ala Ala Lys Gly
 245 250 255
 Leu Gly Ile Ser Pro Ala Val Thr Ala Thr Thr Trp Val Arg Asp Arg

1069

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 Ile Gly Tyr His Glu Ile Glu Gln Asp Ala Gly Thr Gly Arg Ala Ile
 135 140 145

gcg tat gcc acg gat gat gtg gat gca ggt gcc cag gtt gca cag cta 595
 Ala Tyr Ala Thr Asp Asp Val Asp Ala Gly Ala Gln Val Ala Gln Leu
 150 155 160 165

att aag agt ttt ggg ttt gtt cct tta aat att ggc gca ttg gaa aac 643
 Ile Lys Ser Phe Gly Phe Val Pro Leu Asn Ile Gly Ala Leu Glu Asn
 170 175 180

ggc cgt att ctg gaa cct ggc caa gaa gct ttc ggc gcg cac ctt aat 691
 Gly Arg Ile Leu Glu Pro Gly Gln Glu Ala Phe Gly Ala His Leu Asn
 185 190 195

aaa gat tcg cgc cta gaa ctt gtt aat cag cgg tagtacctcg atcttcagcc 744
 Lys Asp Ser Arg Leu Glu Leu Val Asn Gln Arg
 200 205

aac 747

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 <212> PRT
 <213> Corynebacterium glutamicum

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Val Ala Gly Ser Gly Ala Val Asp Lys Ile Ala Leu Thr Ala Glu Ile
 35 40 45

Leu Met Pro Gly Ala Val Pro Ser Thr Ala Asp Gln Ala Val Lys Asp
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Ala Asp Ile Val Phe Leu Ala Val Pro Leu His Lys Phe Arg Ser Val
 65 70 75 80

Asn Pro Ala Thr Leu Glu Gly Lys Ile Val Ile Asp Thr Met Asn His
 85 90 95

Trp Val Pro Val Asn Gly Glu Leu Glu Glu Ile Asp Gln Asp Pro Arg
 100 105 110

Ser Thr Ser Glu Ile Ile Ala Glu Phe Phe Ala Gly Ser Thr Met Val
 115 120 125

Lys Ser Phe Asn His Ile Gly Tyr His Glu Ile Glu Gln Asp Ala Gly
 130 135 140

Thr Gly Arg Ala Ile Ala Tyr Ala Thr Asp Asp Val Asp Ala Gly Ala
 145 150 155 160

Gln Val Ala Gln Leu Ile Lys Ser Phe Gly Phe Val Pro Leu Asn Ile
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<210> 755
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 <212> DNA
 <213> Corynebacterium glutamicum

<220>
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 <222> (101)..(910)
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 Met Lys Gly Glu Phe
 1 5

cac gcc ccc gat ttg gac aaa gaa ttt ttc ccg ggg cac gta acc gat 163
 His Ala Pro Asp Leu Asp Lys Glu Phe Phe Pro Gly His Val Thr Asp
 10 15 20

agt ggt gaa gtc gtg aac atg ctg ttc acc gat ttc gct aat ggt tgg 211
 Ser Gly Glu Val Val Asn Met Leu Phe Thr Asp Phe Ala Asn Gly Trp
 25 30 35

ttc gca atg gac cgc atc gta ttg atc cgt ctt ctt atg acg gca gtc 259
 Phe Ala Met Asp Arg Ile Val Leu Ile Arg Leu Leu Met Thr Ala Val
 40 45 50

gtt gtg gtc ttc ttc ctt tgg gct atg cgc aag cca aag ctt gtt ccg 307
 Val Val Val Phe Phe Leu Trp Ala Met Arg Lys Pro Lys Leu Val Pro
 55 60 65

cat ggc gtc cag aat ttt gca gag tac gca ctc gat ttc gtt ggt att 355
 His Gly Val Gln Asn Phe Ala Glu Tyr Ala Leu Asp Phe Val Gly Ile
 70 75 80 85

cac atc gct gaa gac atc ctc gga aag aag aaa ggt cgt cgg ttc ctg 403
 His Ile Ala Glu Asp Ile Leu Gly Lys Lys Lys Gly Arg Arg Phe Leu
 90 95 100

ccg atc ctg gcc acc atc ttc ttc gcg gct ctg ttg atg aac ctt gca 451
 Pro Ile Leu Ala Thr Ile Phe Phe Ala Ala Leu Leu Met Asn Leu Ala
 105 110 115

acg atc atc ccg gga cta aac atc tcc tcc aac tca cgt att gca ttc 499
 Thr Ile Ile Pro Gly Leu Asn Ile Ser Ser Asn Ser Arg Ile Ala Phe
 120 125 130

cca atc gtg atg gcg gta gct ggt tac atc gcg ttt atc tac gca ggc 547

Pro Ile Val Met Ala Val Ala Gly Tyr Ile Ala Phe Ile Tyr Ala Gly
 135 140 145

tct aag cgt tac gga ttc ttc aaa tat gtg aag tct tct gtt gtg att 595
 Ser Lys Arg Tyr Gly Phe Phe Lys Tyr Val Lys Ser Ser Val Val Ile
 150 155 160 165

cgc aac att cca cca gca ctt cac gtc ttg gtg gtt cca att gag ttc 643
 Pro Asn Ile Pro Ala Leu His Val Leu Val Val Pro Ile Glu Phe
 170 175 180

ttc tct aca ttc atc ttg agg cca gtc acc ctg gca ctg cgt ttg atg 691
 Phe Ser Thr Phe Ile Leu Arg Pro Val Thr Leu Ala Leu Arg Leu Met
 185 190 195

gcc aac ttc ctt gct ggc cac atc atc ctg gtt ctg ctt ttc tcc gca 739
 Ala Asn Phe Leu Ala Gly His Ile Ile Leu Val Leu Leu Phe Ser Ala
 200 205 210

acg aac ttc ttc ttc ttc cag ttc aac gga tgg aca gca atg tcc ggc 787
 Thr Asn Phe Phe Phe Phe Gln Phe Asn Gly Trp Thr Ala Met Ser Gly
 215 220 225

gta acc atc ttg atg gca gta ctc ttc acg gtt tac gag atc att gtt 835
 Val Thr Ile Leu Met Ala Val Leu Phe Thr Val Tyr Glu Ile Ile Val
 230 235 240 245

atc ttc ctg cag gca tac atc ttc gct ctg ctg gtc gct gta tac att 883
 Ile Phe Leu Gln Ala Tyr Ile Phe Ala Leu Leu Val Ala Val Tyr Ile
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gag ctt tca ctt cac gcg gat tct cac tagatgaaaa aggtcgctat 930
 Glu Leu Ser Leu His Ala Asp Ser His
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taa 933

<210> 756

<211> 270

<212> PRT

<213> Corynebacterium glutamicum

<400> 756

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 35 40 45

Leu Met Thr Ala Val Val Val Val Phe Phe Leu Trp Ala Met Arg Lys
 50 55 60

Pro Lys Leu Val Pro His Gly Val Gln Asn Phe Ala Glu Tyr Ala Leu
 65 70 75 80

Asp Phe Val Gly Ile His Ile Ala Glu Asp Ile Leu Gly Lys Lys Lys
 85 90 95

Gly Arg Arg Phe Leu Pro Ile Leu Ala Thr Ile Phe Phe Ala Ala Leu
 100 105 110
 Leu Met Asn Leu Ala Thr Ile Ile Pro Gly Leu Asn Ile Ser Ser Asn
 115 120 125
 Ser Arg Ile Ala Phe Pro Ile Val Met Ala Val Ala Gly Tyr Ile Ala
 130 135 140
 Phe Ile Tyr Ala Gly Ser Lys Arg Tyr Gly Phe Phe Lys Tyr Val Lys
 145 150 155 160
 Ser Ser Val Val Ile Pro Asn Ile Pro Pro Ala Leu His Val Leu Val
 165 170 175
 Val Pro Ile Glu Phe Phe Ser Thr Phe Ile Leu Arg Pro Val Thr Leu
 180 185 190
 Ala Leu Arg Leu Met Ala Asn Phe Leu Ala Gly His Ile Ile Leu Val
 195 200 205
 Leu Leu Phe Ser Ala Thr Asn Phe Phe Phe Phe Gln Phe Asn Gly Trp
 210 215 220
 Thr Ala Met Ser Gly Val Thr Ile Leu Met Ala Val Leu Phe Thr Val
 225 230 235 240
 Tyr Glu Ile Ile Val Ile Phe Leu Gln Ala Tyr Ile Phe Ala Leu Leu
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 Val Ala Val Tyr Ile Glu Leu Ser Leu His Ala Asp Ser His
 260 265 270

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 <212> DNA
 <213> Corynebacterium glutamicum

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 <223> FRXA01204

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 Met Lys Gly Glu Phe
 1 5

cac gcc ccc gat ttg gac aaa gaa ttt ttc ccg ggg cac gta acc gat 163
 His Ala Pro Asp Leu Asp Lys Glu Phe Phe Pro Gly His Val Thr Asp
 10 15 20

agt ggt gaa gtc gtg aac atg ctg ttc acc gat ttc gct aat ggt tgg 211
 Ser Gly Glu Val Val Asn Met Leu Phe Thr Asp Phe Ala Asn Gly Trp
 25 30 35

ttc gca atg gac cgc atc gta ttg atc cgt ctt ctt atg acg gca gtc 259

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gtt	gtg	gtc	ttc	ttc	ctt	tgg	gct	atg	cgc	aag	cca	aag	ctt	gtt	ccg	307	
Val	Val	Val	Phe	Phe	Leu	Trp	Ala	Met	Arg	Lys	Pro	Lys	Leu	Val	Pro		
	55					60					65						
cat	ggc	gtc	cag	aat	ttt	gca	gag	tac	gca	ctc	gat	ttc	gtt	ggg	att	355	
His	Gly	Val	Gln	Asn	Phe	Ala	Glu	Tyr	Ala	Leu	Asp	Phe	Val	Gly	Ile		
	70				75					80					85		
cac	atc	gct	gaa	gac	atc	ctc	gga	aag	aag	aaa	ggg	cgt	cgg	ttc	ctg	403	
His	Ile	Ala	Glu	Asp	Ile	Leu	Gly	Lys	Lys	Lys	Gly	Arg	Arg	Phe	Leu		
				90					95					100			
ccg	atc	ctg	gcc	acc	atc	ttc	ttc	gcg	gct	ctg	ttg	atg	aac	ctt	gca	451	
Pro	Ile	Leu	Ala	Thr	Ile	Phe	Phe	Ala	Ala	Leu	Leu	Met	Asn	Leu	Ala		
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Thr	Ile	Ile	Pro	Gly	Leu	Asn	Ile	Ser	Ser	Asn	Ser	Arg	Ile	Ala	Phe		
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cca	atc	gtg	atg	gcg	gta	gct	ggg	tac	atc	gcg	ttt	atc	tac	gca	ggc	547	
Pro	Ile	Val	Met	Ala	Val	Ala	Gly	Tyr	Ile	Ala	Phe	Ile	Tyr	Ala	Gly		
	135					140					145						
tct	aag	cgt	tac	gga	ttc	ttc	aaa	tat	gtg	aag	tct	tct	gtt	gtg	att	595	
Ser	Lys	Arg	Tyr	Gly	Phe	Phe	Lys	Tyr	Val	Lys	Ser	Ser	Val	Val	Ile		
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ccg	aac	att	cca	cca	gca	ctt	cac	gtc	ttg	gtg	gtt	cca	att	gag	ttc	643	
Pro	Asn	Ile	Pro	Pro	Ala	Leu	His	Val	Leu	Val	Val	Pro	Ile	Glu	Phe		
				170					175					180			
ttc	tct	aca	ttc	atc	ttg	agg	cca	gtc	acc	ctg	gca	ctg	cgt	ttg	atg	691	
Phe	Ser	Thr	Phe	Ile	Leu	Arg	Pro	Val	Thr	Leu	Ala	Leu	Arg	Leu	Met		
			185					190					195				
gcc	aac	ttc	ctt	gct	ggc	cac	atc	atc	ctg	gtt	ctg	ctt	ttc	ttc	gca	739	
Ala	Asn	Phe	Leu	Ala	Gly	His	Ile	Ile	Leu	Val	Leu	Leu	Phe	Phe	Ala		
	200					205						210					
acg	aac	ttc	ttc	ttc	ttc	cag	ttc	aac	gga	tgg	aca	gca	atg	tcc	ggc	787	
Thr	Asn	Phe	Phe	Phe	Phe	Gln	Phe	Asn	Gly	Trp	Thr	Ala	Met	Ser	Gly		
	215					220					225						
gta	acc	atc	ttg	atg	gca	gta	ctc	ttc	acg	gtt	tac	gag	atc	att	gtt	835	
Val	Thr	Ile	Leu	Met	Ala	Val	Leu	Phe	Thr	Val	Tyr	Glu	Ile	Ile	Val		
	230				235					240					245		
atc	ttc	ctg	cag	gca	tac	atc	ttc	gct								862	
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<210> 758

<211> 254

<212> PRT

<213> Corynebacterium glutamicum

<400> 758

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Phe Ala Asn Gly Trp Phe Ala Met Asp Arg Ile Val Leu Ile Arg Leu
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Leu Met Thr Ala Val Val Val Val Phe Phe Leu Trp Ala Met Arg Lys
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Pro Lys Leu Val Pro His Gly Val Gln Asn Phe Ala Glu Tyr Ala Leu
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Asp Phe Val Gly Ile His Ile Ala Glu Asp Ile Leu Gly Lys Lys Lys
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Gly Arg Arg Phe Leu Pro Ile Leu Ala Thr Ile Phe Phe Ala Ala Leu
          100          105          110

Leu Met Asn Leu Ala Thr Ile Ile Pro Gly Leu Asn Ile Ser Ser Asn
          115          120          125

Ser Arg Ile Ala Phe Pro Ile Val Met Ala Val Ala Gly Tyr Ile Ala
          130          135          140

Phe Ile Tyr Ala Gly Ser Lys Arg Tyr Gly Phe Phe Lys Tyr Val Lys
          145          150          155          160

Ser Ser Val Val Ile Pro Asn Ile Pro Pro Ala Leu His Val Leu Val
          165          170          175

Val Pro Ile Glu Phe Phe Ser Thr Phe Ile Leu Arg Pro Val Thr Leu
          180          185          190

Ala Leu Arg Leu Met Ala Asn Phe Leu Ala Gly His Ile Ile Leu Val
          195          200          205

Leu Leu Phe Phe Ala Thr Asn Phe Phe Phe Phe Gln Phe Asn Gly Trp
          210          215          220

Thr Ala Met Ser Gly Val Thr Ile Leu Met Ala Val Leu Phe Thr Val
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Tyr Glu Ile Ile Val Ile Phe Leu Gln Ala Tyr Ile Phe Ala
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<211> 1764

<212> DNA

<213> Corynebacterium glutamicum

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<221> CDS

<222> (101)..(1741)

<223> RXA01201

<400> 759

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                                     Met Ala Glu Leu Thr
                                     1 5
atc tcc tcc gat gag atc cgt agc gcg att gcg aac tac acc tcg agc 163
Ile Ser Ser Asp Glu Ile Arg Ser Ala Ile Ala Asn Tyr Thr Ser Ser
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Tyr Ser Ala Glu Ala Ser Arg Glu Glu Val Gly Val Val Ile Ser Ala
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gct gac ggt atc gcc cag gtt tcg ggc ctc ccg tca gta atg gcg aat 259
Ala Asp Gly Ile Ala Gln Val Ser Gly Leu Pro Ser Val Met Ala Asn
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Glu Leu Leu Glu Phe Pro Gly Gly Val Ile Gly Val Ala Gln Asn Leu
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gaa gct gac cga gtc ggc gtc gtg gtc ctg ggt aac tac gag cta ctt 355
Glu Ala Asp Arg Val Gly Val Val Val Leu Gly Asn Tyr Glu Leu Leu
          70          75          80          85
aaa gaa ggc gac caa gtt cgt cgt act gga gac gtt ctg tct atc cca 403
Lys Glu Gly Asp Gln Val Arg Arg Thr Gly Asp Val Leu Ser Ile Pro
          90          95          100
gtc ggc gag gca ttc ctt ggc cgc gtt atc aac ccc ctt ggc cag cca 451
Val Gly Glu Ala Phe Leu Gly Arg Val Ile Asn Pro Leu Gly Gln Pro
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Ile Asp Gly Leu Gly Glu Ile Ala Ser Glu Glu Asp Arg Val Leu Glu
          120          125          130
ctt cag gca cca acc gtg ctt gag cgc cag cct gtc gag gag cct ttg 547
Leu Gln Ala Pro Thr Val Leu Glu Arg Gln Pro Val Glu Glu Pro Leu
          135          140          145
gca acc ggc atc aag gct atc gat gca atg acc cca atc ggc cgc ggt 595
Ala Thr Gly Ile Lys Ala Ile Asp Ala Met Thr Pro Ile Gly Arg Gly
          150          155          160          165
cag cgt cag ctg atc att ggt gac cgt aag act ggc aag acc gca gtc 643
Gln Arg Gln Leu Ile Ile Gly Asp Arg Lys Thr Gly Lys Thr Ala Val
          170          175          180
tgt gtc gat acc atc ctt aac cag aag gcc aac tgg gag acc ggc gac 691
Cys Val Asp Thr Ile Leu Asn Gln Lys Ala Asn Trp Glu Thr Gly Asp
          185          190          195
aag acc aag cag gtt cgc tgc atc tac gtc gca atc ggt cag aag ggc 739
Lys Thr Lys Gln Val Arg Cys Ile Tyr Val Ala Ile Gly Gln Lys Gly
          200          205          210
tcc acc att gca gcc ctg cgt aag acc ctc gag gag cag ggc gct ctc 787
Ser Thr Ile Ala Ala Leu Arg Lys Thr Leu Glu Glu Gln Gly Ala Leu
          215          220          225

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Lys Trp Leu Ala Pro Phe Ala Gly Ala Ala Leu Ala Gln His Trp Met	
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tac cag ggc aac cac gtc ctg gtc atc tac gat gat ctg acc aag cag	931
Tyr Gln Gly Asn His Val Leu Val Ile Tyr Asp Asp Leu Thr Lys Gln	
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gct gag gca tac cgt gct atc tcc ctg ctg ctg cgt cgc cca ccg ggc	979
Ala Glu Ala Tyr Arg Ala Ile Ser Leu Leu Leu Arg Arg Pro Pro Gly	
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cgc gaa gca tac cca ggt gac gtc ttc tac ctg cac tcc cgt ctg ctg	1027
Arg Glu Ala Tyr Pro Gly Asp Val Phe Tyr Leu His Ser Arg Leu Leu	
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gag cgc gct gcg aag ctg tcc gat gaa cta ggc gca ggt tct att aca	1075
Glu Arg Ala Ala Lys Leu Ser Asp Glu Leu Gly Ala Gly Ser Ile Thr	
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Ala Leu Pro Ile Ile Glu Thr Lys Ala Asn Asp Val Ser Ala Phe Ile	
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cct acc aac gtg att tcc atc acc gac ggt cag gta ttc ctt gag tcc	1171
Pro Thr Asn Val Ile Ser Ile Thr Asp Gly Gln Val Phe Leu Glu Ser	
345 350 355	
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Asp Leu Phe Asn Arg Gly Val Arg Pro Ala Ile Asn Val Gly Val Ser	
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gtc tcc cgt gtc ggt ggc gca gct cag acc aag ggt atg aag aag gtt	1267
Val Ser Arg Val Gly Gly Ala Ala Gln Thr Lys Gly Met Lys Lys Val	
375 380 385	
gcc ggt tct ctc cgt ctg gat ctg gct gca ttc cgc gac ctg gaa gca	1315
Ala Gly Ser Leu Arg Leu Asp Leu Ala Ala Phe Arg Asp Leu Glu Ala	
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Phe Ala Thr Phe Ala Ser Asp Leu Asp Ala Ala Ser Lys Ser Gln Leu	
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Glu Arg Gly Gln Arg Leu Val Gln Leu Ile Gln Ser Glu Asn Ala	
425 430 435	
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Pro Gln Ala Val Glu Tyr Gln Ile Ile Ser Leu Trp Leu Ala Gly Glu	
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Gly Ala Phe Asp Asn Val Pro Val Glu Asp Val Arg Arg Phe Glu Ser	
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 Glu Leu His Glu Tyr Leu Gly Ser Asn Ala Ala Gln Val Tyr Glu Gln
 470 475 480 485
 atc gct ggt gga gct cag ctt tcc gac gag tcc aag gaa acc ttg ctc 1603
 Ile Ala Gly Gly Ala Gln Leu Ser Asp Glu Ser Lys Glu Thr Leu Leu
 490 495 500
 aag gca acc gaa gat ttc aag agc gct ttc cag acc acc gat ggc acc 1651
 Lys Ala Thr Glu Asp Phe Lys Ser Ala Phe Gln Thr Thr Asp Gly Thr
 505 510 515
 cct gtc atc aac gag cct gag gtt gaa gca ctc gat gca ggc cag gtc 1699
 Pro Val Ile Asn Glu Pro Glu Val Glu Ala Leu Asp Ala Gly Gln Val
 520 525 530
 aag aaa gac cag ctc acc gtt tcc cgc aag gtc agc aag aag 1741
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 taaggcagcg agcctacact aaa 1764

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 <212> PRT
 <213> Corynebacterium glutamicum

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 35 40 45
 Ser Val Met Ala Asn Glu Leu Leu Glu Phe Pro Gly Gly Val Ile Gly
 50 55 60
 Val Ala Gln Asn Leu Glu Ala Asp Arg Val Gly Val Val Val Leu Gly
 65 70 75 80
 Asn Tyr Glu Leu Leu Lys Glu Gly Asp Gln Val Arg Arg Thr Gly Asp
 85 90 95
 Val Leu Ser Ile Pro Val Gly Glu Ala Phe Leu Gly Arg Val Ile Asn
 100 105 110
 Pro Leu Gly Gln Pro Ile Asp Gly Leu Gly Glu Ile Ala Ser Glu Glu
 115 120 125
 Asp Arg Val Leu Glu Leu Gln Ala Pro Thr Val Leu Glu Arg Gln Pro
 130 135 140
 Val Glu Glu Pro Leu Ala Thr Gly Ile Lys Ala Ile Asp Ala Met Thr
 145 150 155 160
 Pro Ile Gly Arg Gly Gln Arg Gln Leu Ile Ile Gly Asp Arg Lys Thr
 165 170 175

Gly Lys Thr Ala Val Cys Val Asp Thr Ile Leu Asn Gln Lys Ala Asn
 180 185 190
 Trp Glu Thr Gly Asp Lys Thr Lys Gln Val Arg Cys Ile Tyr Val Ala
 195 200 205
 Ile Gly Gln Lys Gly Ser Thr Ile Ala Ala Leu Arg Lys Thr Leu Glu
 210 215 220
 Glu Gln Gly Ala Leu Glu Tyr Thr Thr Ile Val Ala Ala Pro Ala Ser
 225 230 235 240
 Asp Ala Ala Gly Phe Lys Trp Leu Ala Pro Phe Ala Gly Ala Ala Leu
 245 250 255
 Ala Gln His Trp Met Tyr Gln Gly Asn His Val Leu Val Ile Tyr Asp
 260 265 270
 Asp Leu Thr Lys Gln Ala Glu Ala Tyr Arg Ala Ile Ser Leu Leu Leu
 275 280 285
 Arg Arg Pro Pro Gly Arg Glu Ala Tyr Pro Gly Asp Val Phe Tyr Leu
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 His Ser Arg Leu Leu Glu Arg Ala Ala Lys Leu Ser Asp Glu Leu Gly
 305 310 315 320
 Ala Gly Ser Ile Thr Ala Leu Pro Ile Ile Glu Thr Lys Ala Asn Asp
 325 330 335
 Val Ser Ala Phe Ile Pro Thr Asn Val Ile Ser Ile Thr Asp Gly Gln
 340 345 350
 Val Phe Leu Glu Ser Asp Leu Phe Asn Arg Gly Val Arg Pro Ala Ile
 355 360 365
 Asn Val Gly Val Ser Val Ser Arg Val Gly Gly Ala Ala Gln Thr Lys
 370 375 380
 Gly Met Lys Lys Val Ala Gly Ser Leu Arg Leu Asp Leu Ala Ala Phe
 385 390 395 400
 Arg Asp Leu Glu Ala Phe Ala Thr Phe Ala Ser Asp Leu Asp Ala Ala
 405 410 415
 Ser Lys Ser Gln Leu Glu Arg Gly Gln Arg Leu Val Gln Leu Leu Ile
 420 425 430
 Gln Ser Glu Asn Ala Pro Gln Ala Val Glu Tyr Gln Ile Ile Ser Leu
 435 440 445
 Trp Leu Ala Gly Glu Gly Ala Phe Asp Asn Val Pro Val Glu Asp Val
 450 455 460
 Arg Arg Phe Glu Ser Glu Leu His Glu Tyr Leu Gly Ser Asn Ala Ala
 465 470 475 480
 Gln Val Tyr Glu Gln Ile Ala Gly Gly Ala Gln Leu Ser Asp Glu Ser
 485 490 495

Lys Glu Thr Leu Leu Lys Ala Thr Glu Asp Phe Lys Ser Ala Phe Gln
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Ser Lys Lys
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 <223> RXN01193

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 Met Thr Thr Ala Leu
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 Glu Glu Gln Asn Ala Gln Gln Ala Ala Thr Ala Gly Arg Val Val Arg
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gtc att ggt gcg gtc gtc gac gtg gag ttt ccc cgc ggc gag ctg cca 211
 Val Ile Gly Ala Val Val Asp Val Glu Phe Pro Arg Gly Glu Leu Pro
 25 30 35

gca ctg tac aac gca ctt act gta gag gta acc ctc gaa tca gtt aag 259
 Ala Leu Tyr Asn Ala Leu Thr Val Glu Val Thr Leu Glu Ser Val Lys
 40 45 50

aag acc gtt gtt ctc gag gtt gct cag cac ctc ggc gac aac ctc atc 307
 Lys Thr Val Val Leu Glu Val Ala Gln His Leu Gly Asp Asn Leu Ile
 55 60 65

cgc acc atc gct atg gca cca acc gac gga ctt gtc cgc ggt gct gct 355
 Arg Thr Ile Ala Met Ala Pro Thr Asp Gly Leu Val Arg Gly Ala Ala
 70 75 80 85

gta acc gat act gca cgc cca att tcc gta cca gtg ggc gat gtt gtt 403
 Val Thr Asp Thr Ala Arg Pro Ile Ser Val Pro Val Gly Asp Val Val
 90 95 100

aag ggc cac gta ttc aac gct ttg ggc gac tgc cta gac gac gtt tcc 451
 Lys Gly His Val Phe Asn Ala Leu Gly Asp Cys Leu Asp Asp Val Ser
 105 110 115

ctg aac aac aac cca gag atc gag cgt tgg ggc atc cac cgc gag cca 499
 Leu Asn Asn Asn Pro Glu Ile Glu Arg Trp Gly Ile His Arg Glu Pro
 120 125 130

cca tca ttc gat cag ctt gag ggt aag acc gag atc ctg gaa aca ggc	547
Pro Ser Phe Asp Gln Leu Glu Gly Lys Thr Glu Ile Leu Glu Thr Gly	
135 140 145	
atc aag gtt atc gac ctt ctc acc cct tac gtt aag ggt gga aag atc	595
Ile Lys Val Ile Asp Leu Leu Thr Pro Tyr Val Lys Gly Gly Lys Ile	
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Gly Leu Phe Gly Gly Ala Gly Val Gly Lys Thr Val Leu Ile Gln Glu	
170 175 180	
atg atc acc cgt att gca cgt gag ttc tcc ggt act tcc gtg ttc gca	691
Met Ile Thr Arg Ile Ala Arg Glu Phe Ser Gly Thr Ser Val Phe Ala	
185 190 195	
ggt gtt ggt gag cgt acc cgt gag ggc acc gac ctc ttc ctc gaa atg	739
Gly Val Gly Glu Arg Thr Arg Glu Gly Thr Asp Leu Phe Leu Glu Met	
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gaa gaa atg ggc gtt ctc cag gac acc gcc ctg gtg ttc ggt cag atg	787
Glu Glu Met Gly Val Leu Gln Asp Thr Ala Leu Val Phe Gly Gln Met	
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Asp Glu Pro Pro Gly Val Gly Met Arg Val Ala Leu Ser Gly Leu Thr	
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Met Ala Glu Tyr Phe Arg Asp Val Gln Asn Gln Asp Val Leu Leu Phe	
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Ile Asp Asn Ile Phe Arg Phe Thr Gln Ala Gly Ser Glu Val Ser Thr	
265 270 275	
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Asp Glu Met Gly Val Leu Gln Glu Arg Ile Thr Ser Thr Lys Gly Arg	
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Asp Pro Ala Pro Ala Thr Thr Phe Ala His Leu Asp Ala Thr Thr Glu	
330 335 340	
ctt gac cgc tcc att gct tcc aag ggt att tac cca gca gtg aac cca	1171
Leu Asp Arg Ser Ile Ala Ser Lys Gly Ile Tyr Pro Ala Val Asn Pro	
345 350 355	
ctg acc tcc acc tct cgt att ctc gag cca gca atc gtt ggt gag cgt	1219
Leu Thr Ser Thr Ser Arg Ile Leu Glu Pro Ala Ile Val Gly Glu Arg	
360 365 370	

cac tac gag gtt tct cag cgt gtc atc ggc att ctg cag aag aac aag 1267
 His Tyr Glu Val Ser Gln Arg Val Ile Gly Ile Leu Gln Lys Asn Lys
 375 380 385

gaa ctt cag gac atc atc gcc atc ctt ggt atg gac gag ctt tct gaa 1315
 Glu Leu Gln Asp Ile Ile Ala Ile Leu Gly Met Asp Glu Leu Ser Glu
 390 395 400 405

gag gac aag atc acc gtt gca cgt gcg cgt cgc atc gag cgc ttc ctg 1363
 Glu Asp Lys Ile Thr Val Ala Arg Ala Arg Arg Ile Glu Arg Phe Leu
 410 415 420

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 Gly Gln Asn Phe Phe Val Ala Glu Lys Phe Thr Gly Leu Pro Gly Ser
 425 430 435

tac gtg cca ctg acc gac acc gtc gac gct ttc gag cgt att tgc aac 1459
 Tyr Val Pro Leu Thr Asp Thr Val Asp Ala Phe Glu Arg Ile Cys Asn
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 Gly Asp Phe Asp His Tyr Pro Glu Gln Ala Phe Asn Gly Leu Gly Gly
 455 460 465

ttg gac gat gtc gaa gct gca tac aag aag ctg acc gga aag 1549
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<211> 483

<212> PRT

<213> Corynebacterium glutamicum

<400> 762

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Arg Gly Glu Leu Pro Ala Leu Tyr Asn Ala Leu Thr Val Glu Val Thr
 35 40 45

Leu Glu Ser Val Lys Lys Thr Val Val Leu Glu Val Ala Gln His Leu
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Gly Asp Asn Leu Ile Arg Thr Ile Ala Met Ala Pro Thr Asp Gly Leu
 65 70 75 80

Val Arg Gly Ala Ala Val Thr Asp Thr Ala Arg Pro Ile Ser Val Pro
 85 90 95

Val Gly Asp Val Val Lys Gly His Val Phe Asn Ala Leu Gly Asp Cys
 100 105 110

Leu Asp Asp Val Ser Leu Asn Asn Asn Pro Glu Ile Glu Arg Trp Gly
 115 120 125

Ile His Arg Glu Pro Pro Ser Phe Asp Gln Leu Glu Gly Lys Thr Glu
 130 135 140
 Ile Leu Glu Thr Gly Ile Lys Val Ile Asp Leu Leu Thr Pro Tyr Val
 145 150 155 160
 Lys Gly Gly Lys Ile Gly Leu Phe Gly Gly Ala Gly Val Gly Lys Thr
 165 170 175
 Val Leu Ile Gln Glu Met Ile Thr Arg Ile Ala Arg Glu Phe Ser Gly
 180 185 190
 Thr Ser Val Phe Ala Gly Val Gly Glu Arg Thr Arg Glu Gly Thr Asp
 195 200 205
 Leu Phe Leu Glu Met Glu Glu Met Gly Val Leu Gln Asp Thr Ala Leu
 210 215 220
 Val Phe Gly Gln Met Asp Glu Pro Pro Gly Val Gly Met Arg Val Ala
 225 230 235 240
 Leu Ser Gly Leu Thr Met Ala Glu Tyr Phe Arg Asp Val Gln Asn Gln
 245 250 255
 Asp Val Leu Leu Phe Ile Asp Asn Ile Phe Arg Phe Thr Gln Ala Gly
 260 265 270
 Ser Glu Val Ser Thr Leu Leu Gly Arg Met Pro Ser Ala Val Gly Tyr
 275 280 285
 Gln Pro Thr Leu Ala Asp Glu Met Gly Val Leu Gln Glu Arg Ile Thr
 290 295 300
 Ser Thr Lys Gly Arg Ser Ile Thr Ser Leu Gln Ala Val Tyr Val Pro
 305 310 315 320
 Ala Asp Asp Tyr Thr Asp Pro Ala Pro Ala Thr Thr Phe Ala His Leu
 325 330 335
 Asp Ala Thr Thr Glu Leu Asp Arg Ser Ile Ala Ser Lys Gly Ile Tyr
 340 345 350
 Pro Ala Val Asn Pro Leu Thr Ser Thr Ser Arg Ile Leu Glu Pro Ala
 355 360 365
 Ile Val Gly Glu Arg His Tyr Glu Val Ser Gln Arg Val Ile Gly Ile
 370 375 380
 Leu Gln Lys Asn Lys Glu Leu Gln Asp Ile Ile Ala Ile Leu Gly Met
 385 390 395 400
 Asp Glu Leu Ser Glu Glu Asp Lys Ile Thr Val Ala Arg Ala Arg Arg
 405 410 415
 Ile Glu Arg Phe Leu Gly Gln Asn Phe Phe Val Ala Glu Lys Phe Thr
 420 425 430
 Gly Leu Pro Gly Ser Tyr Val Pro Leu Thr Asp Thr Val Asp Ala Phe
 435 440 445
 Glu Arg Ile Cys Asn Gly Asp Phe Asp His Tyr Pro Glu Gln Ala Phe

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Thr Gly Lys

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 <222> (15)..(755)
 <223> FRXA01193

<400> 763

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 Tyr Phe Arg Asp Val Gln Asn Gln Asp Val Leu Leu Phe Ile Asp Asn
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atc ttc cgt ttc acc cag gca ggt tct gag gtt tcc acc ctt ctg ggt 146
 Ile Phe Arg Phe Thr Gln Ala Gly Ser Glu Val Ser Thr Leu Leu Gly
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cgt atg cct tcc gcc gtg ggt tac cag cca acc ctg gct gac gag atg 194
 Arg Met Pro Ser Ala Val Gly Tyr Gln Pro Thr Leu Ala Asp Glu Met
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ggt gtt ctc cag gag cgc att acc tcc acc aag ggc cgt tcg att acc 242
 Gly Val Leu Gln Glu Arg Ile Thr Ser Thr Lys Gly Arg Ser Ile Thr
 65 70 75

tct ctg cag gcc gtt tac gtt cct gcc gat gac tac acc gac ccg gct 290
 Ser Leu Gln Ala Val Tyr Val Pro Ala Asp Asp Tyr Thr Asp Pro Ala
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cca gcg acc acc ttc gct cac ttg gat gca acc acc gag ctt gac cgc 338
 Pro Ala Thr Thr Phe Ala His Leu Asp Ala Thr Thr Glu Leu Asp Arg
 95 100 105

tcc att gct tcc aag ggt att tac cca gca gtg aac cca ctg acc tcc 386
 Ser Ile Ala Ser Lys Gly Ile Tyr Pro Ala Val Asn Pro Leu Thr Ser
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acc tct cgt att ctc gag cca gca atc gtt ggt gag cgt cac tac gag 434
 Thr Ser Arg Ile Leu Glu Pro Ala Ile Val Gly Glu Arg His Tyr Glu
 125 130 135 140

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 Val Ser Gln Arg Val Ile Gly Ile Leu Gln Lys Asn Lys Glu Leu Gln
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gac atc atc gcc atc ctt ggt atg gac gag ctt tct gaa gag gac aag 530

Asp Ile Ile Ala Ile Leu Gly Met Asp Glu Leu Ser Glu Glu Asp Lys
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 Ile Thr Val Ala Arg Ala Arg Arg Ile Glu Arg Phe Leu Gly Gln Asn
 175 180 185
 ttc ttc gtt gca gag aag ttc acc ggt ctt cct ggc tcc tac gtg cca 626
 Phe Phe Val Ala Glu Lys Phe Thr Gly Leu Pro Gly Ser Tyr Val Pro
 190 195 200
 ctg acc gac acc gtc gac gct ttc gag cgt att tgc aac ggc gac ttc 674
 Leu Thr Asp Thr Val Asp Ala Phe Glu Arg Ile Cys Asn Gly Asp Phe
 205 210 215 220
 gac cac tac cca gag cag gct ttc aac ggc ctc ggt ggt ttg gac gat 722
 Asp His Tyr Pro Glu Gln Ala Phe Asn Gly Leu Gly Gly Leu Asp Asp
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 gtc gaa gct gca tac aag aag ctg acc gga aag taaggtagag acacatggct 775
 Val Glu Ala Ala Tyr Lys Lys Leu Thr Gly Lys
 240 245
 gaa 778

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 <212> PRT
 <213> Corynebacterium glutamicum

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 Thr Gln Ala Gly Ser Glu Val Ser Thr Leu Leu Gly Arg Met Pro Ser
 35 40 45
 Ala Val Gly Tyr Gln Pro Thr Leu Ala Asp Glu Met Gly Val Leu Gln
 50 55 60
 Glu Arg Ile Thr Ser Thr Lys Gly Arg Ser Ile Thr Ser Leu Gln Ala
 65 70 75 80
 Val Tyr Val Pro Ala Asp Asp Tyr Thr Asp Pro Ala Pro Ala Thr Thr
 85 90 95
 Phe Ala His Leu Asp Ala Thr Thr Glu Leu Asp Arg Ser Ile Ala Ser
 100 105 110
 Lys Gly Ile Tyr Pro Ala Val Asn Pro Leu Thr Ser Thr Ser Arg Ile
 115 120 125
 Leu Glu Pro Ala Ile Val Gly Glu Arg His Tyr Glu Val Ser Gln Arg
 130 135 140
 Val Ile Gly Ile Leu Gln Lys Asn Lys Glu Leu Gln Asp Ile Ile Ala
 145 150 155 160

Ile Leu Gly Met Asp Glu Leu Ser Glu Glu Asp Lys Ile Thr Val Ala
 165 170 175

Arg Ala Arg Arg Ile Glu Arg Phe Leu Gly Gln Asn Phe Phe Val Ala
 180 185 190

Glu Lys Phe Thr Gly Leu Pro Gly Ser Tyr Val Pro Leu Thr Asp Thr
 195 200 205

Val Asp Ala Phe Glu Arg Ile Cys Asn Gly Asp Phe Asp His Tyr Pro
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Tyr Lys Lys Leu Thr Gly Lys
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 <212> DNA
 <213> Corynebacterium glutamicum

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 Met Thr Thr Ala Leu
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gaa gag cag aac gca cag cag gca gcc act gcc ggc cgt gtc gtg cgt 163
 Glu Glu Gln Asn Ala Gln Gln Ala Ala Thr Ala Gly Arg Val Val Arg
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gtc att ggt gcg gtc gtc gac gtg gag ttt ccc cgc ggc gag ctg cca 211
 Val Ile Gly Ala Val Val Asp Val Glu Phe Pro Arg Gly Glu Leu Pro
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gca ctg tac aac gca ctt act gta gag gta acc ctc gaa tca gtt aag 259
 Ala Leu Tyr Asn Ala Leu Thr Val Glu Val Thr Leu Glu Ser Val Lys
 40 45 50

aag acc gtt gtt ctc gag gtt gct cag cac ctc ggc gac aac ctc atc 307
 Lys Thr Val Val Leu Glu Val Ala Gln His Leu Gly Asp Asn Leu Ile
 55 60 65

cgc acc atc gct atg gca cca acc gac gga ctt gtc cgc ggt gct gct 355
 Arg Thr Ile Ala Met Ala Pro Thr Asp Gly Leu Val Arg Gly Ala Ala
 70 75 80 85

gta acc gat act gca cgc cca att tcc gta cca gtg ggc gat gtt gtt 403
 Val Thr Asp Thr Ala Arg Pro Il Ser Val Pro Val Gly Asp Val Val
 90 95 100

aag ggc cac gta ttc aac gct ttg ggc gac tgc cta gac gac gtt tcc 451
 Lys Gly His Val Phe Asn Ala Leu Gly Asp Cys Leu Asp Asp Val Ser
 105 110 115

 ctg aac aac aac cca gag atc gag cgt tgg ggc atc cac cgc gag cca 499
 Leu Asn Asn Asn Pro Glu Ile Glu Arg Trp Gly Ile His Arg Glu Pro
 120 125 130

 cca tca ttc gat cag ctt gag ggt aag acc gag atc ctg gaa aca ggc 547
 Pro Ser Phe Asp Gln Leu Glu Gly Lys Thr Glu Ile Leu Glu Thr Gly
 135 140 145

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 Ile Lys Val Ile Asp Leu Leu Thr Pro Tyr Val Lys Gly Gly Lys Ile
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 ggc ctc ttc ggt ggt gca ggt gtg ggt aag acc gtt ctt atc cag gaa 643
 Gly Leu Phe Gly Gly Ala Gly Val Gly Lys Thr Val Leu Ile Gln Glu
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 atg atc acc cgt att gca cgt gag ttc tcc ggt act tcc gtg ttc gca 691
 Met Ile Thr Arg Ile Ala Arg Glu Phe Ser Gly Thr Ser Val Phe Ala
 185 190 195

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<210> 766

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<212> PRT

<213> Corynebacterium glutamicum

<400> 766

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 Leu Glu Ser Val Lys Lys Thr Val Val Leu Glu Val Ala Gln His Leu
 50 55 60

 Gly Asp Asn Leu Ile Arg Thr Ile Ala Met Ala Pro Thr Asp Gly Leu
 65 70 75 80

 Val Arg Gly Ala Ala Val Thr Asp Thr Ala Arg Pro Ile Ser Val Pro
 85 90 95

 Val Gly Asp Val Val Lys Gly His Val Phe Asn Ala Leu Gly Asp Cys
 100 105 110

 Leu Asp Asp Val Ser Leu Asn Asn Asn Pro Glu Ile Glu Arg Trp Gly
 115 120 125

 Ile His Arg Glu Pro Pro Ser Phe Asp Gln Leu Glu Gly Lys Thr Glu
 130 135 140

Ile Leu Glu Thr Gly Ile Lys Val Ile Asp Leu Leu Thr Pro Tyr Val
 145 150 155 160

Lys Gly Gly Lys Ile Gly Leu Phe Gly Gly Ala Gly Val Gly Lys Thr
 165 170 175

Val Leu Ile Gln Glu Met Ile Thr Arg Ile Ala Arg Glu Phe Ser Gly
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Thr Ser Val Phe Ala Gly Val Gly Lys Arg Thr Arg Glu Gly Thr Asp
 195 200 205

Leu Phe Leu Glu Met
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 <212> DNA
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 <223> RXN02821

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 Met Asn Glu Ile Ile
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ctg gca cag gac gca acc gag tcc acc atc acc gga ctt ggc gct gtc 163
 Leu Ala Gln Asp Ala Thr Glu Ser Thr Ile Thr Gly Leu Gly Ala Val
 10 15 20

ggc tac ggc atc gca acc atc gga cct ggc ctc ggc atc ggc atc ctg 211
 Gly Tyr Gly Ile Ala Thr Ile Gly Pro Gly Leu Gly Ile Gly Ile Leu
 25 30 35

gtt ggt aag gct ctc gag ggt atg gca cgt cag cct gag atg gct gga 259
 Val Gly Lys Ala Leu Glu Gly Met Ala Arg Gln Pro Glu Met Ala Gly
 40 45 50

cag ctc cgt acc acc atg ttc ctg ggc atc gcc ttc gtt gag gcc ctg 307
 Gln Leu Arg Thr Thr Met Phe Leu Gly Ile Ala Phe Val Glu Ala Leu
 55 60 65

gca ctg atc ggc ctt gtt gct ggc ttc ctg ttc taatcagcta acttaaccga 360
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 <212> PRT
 <213> Corynebacterium glutamicum

<400> 768

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 35 40 45

Pro Glu Met Ala Gly Gln Leu Arg Thr Thr Met Phe Leu Gly Ile Ala
 50 55 60

Phe Val Glu Ala Leu Ala Leu Ile Gly Leu Val Ala Gly Phe Leu Phe
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<212> DNA

<213> Corynebacterium glutamicum

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<223> FRXA02821

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 Val Gly Tyr Gly Ile
 1 5

gca acc atc gga cct ggc ctc ggc atc ggc atc ttg gtt ggt aag gct 163
 Ala Thr Ile Gly Pro Gly Leu Gly Ile Gly Ile Leu Val Gly Lys Ala
 10 15 20

ctc gag ggt atg gca cgt cag cct gag atg gct gga cag ctc cgt acc 211
 Leu Glu Gly Met Ala Arg Gln Pro Glu Met Ala Gly Gln Leu Arg Thr
 25 30 35

acc atg ttc ctg ggc atc gcc ttc gtt gag gcc ctg gca ctg atc ggc 259
 Thr Met Phe Leu Gly Ile Ala Phe Val Glu Ala Leu Ala Leu Ile Gly
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<212> PRT

<213> Corynebacterium glutamicum

<400> 770

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 35 40 45
 Leu Ala Leu Ile Gly Leu Val Ala Gly Phe Leu Phe
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 <212> DNA
 <213> *Corynebacterium glutamicum*

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 <222> (1)..(609)
 <223> RXA01200

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 Asp Ala Ala Glu Gln Thr Trp Ser Thr Pro Arg Glu Phe Arg Ala Gly
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 cta gtc caa ctt ggc cgt cgc gcc ctt ctt cgc tct gcg gag aaa cag 144
 Leu Val Gln Leu Gly Arg Arg Ala Leu Leu Arg Ser Ala Glu Lys Gln
 35 40 45
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 Gly Gln Leu Gly Gln Val Glu Asp Glu Leu Phe Arg Leu Ser Arg Ile
 50 55 60
 ctg gat cgc gaa agc aag ctg act cag ctt ctt tca gat cgc act cag 240
 Leu Asp Arg Glu Ser Lys Leu Thr Gln Leu Leu Ser Asp Arg Thr Gln
 65 70 75 80
 gaa att ggc ggt cga cgt gac ctc ctg gct aag gtg ctc tac ggc aag 288
 Glu Ile Gly Gly Arg Arg Asp Leu Leu Ala Lys Val Leu Tyr Gly Lys
 85 90 95
 gta act gct gtt acc gaa gcc ctc gca ctg cag gct att ggt cgc cct 336
 Val Thr Ala Val Thr Glu Ala Leu Ala Leu Gln Ala Ile Gly Arg Pro
 100 105 110
 gag cac aac cca att gac gat atc gca gct ttg gct ggc gct gta gca 384
 Glu His Asn Pro Ile Asp Asp Ile Ala Ala Leu Ala Gly Ala Val Ala
 115 120 125
 gag cta cag ggt cgt tcc gtt gca cat gtc gtt acc gca gtt gaa ctc 432
 Glu Leu Gln Gly Arg Ser Val Ala His Val Val Thr Ala Val Glu Leu
 130 135 140
 aac gag gga cag caa caa gcg cta gct gaa aag ctg gga cgt att tat 480

Asn Glu Gly Gln Gln Gln Ala Leu Ala Glu Lys Leu Gly Arg Ile Tyr
 145 150 155 160
 ggt cgt gcg atg agc atc cac tcc gag gtt gat acc agc ctc ctc ggt 528
 Gly Arg Ala Met Ser Ile His Ser Glu Val Asp Thr Ser Leu Leu Gly
 165 170 175
 gga atg atc atc cgc gtc gga gac gaa gta att gac ggc agc acc tcg 576
 Gly Met Ile Ile Arg Val Gly Asp Glu Val Ile Asp Gly Ser Thr Ser
 180 185 190
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 Gly Lys Leu Glu Arg Leu Arg Ala Ser Phe Ala
 195 200
 caa 632

<210> 772
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 <212> PRT
 <213> Corynebacterium glutamicum

<400> 772
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 35 40 45
 Gly Gln Leu Gly Gln Val Glu Asp Glu Leu Phe Arg Leu Ser Arg Ile
 50 55 60
 Leu Asp Arg Glu Ser Lys Leu Thr Gln Leu Leu Ser Asp Arg Thr Gln
 65 70 75 80
 Glu Ile Gly Gly Arg Arg Asp Leu Leu Ala Lys Val Leu Tyr Gly Lys
 85 90 95
 Val Thr Ala Val Thr Glu Ala Leu Ala Leu Gln Ala Ile Gly Arg Pro
 100 105 110
 Glu His Asn Pro Ile Asp Asp Ile Ala Ala Leu Ala Gly Ala Val Ala
 115 120 125
 Glu Leu Gln Gly Arg Ser Val Ala His Val Val Thr Ala Val Glu Leu
 130 135 140
 Asn Glu Gly Gln Gln Gln Ala Leu Ala Glu Lys Leu Gly Arg Ile Tyr
 145 150 155 160
 Gly Arg Ala Met Ser Ile His Ser Glu Val Asp Thr Ser Leu Leu Gly
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Met Ala Glu Ile Thr																115
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Val Glu Leu Val Ser Val Glu Arg Met Leu Trp Ala Gly Gln Ala Ser																
10 15 20																
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Ile Val Thr Ala Gln Thr Thr Glu Gly Glu Ile Gly Val Leu Pro Asp																
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cac gag cct ctt ctc ggc caa ttg gtt gag aac ggt gtc gtg acc atc																259
His Glu Pro Leu Leu Gly Gln Leu Val Glu Asn Gly Val Val Thr Ile																
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Gln Pro Ile Asp Gly Glu Lys Leu Ile Ala Gly Val Ser Asp Gly Phe																
55 60 65																
ctc tcc gta tct aag gaa aag gtg acg atc ctc gcg gac ttc gcc gtc																355
Leu Ser Val Ser Lys Glu Lys Val Thr Ile Leu Ala Asp Phe Ala Val																
70 75 80 85																
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Trp Ala Asn Glu Val Asp Thr Ala Ser Ala Glu Ala Asp Leu Asn Ser																
90 95 100																
gac gac gag ctg gcc aag gca cac gcc gag gct ggg ctg cgc gcg gtc																451
Asp Asp Glu Leu Ala Lys Ala His Ala Glu Ala Gly Leu Arg Ala Val																
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<212> PRT
<213> Corynebacterium glutamicum
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				1													5	
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Glu	Leu	Arg	Asp	Arg	Ile	Arg	Ser	Val	Asn	Ser	Thr	Lys	Lys	Ile	Thr			
				10											15	20		
aag	gct	caa	gag	ctc	atc	gcc	acc	tct	cgc	atc	acc	aag	gca	cag	ggt	211		
Lys	Ala	Gln	Glu	Leu	Ile	Ala	Thr	Ser	Arg	Ile	Thr	Lys	Ala	Gln	Gly			
				25											30	35		
cgc	gtc	gcg	gca	gct	gcg	ccg	tac	gcc	gag	gaa	atc	cag	cgc	gtg	ctg	259		
Arg	Val	Ala	Ala	Ala	Ala	Pro	Tyr	Ala	Glu	Glu	Ile	Gln	Arg	Val	Leu			
				40											45	50		
gag	cgc	ctc	gcg	tcg	gca	agc	tcc	cta	gac	cac	cca	atg	ctg	cgt	gag	307		
Glu	Arg	Leu	Ala	Ser	Ala	Ser	Ser	Leu	Asp	His	Pro	Met	Leu	Arg	Glu			
				55											60	65		
cgt	gaa	ggc	ggc	aag	cga	gcc	gcc	gtg	ctc	gtg	ggt	act	tct	gac	cgc	355		
Arg	Glu	Gly	Gly	Lys	Arg	Ala	Ala	Val	Leu	Val	Val	Thr	Ser	Asp	Arg			
				70											75	80		
ggc	atg	gct	ggt	ggc	tac	aac	cac	aac	ggt	ctg	aaa	aag	gca	gcg	gag	403		

Gly	Met	Ala	Gly	Gly	Tyr	Asn	His	Asn	Val	Leu	Lys	Lys	Ala	Ala	Glu		
				90					95						100		
ctg	gaa	aag	ctt	ctt	gct	gaa	agt	gga	tac	gaa	gtg	gtt	cgt	tat	gtc	451	
Leu	Glu	Lys	Leu	Leu	Ala	Glu	Ser	Gly	Tyr	Glu	Val	Val	Arg	Tyr	Val		
			105					110					115				
acc	ggc	aaa	aag	ggc	gtc	gac	tac	tac	aag	ttc	cgc	gct	gaa	gat	gtg	499	
Thr	Gly	Lys	Lys	Gly	Val	Asp	Tyr	Tyr	Lys	Phe	Arg	Ala	Glu	Asp	Val		
		120					125					130					
gct	ggc	acc	tgg	act	gga	ttc	tca	cag	gat	cca	gac	tgg	gca	gct	acc	547	
Ala	Gly	Thr	Trp	Thr	Gly	Phe	Ser	Gln	Asp	Pro	Asp	Trp	Ala	Ala	Thr		
		135				140					145						
cac	aac	gtg	cgc	cgt	cac	ctc	att	gat	ggc	ttc	acc	gcc	agc	tct	gaa	595	
His	Asn	Val	Arg	Arg	His	Leu	Ile	Asp	Gly	Phe	Thr	Ala	Ser	Ser	Glu		
150					155					160					165		
ggc	gaa	gct	gca	tgg	cgc	gag	gga	ctg	aac	cta	cca	gaa	ggc	cag	gat	643	
Gly	Glu	Ala	Ala	Trp	Arg	Glu	Gly	Leu	Asn	Leu	Pro	Glu	Gly	Gln	Asp		
				170				175						180			
atc	cag	ggc	ttc	gac	cag	gtt	cac	gtg	gtc	tac	acc	gag	ttc	atc	tcc	691	
Ile	Gln	Gly	Phe	Asp	Gln	Val	His	Val	Val	Tyr	Thr	Glu	Phe	Ile	Ser		
			185					190					195				
atg	ctg	act	caa	aac	cca	gta	gtg	cac	caa	ctg	ctg	cct	gtt	gag	cca	739	
Met	Leu	Thr	Gln	Asn	Pro	Val	Val	His	Gln	Leu	Leu	Pro	Val	Glu	Pro		
		200					205					210					
gtc	atc	gaa	gat	gaa	att	ttc	gaa	aaa	ggc	gag	gat	ctg	ctg	tcc	tct	787	
Val	Ile	Glu	Asp	Glu	Ile	Phe	Glu	Lys	Gly	Glu	Asp	Leu	Leu	Ser	Ser		
		215				220					225						
tcc	ggc	gaa	gtc	gaa	ccc	gac	tac	gag	ttc	gag	ccg	gat	gca	gac	act	835	
Ser	Gly	Glu	Val	Glu	Pro	Asp	Tyr	Glu	Phe	Glu	Pro	Asp	Ala	Asp	Thr		
230					235				240						245		
ctg	ctt	gag	gca	ctg	ctt	ccg	cag	tac	gtc	tct	cgt	agg	ctg	ttc	tcc	883	
Leu	Leu	Glu	Ala	Leu	Leu	Pro	Gln	Tyr	Val	Ser	Arg	Arg	Leu	Phe	Ser		
				250					255					260			
atc	ttc	ttg	gag	gct	gca	gct	gca	gag	tcc	gct	tca	cgt	cga	aac	gcg	931	
Ile	Phe	Leu	Glu	Ala	Ala	Ala	Ala	Glu	Ser	Ala	Ser	Arg	Arg	Asn	Ala		
			265					270					275				
atg	aag	tct	gcg	act	gac	aac	gct	acg	gaa	ctg	gtc	aag	gac	ctg	tcc	979	
Met	Lys	Ser	Ala	Thr	Asp	Asn	Ala	Thr	Glu	Leu	Val	Lys	Asp	Leu	Ser		
		280					285					290					
cgt	gtg	gcc	aac	cag	gca	cgt	cag	gca	cag	atc	acc	cag	gaa	atc	aca	1027	
Arg	Val	Ala	Asn	Gln	Ala	Arg	Gln	Ala	Gln	Ile	Thr	Gln	Glu	Ile	Thr		
		295				300					305						
gag	att	gtt	ggc	gca	ggc	gcg	ctc	gcc	gac	agc	gga	gaa	agt	gac		1075	
Glu	Ile	Val	Gly	Gly	Ala	Gly	Ala	Leu	Ala	Asp	Ser	Gly	Glu	Ser	Asp		
310					315				320						325		
taattatgac	tacagctctt	gaa														1098	

<210> 776

<211> 325

<212> PRT

<213> Corynebacterium glutamicum

<400> 776

Met Ala Thr Ile Arg Glu Leu Arg Asp Arg Ile Arg Ser Val Asn Ser
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Thr Lys Lys Ile Thr Lys Ala Gln Glu Leu Ile Ala Thr Ser Arg Ile
 20 25 30

Thr Lys Ala Gln Gly Arg Val Ala Ala Ala Ala Pro Tyr Ala Glu Glu
 35 40 45

Ile Gln Arg Val Leu Glu Arg Leu Ala Ser Ala Ser Ser Leu Asp His
 50 55 60

Pro Met Leu Arg Glu Arg Glu Gly Gly Lys Arg Ala Ala Val Leu Val
 65 70 75 80

Val Thr Ser Asp Arg Gly Met Ala Gly Gly Tyr Asn His Asn Val Leu
 85 90 95

Lys Lys Ala Ala Glu Leu Glu Lys Leu Leu Ala Glu Ser Gly Tyr Glu
 100 105 110

Val Val Arg Tyr Val Thr Gly Lys Lys Gly Val Asp Tyr Tyr Lys Phe
 115 120 125

Arg Ala Glu Asp Val Ala Gly Thr Trp Thr Gly Phe Ser Gln Asp Pro
 130 135 140

Asp Trp Ala Ala Thr His Asn Val Arg Arg His Leu Ile Asp Gly Phe
 145 150 155 160

Thr Ala Ser Ser Glu Gly Glu Ala Ala Trp Arg Glu Gly Leu Asn Leu
 165 170 175

Pro Glu Gly Gln Asp Ile Gln Gly Phe Asp Gln Val His Val Val Tyr
 180 185 190

Thr Glu Phe Ile Ser Met Leu Thr Gln Asn Pro Val Val His Gln Leu
 195 200 205

Leu Pro Val Glu Pro Val Ile Glu Asp Glu Ile Phe Glu Lys Gly Glu
 210 215 220

Asp Leu Leu Ser Ser Ser Gly Glu Val Glu Pro Asp Tyr Glu Phe Glu
 225 230 235 240

Pro Asp Ala Asp Thr Leu Leu Glu Ala Leu Leu Pro Gln Tyr Val Ser
 245 250 255

Arg Arg Leu Phe Ser Ile Phe Leu Glu Ala Ala Ala Ala Glu Ser Ala
 260 265 270

Ser Arg Arg Asn Ala Met Lys Ser Ala Thr Asp Asn Ala Thr Glu Leu
 275 280 285

Val Lys Asp Leu Ser Arg Val Ala Asn Gln Ala Arg Gln Ala Gln Ile
 290 295 300

Thr Gln Glu Ile Thr Glu Ile Val Gly Gly Ala Gly Ala Leu Ala Asp
 305 310 315 320

Ser Gly Glu Ser Asp
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<210> 777

<211> 1773

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1750)

<223> RXN02434

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 Met Arg Thr Phe Ala
 1 5

gct tat att gcc att gat ggc ctc agc ttt tcc tac ccc aac acc cac 163
 Ala Tyr Ile Ala Ile Asp Gly Leu Ser Phe Ser Tyr Pro Asn Thr His
 10 15 20

gtt tta agc gat att tcg ctc acc gtt gcc aat ggc gat atc gcc gga 211
 Val Leu Ser Asp Ile Ser Leu Thr Val Ala Asn Gly Asp Ile Ala Gly
 25 30 35

ctg att ggt gaa aac ggc gca gga aaa tcc acc ctg ctc agc ctc atc 259
 Leu Ile Gly Glu Asn Gly Ala Gly Lys Ser Thr Leu Leu Ser Leu Ile
 40 45 50

gct ggc gtc atg gaa ccc gac cag ggc agg att tac ctc ccc gaa cgc 307
 Ala Gly Val Met Glu Pro Asp Gln Gly Arg Ile Tyr Leu Pro Glu Arg
 55 60 65

acc gga ttc atc gcc caa gaa aca gac tta ccg ttt gaa caa ccc gtg 355
 Thr Gly Phe Ile Ala Gln Glu Thr Asp Leu Pro Phe Glu Gln Pro Val
 70 75 80 85

cag tcg ctt atc gac gcc gcc gtc gcc cca gtg cgc gcg gtc gat gcc 403
 Gln Ser Leu Ile Asp Ala Ala Val Ala Pro Val Arg Ala Val Asp Ala
 90 95 100

gcg att aca gat ttg tcc acc aag ctt ggc gac gcc tcc ctc agc gcc 451
 Ala Ile Thr Asp Leu Ser Thr Lys Leu Gly Asp Ala Ser Leu Ser Ala
 105 110 115

gaa gag cag gcg caa gtc gcc aca gat ttc gat gca gcg cta ggc gct 499
 Glu Glu Gln Ala Gln Val Ala Thr Asp Phe Asp Ala Ala Leu Gly Ala
 120 125 130

gca gaa gaa ctc gga ctg tgg gaa tta gat gca cgt att gaa acc atc 547
 Ala Glu Glu Leu Gly Leu Trp Glu Leu Asp Ala Arg Ile Glu Thr Ile

135	140	145	
gtc gcg ggt ctc ggc ctt gcc gag gtg gat cgc agc act ccc att ggt Val Ala Gly Leu Gly Leu Ala Glu Val Asp Arg Ser Thr Pro Ile Gly 150 155 160 165			595
gag ctt tcc ggc ggt cag cgc cgc aga ttc gca ttg gca gcg ctg ctg Glu Leu Ser Gly Gly Gln Arg Arg Arg Phe Ala Leu Ala Ala Leu Leu 170 175 180			643
ttg gaa cca cac gat gct ctg att ttc gat gag ccc acc aac cac ctc Leu Glu Pro His Asp Ala Leu Ile Phe Asp Glu Pro Thr Asn His Leu 185 190 195			691
gac gac aca gcc gta gat ttc ctc atc tcg gag att tcc cgt ttc aaa Asp Asp Thr Ala Val Asp Phe Leu Ile Ser Glu Ile Ser Arg Phe Lys 200 205 210			739
ggt cca gtg ctg atc gcc agc cac gat cgc ttc ttc ctc gac tcc gtc Gly Pro Val Leu Ile Ala Ser His Asp Arg Phe Phe Leu Asp Ser Val 215 220 225			787
tgt acc gag tta atc gac ctc gat cct gca ctt gga cct gag ggc gga Cys Thr Glu Leu Ile Asp Leu Asp Pro Ala Leu Gly Pro Glu Gly Gly 230 235 240 245			835
tcc ggc gaa gaa gta aaa caa gcc gtg tct ttt ggt ggt gga ttt tct Ser Gly Glu Glu Val Lys Gln Ala Val Ser Phe Gly Gly Gly Phe Ser 250 255 260			883
gaa tac atc aaa gaa cgc gag acc cgc cgc acc cgc tgg gct cag ttg Glu Tyr Ile Lys Glu Arg Glu Thr Arg Arg Thr Arg Trp Ala Gln Leu 265 270 275			931
tac acc gca caa gaa acc gag cgg gaa aaa ctc gaa gaa acc acc ggc Tyr Thr Ala Gln Glu Thr Glu Arg Glu Lys Leu Glu Glu Thr Thr Gly 280 285 290			979
acc acc gaa tcg gat att ttc cac agc tcg gtt tcc aaa tcg gaa gct Thr Thr Glu Ser Asp Ile Phe His Ser Ser Val Ser Lys Ser Glu Ala 295 300 305			1027
aaa atc acc gcg aaa ttt tac gca gac cgg gca gct aaa act caa ggc Lys Ile Thr Ala Lys Phe Tyr Ala Asp Arg Ala Ala Lys Thr Gln Gly 310 315 320 325			1075
aac cgc gtc cgc tcc gcc aaa aac cgc ctg aag gaa ttg gaa cgc tat Asn Arg Val Arg Ser Ala Lys Asn Arg Leu Lys Glu Leu Glu Arg Tyr 330 335 340			1123
gaa atc cca gca cct cca aag cca ctg gaa ttc caa ggc atc cca gaa Glu Ile Pro Ala Pro Pro Lys Pro Leu Glu Phe Gln Gly Ile Pro Glu 345 350 355			1171
gcc tcc gga aac ggt cac ggt gaa aca cta gaa gtg cgg gct att gct Ala Ser Gly Asn Gly His Gly Glu Thr Leu Glu Val Arg Ala Ile Ala 360 365 370			1219
gtg gaa aac agg ctt caa ccc ttg act ttc cac atc gat ccc ggc gac Val Glu Asn Arg Leu Gln Pro Leu Thr Phe His Ile Asp Pro Gly Asp 375 380 385			1267

cac atc ctg gtc gaa ggc ccc aac ggt gtc ggt aaa tcc acc ctg ctg 1315
 His Ile Leu Val Glu Gly Pro Asn Gly Val Gly Lys Ser Thr Leu Leu
 390 395 400 405
 agc gtt ctg gaa ggc gtg ctt gaa cca acc gaa ggt gaa ttg atc gtc 1363
 Ser Val Leu Glu Gly Val Leu Glu Pro Thr Glu Gly Glu Leu Ile Val
 410 415 420
 ccc gaa ggg ctg aaa gtt gcg cgc ctg aaa cag gac gat cag tgg acg 1411
 Pro Glu Gly Leu Lys Val Ala Arg Leu Lys Gln Asp Asp Gln Trp Thr
 425 430 435
 gaa aag cag ttg aac acc ccc gtc gac gaa ctg ttc gcc gcc cta tcg 1459
 Glu Lys Gln Leu Asn Thr Pro Val Asp Glu Leu Phe Ala Ala Leu Ser
 440 445 450
 aaa ggt ccg gtc gga ctc aac ctc gtg gag atg ggg ctg ttg agg gag 1507
 Lys Gly Pro Val Gly Leu Asn Leu Val Glu Met Gly Leu Leu Arg Glu
 455 460 465
 acg tcg caa agc agc ccg cta cgg gcc cta tcg ctc ggc caa cgc cgg 1555
 Thr Ser Gln Ser Ser Pro Leu Arg Ala Leu Ser Leu Gly Gln Arg Arg
 470 475 480 485
 cgc gtc tcg ctc ggg ctc atc ctg gcg agc cca cca gat ctt ttg ctt 1603
 Arg Val Ser Leu Gly Leu Ile Leu Ala Ser Pro Pro Asp Leu Leu Leu
 490 495 500
 ctt gac gag ccc acc aac cac ctc tcc ctc gcg ctg agc gaa gaa ctc 1651
 Leu Asp Glu Pro Thr Asn His Leu Ser Leu Ala Leu Ser Glu Glu Leu
 505 510 515
 gag tcg gcg ata gaa aaa ttc ccc ggt cgc gtt att ctg gcc agc cac 1699
 Glu Ser Ala Ile Glu Lys Phe Pro Gly Arg Val Ile Leu Ala Ser His
 520 525 530
 gat agg tgg atc aga aaa cgt tgg acg ggg aag aaa atc agc ctg agc 1747
 Asp Arg Trp Ile Arg Lys Arg Trp Thr Gly Lys Lys Ile Ser Leu Ser
 535 540 545
 cgt taaaccctac tgaacaggaa cct 1773
 Arg
 550

<210> 778

<211> 550

<212> PRT

<213> Corynebacterium glutamicum

<400> 778

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Tyr Pro Asn Thr His Val Leu Ser Asp Ile Ser Leu Thr Val Ala Asn
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Gly Asp Ile Ala Gly Leu Ile Gly Glu Asn Gly Ala Gly Lys Ser Thr
 35 40 45

Leu Leu Ser Leu Ile Ala Gly Val Met Glu Pro Asp Gln Gly Arg Ile
 50 55 60
 Tyr Leu Pro Glu Arg Thr Gly Phe Ile Ala Gln Glu Thr Asp Leu Pro
 65 70 75 80
 Phe Glu Gln Pro Val Gln Ser Leu Ile Asp Ala Ala Val Ala Pro Val
 85 90 95
 Arg Ala Val Asp Ala Ala Ile Thr Asp Leu Ser Thr Lys Leu Gly Asp
 100 105 110
 Ala Ser Leu Ser Ala Glu Glu Gln Ala Gln Val Ala Thr Asp Phe Asp
 115 120 125
 Ala Ala Leu Gly Ala Ala Glu Glu Leu Gly Leu Trp Glu Leu Asp Ala
 130 135 140
 Arg Ile Glu Thr Ile Val Ala Gly Leu Gly Leu Ala Glu Val Asp Arg
 145 150 155 160
 Ser Thr Pro Ile Gly Glu Leu Ser Gly Gly Gln Arg Arg Arg Phe Ala
 165 170 175
 Leu Ala Ala Leu Leu Leu Glu Pro His Asp Ala Leu Ile Phe Asp Glu
 180 185 190
 Pro Thr Asn His Leu Asp Asp Thr Ala Val Asp Phe Leu Ile Ser Glu
 195 200 205
 Ile Ser Arg Phe Lys Gly Pro Val Leu Ile Ala Ser His Asp Arg Phe
 210 215 220
 Phe Leu Asp Ser Val Cys Thr Glu Leu Ile Asp Leu Asp Pro Ala Leu
 225 230 235 240
 Gly Pro Glu Gly Gly Ser Gly Glu Glu Val Lys Gln Ala Val Ser Phe
 245 250 255
 Gly Gly Gly Phe Ser Glu Tyr Ile Lys Glu Arg Glu Thr Arg Arg Thr
 260 265 270
 Arg Trp Ala Gln Leu Tyr Thr Ala Gln Glu Thr Glu Arg Glu Lys Leu
 275 280 285
 Glu Glu Thr Thr Gly Thr Thr Glu Ser Asp Ile Phe His Ser Ser Val
 290 295 300
 Ser Lys Ser Glu Ala Lys Ile Thr Ala Lys Phe Tyr Ala Asp Arg Ala
 305 310 315 320
 Ala Lys Thr Gln Gly Asn Arg Val Arg Ser Ala Lys Asn Arg Leu Lys
 325 330 335
 Glu Leu Glu Arg Tyr Glu Ile Pro Ala Pro Pro Lys Pro Leu Glu Phe
 340 345 350
 Gln Gly Ile Pro Glu Ala Ser Gly Asn Gly His Gly Glu Thr Leu Glu
 355 360 365
 Val Arg Ala Ile Ala Val Glu Asn Arg Leu Gln Pro Leu Thr Phe His

370 375 380
 Ile Asp Pro Gly Asp His Ile Leu Val Glu Gly Pro Asn Gly Val Gly
 385 390 395 400
 Lys Ser Thr Leu Leu Ser Val Leu Glu Gly Val Leu Glu Pro Thr Glu
 405 410 415
 Gly Glu Leu Ile Val Pro Glu Gly Leu Lys Val Ala Arg Leu Lys Gln
 420 425 430
 Asp Asp Gln Trp Thr Glu Lys Gln Leu Asn Thr Pro Val Asp Glu Leu
 435 440 445
 Phe Ala Ala Leu Ser Lys Gly Pro Val Gly Leu Asn Leu Val Glu Met
 450 455 460
 Gly Leu Leu Arg Glu Thr Ser Gln Ser Ser Pro Leu Arg Ala Leu Ser
 465 470 475 480
 Leu Gly Gln Arg Arg Arg Val Ser Leu Gly Leu Ile Leu Ala Ser Pro
 485 490 495
 Pro Asp Leu Leu Leu Leu Asp Glu Pro Thr Asn His Leu Ser Leu Ala
 500 505 510
 Leu Ser Glu Glu Leu Glu Ser Ala Ile Glu Lys Phe Pro Gly Arg Val
 515 520 525
 Ile Leu Ala Ser His Asp Arg Trp Ile Arg Lys Arg Trp Thr Gly Lys
 530 535 540
 Lys Ile Ser Leu Ser Arg
 545 550

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 <211> 1407
 <212> DNA
 <213> Corynebacterium glutamicum

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 <222> (101)..(1384)
 <223> RXN00684

<400> 779
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 Met Thr Ser Gln Thr 5
 tcc caa caa tcc acc tca acc ggt gga tgc cca ttc ggg cac aca tca 163
 Ser Gln Gln Ser Thr Ser Thr Gly Gly Cys Pro Phe Gly His Thr Ser 20
 10 15
 gag tcc acc agc cat cac ggc tac cag cct ttc gat atg cac aac ccg 211
 Glu Ser Thr Ser His His Gly Tyr Gln Pro Phe Asp Met His Asn Pro 35
 25 30

ttt cct gca tat aaa gaa ctc cgt cag gaa gag cca gtg atg ttc gat	259
Phe Pro Ala Tyr Lys Glu Leu Arg Gln Glu Glu Pro Val Met Phe Asp	
40 45 50	
gag cgc atc ggc tac tgg gtg gta acc aaa tat gac gac atc aaa acc	307
Glu Arg Ile Gly Tyr Trp Val Val Thr Lys Tyr Asp Asp Ile Lys Thr	
55 60 65	
acc ttt gat gac tgg gaa aca ttc tcc tct gaa aat gca caa gcc cca	355
Thr Phe Asp Asp Trp Glu Thr Phe Ser Ser Glu Asn Ala Gln Ala Pro	
70 75 80 85	
gtc cgc aag cgt gga cct cag gca acc caa atc atg acc gat ggc ggc	403
Val Arg Lys Arg Gly Pro Gln Ala Thr Gln Ile Met Thr Asp Gly Gly	
90 95 100	
ttc act gca tac tcc gga tta tca gct cgt att cca cca gag cac acc	451
Phe Thr Ala Tyr Ser Gly Leu Ser Ala Arg Ile Pro Pro Glu His Thr	
105 110 115	
cgc atc cgc gca atc gca caa aag gcc ttc acg cca cgc cgc tat aaa	499
Arg Ile Arg Ala Ile Ala Gln Lys Ala Phe Thr Pro Arg Arg Tyr Lys	
120 125 130	
gca ctc gaa cca gat atc cga gca atg gtg att gat cgt gtg gag aaa	547
Ala Leu Glu Pro Asp Ile Arg Ala Met Val Ile Asp Arg Val Glu Lys	
135 140 145	
atg ttg gcg aat gat caa cac gtc ggc gat atg gtg tca gat ctt gcc	595
Met Leu Ala Asn Asp Gln His Val Gly Asp Met Val Ser Asp Leu Ala	
150 155 160 165	
tac gac att cca acc atc acg atc ctg acg ctg atc ggt gca gat att	643
Tyr Asp Ile Pro Thr Ile Thr Ile Leu Thr Leu Ile Gly Ala Asp Ile	
170 175 180	
ttc atg gtg gtc acc tac aag cgg tgg tca gat tcc cgt gcg gcc atg	691
Phe Met Val Thr Tyr Lys Arg Trp Ser Asp Ser Arg Ala Ala Met	
185 190 195	
acc tgg ggc gat ctt agt gat gaa gag cag atc cca cac gca cac aat	739
Thr Trp Gly Asp Leu Ser Asp Glu Glu Gln Ile Pro His Ala His Asn	
200 205 210	
ttg gtt gag tac tgg cag gaa tgc caa cgc atg gta gct gat gca cat	787
Leu Val Glu Tyr Trp Gln Glu Cys Gln Arg Met Val Ala Asp Ala His	
215 220 225	
gca cac ggt ggc gac aac ctc acc gct gat cta gtg cga gca cag caa	835
Ala His Gly Gly Asp Asn Leu Thr Ala Asp Leu Val Arg Ala Gln Gln	
230 235 240 245	
gag ggt caa gaa atc acc gat cat gag att gct tct ttg ctg tac tcc	883
Glu Gly Gln Glu Ile Thr Asp His Glu Ile Ala Ser Leu Leu Tyr Ser	
250 255 260	
ctg ctt ttt gcg ggg cac gaa aca acc acc acg ttg atc tcc aat tgt	931
Leu Leu Phe Ala Gly His Glu Thr Thr Thr Thr Leu Ile Ser Asn Cys	
265 270 275	
ttc cga gtt ctc ctc gat cat cca gag cag tgg caa gcc att cta gag	979

Phe Arg Val Leu Leu Asp His Pro Glu Gln Trp Gln Ala Ile Leu Glu
 280 285 290
 aat cca aaa ctg att cct gcg gca gtg gat gag gtc ttg cgg tac tcc 1027
 Asn Pro Lys Leu Ile Pro Ala Ala Val Asp Glu Val Leu Arg Tyr Ser
 295 300 305
 ggc tcg atc gtg ggg tgg cgt cga aaa gca tta aaa gac acc gag atc 1075
 Gly Ser Ile Val Gly Trp Arg Arg Lys Ala Leu Lys Asp Thr Glu Ile
 310 315 320 325
 ggc ggc gtt gcc att aag gaa ggc gat ggt gtt ctg ctg ctc atg ggt 1123
 Gly Gly Val Ala Ile Lys Glu Gly Asp Gly Val Leu Leu Leu Met Gly
 330 335 340
 tcc gcg aac cgc gat gaa gct cgc ttt gaa aat ggc gag gaa ttc gat 1171
 Ser Ala Asn Arg Asp Glu Ala Arg Phe Glu Asn Gly Glu Glu Phe Asp
 345 350 355
 atc agc cgc gct aat gcg cgc gag cac ctg tct ttt ggt ttc ggc atc 1219
 Ile Ser Arg Ala Asn Ala Arg Glu His Leu Ser Phe Gly Phe Gly Ile
 360 365 370
 cac tat tgc cta gga aac atg ctg gcc aaa ctt caa gcc aag atc tgt 1267
 His Tyr Cys Leu Gly Asn Met Leu Ala Lys Leu Gln Ala Lys Ile Cys
 375 380 385
 ctc gag gaa gtc acc agg ctt gtt cct tcc ctg cac ttg gtt gcg gac 1315
 Leu Glu Glu Val Thr Arg Leu Val Pro Ser Leu His Leu Val Ala Asp
 390 395 400 405
 aaa gct atc ggg ttc cgg gag aac ctc tcc ttc cgc gtc ccc act tct 1363
 Lys Ala Ile Gly Phe Arg Glu Asn Leu Ser Phe Arg Val Pro Thr Ser
 410 415 420
 gtt ccc gtg act tgg aac gct taacgcttta ttaaataagg aga 1407
 Val Pro Val Thr Trp Asn Ala
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<210> 780

<211> 428

<212> PRT

<213> Corynebacterium glutamicum

<400> 780

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 Asp Met His Asn Pro Phe Pro Ala Tyr Lys Glu Leu Arg Gln Glu Glu
 35 40 45
 Pro Val Met Phe Asp Glu Arg Ile Gly Tyr Trp Val Val Thr Lys Tyr
 50 55 60
 Asp Asp Ile Lys Thr Thr Phe Asp Asp Trp Glu Thr Phe Ser Ser Glu
 65 70 75 80

Asn Ala Gln Ala Pro Val Arg Lys Arg Gly Pro Gln Ala Thr Gln Ile
 85 90 95
 Met Thr Asp Gly Gly Phe Thr Ala Tyr Ser Gly Leu Ser Ala Arg Ile
 100 105 110
 Pro Pro Glu His Thr Arg Ile Arg Ala Ile Ala Gln Lys Ala Phe Thr
 115 120 125
 Pro Arg Arg Tyr Lys Ala Leu Glu Pro Asp Ile Arg Ala Met Val Ile
 130 135 140
 Asp Arg Val Glu Lys Met Leu Ala Asn Asp Gln His Val Gly Asp Met
 145 150 155 160
 Val Ser Asp Leu Ala Tyr Asp Ile Pro Thr Ile Thr Ile Leu Thr Leu
 165 170 175
 Ile Gly Ala Asp Ile Phe Met Val Val Thr Tyr Lys Arg Trp Ser Asp
 180 185 190
 Ser Arg Ala Ala Met Thr Trp Gly Asp Leu Ser Asp Glu Glu Gln Ile
 195 200 205
 Pro His Ala His Asn Leu Val Glu Tyr Trp Gln Glu Cys Gln Arg Met
 210 215 220
 Val Ala Asp Ala His Ala His Gly Gly Asp Asn Leu Thr Ala Asp Leu
 225 230 235 240
 Val Arg Ala Gln Gln Glu Gly Gln Glu Ile Thr Asp His Glu Ile Ala
 245 250 255
 Ser Leu Leu Tyr Ser Leu Leu Phe Ala Gly His Glu Thr Thr Thr Thr
 260 265 270
 Leu Ile Ser Asn Cys Phe Arg Val Leu Leu Asp His Pro Glu Gln Trp
 275 280 285
 Gln Ala Ile Leu Glu Asn Pro Lys Leu Ile Pro Ala Ala Val Asp Glu
 290 295 300
 Val Leu Arg Tyr Ser Gly Ser Ile Val Gly Trp Arg Arg Lys Ala Leu
 305 310 315 320
 Lys Asp Thr Glu Ile Gly Gly Val Ala Ile Lys Glu Gly Asp Gly Val
 325 330 335
 Leu Leu Leu Met Gly Ser Ala Asn Arg Asp Glu Ala Arg Phe Glu Asn
 340 345 350
 Gly Glu Glu Phe Asp Ile Ser Arg Ala Asn Ala Arg Glu His Leu Ser
 355 360 365
 Phe Gly Phe Gly Ile His Tyr Cys Leu Gly Asn Met Leu Ala Lys Leu
 370 375 380
 Gln Ala Lys Ile Cys Leu Glu Glu Val Thr Arg Leu Val Pro Ser Leu
 385 390 395 400
 His Leu Val Ala Asp Lys Ala Ile Gly Phe Arg Glu Asn Leu Ser Phe

405

410

415

Arg Val Pro Thr Ser Val Pro Val Thr Trp Asn Ala
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<210> 781

<211> 978

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(955)

<223> RXN00387

<400> 781

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gatttctccg ccgactacct cgccaacggg ccaggccgag atg ttc cgc tcg aat 115
Met Phe Arg Ser Asn
1 5

att tcc tac gca gtc ggc gac gac atc caa aac gac cca gaa acc tgg 163
Ile Ser Tyr Ala Val Gly Asp Asp Ile Gln Asn Asp Pro Glu Thr Trp
10 15 20

gaa gac tac gaa ctt cgc gtc aac cac cca ctg cgc atc gaa ggc gac 211
Glu Asp Tyr Glu Leu Arg Val Asn His Pro Leu Arg Ile Glu Gly Asp
25 30 35

cgc gtc tac ctt cag ggc cac ggc ttc gcc cca aca ttc acc gtg acc 259
Arg Val Tyr Leu Gln Gly His Gly Phe Ala Pro Thr Phe Thr Val Thr
40 45 50

tgg cca aat ggc gag acc cgc acc cag acc gtg cag tgg cgc cca gac 307
Trp Pro Asn Gly Glu Thr Arg Thr Gln Thr Val Gln Trp Arg Pro Asp
55 60 65

gac ccg acc ttc ttc ctg tcc tca ggc gtg gtc cgt ttc gat cca ccc 355
Asp Pro Thr Phe Phe Leu Ser Ser Gly Val Val Arg Phe Asp Pro Pro
70 75 80 85

gcc ggc atg tac cca gac ctt tac gag cgc cgc caa aac cag ttg gcc 403
Ala Gly Met Tyr Pro Asp Leu Tyr Glu Arg Arg Gln Asn Gln Leu Ala
90 95 100

atc cag gga ctt ttc gca ccg acc gcg gaa tgg gaa ggc gac aac aac 451
Ile Gln Gly Leu Phe Ala Pro Thr Ala Glu Trp Glu Gly Asp Asn Asn
105 110 115

gaa ctg ctg acc tcc tcc tac ccg gcg atg cgt gac cca gcc gtg gcg 499
Glu Leu Leu Thr Ser Ser Tyr Pro Ala Met Arg Asp Pro Ala Val Ala
120 125 130

atc gat att tac cgc ggc gac aat ggc ctc gat acc ggc atc gga cag 547
Ile Asp Ile Tyr Arg Gly Asp Asn Gly Leu Asp Thr Gly Ile Gly Gln
135 140 145

tca ttg ttc agc ctg gac tct agt ctc atg cac agc ggc gtg ctg caa 595
Ser Leu Phe Ser Leu Asp Ser Ser Leu Met His Ser Gly Val Leu Gln

150	155	160	165	
aaa att gag cgc gtc aac ctc caa atc ggc gac acc gtc acc ctg gat				643
Lys Ile Glu Arg Val Asn Leu Gln Ile Gly Asp Thr Val Thr Leu Asp				
	170	175	180	
gat ggc acc acc gtc tcc ttc gac ggc gcg tca gaa ttt gcc aac tac				691
Asp Gly Thr Thr Val Ser Phe Asp Gly Ala Ser Glu Phe Ala Asn Tyr				
	185	190	195	
cag atc agc cgc gac ccc aca caa aac tgg gtg ctg gtc acc acc gtg				739
Gln Ile Ser Arg Asp Pro Thr Gln Asn Trp Val Leu Val Thr Thr Val				
	200	205	210	
att tcg ctg gtc tcc ctg gtt gga tcc ctg atg atc cga cgc cgc cgc				787
Ile Ser Leu Val Ser Leu Val Gly Ser Leu Met Ile Arg Arg Arg Arg				
	215	220	225	
att tgg gtg cgt ttc tat cca caa gaa aac gga acc acc cgc gtg gaa				835
Ile Trp Val Arg Phe Tyr Pro Gln Glu Asn Gly Thr Thr Arg Val Glu				
	230	235	240	245
acc ggc gga ctt gcc cgc acc gac cgc gca ggc tgg ggt ggc gaa tac				883
Thr Gly Gly Leu Ala Arg Thr Asp Arg Ala Gly Trp Gly Gly Glu Tyr				
	250	255	260	
gag aaa ttc cac cgc gaa ctg ctg ggt ctg aag gag gaa gat gaa gac				931
Glu Lys Phe His Arg Glu Leu Leu Gly Leu Lys Glu Glu Asp Glu Asp				
	265	270	275	
gaa gag tac ttc gac cac gac gac taacaccgca atttaaaggc ttt				978
Glu Glu Tyr Phe Asp His Asp Asp				
	280	285		

<210> 782

<211> 285

<212> PRT

<213> Corynebacterium glutamicum

<400> 782

Met Phe Arg Ser Asn Ile Ser Tyr Ala Val Gly Asp Asp Ile Gln Asn				
1	5	10	15	
Asp Pro Glu Thr Trp Glu Asp Tyr Glu Leu Arg Val Asn His Pro Leu				
	20	25	30	
Arg Ile Glu Gly Asp Arg Val Tyr Leu Gln Gly His Gly Phe Ala Pro				
	35	40	45	
Thr Phe Thr Val Thr Trp Pro Asn Gly Glu Thr Arg Thr Gln Thr Val				
	50	55	60	
Gln Trp Arg Pro Asp Asp Pro Thr Phe Phe Leu Ser Ser Gly Val Val				
	65	70	75	80
Arg Phe Asp Pro Pro Ala Gly Met Tyr Pro Asp Leu Tyr Glu Arg Arg				
	85	90	95	
Gln Asn Gln Leu Ala Ile Gln Gly Leu Phe Ala Pro Thr Ala Glu Trp				
	100	105	110	

Glu Gly Asp Asn Asn Glu Leu Leu Thr Ser Ser Tyr Pro Ala Met Arg
 115 120 125
 Asp Pro Ala Val Ala Ile Asp Ile Tyr Arg Gly Asp Asn Gly Leu Asp
 130 135 140
 Thr Gly Ile Gly Gln Ser Leu Phe Ser Leu Asp Ser Ser Leu Met His
 145 150 155 160
 Ser Gly Val Leu Gln Lys Ile Glu Arg Val Asn Leu Gln Ile Gly Asp
 165 170 175
 Thr Val Thr Leu Asp Asp Gly Thr Thr Val Ser Phe Asp Gly Ala Ser
 180 185 190
 Glu Phe Ala Asn Tyr Gln Ile Ser Arg Asp Pro Thr Gln Asn Trp Val
 195 200 205
 Leu Val Thr Thr Val Ile Ser Leu Val Ser Leu Val Gly Ser Leu Met
 210 215 220
 Ile Arg Arg Arg Arg Ile Trp Val Arg Phe Tyr Pro Gln Glu Asn Gly
 225 230 235 240
 Thr Thr Arg Val Glu Thr Gly Gly Leu Ala Arg Thr Asp Arg Ala Gly
 245 250 255
 Trp Gly Gly Glu Tyr Glu Lys Phe His Arg Glu Leu Leu Gly Leu Lys
 260 265 270
 Glu Glu Asp Glu Asp Glu Glu Tyr Phe Asp His Asp Asp
 275 280 285

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